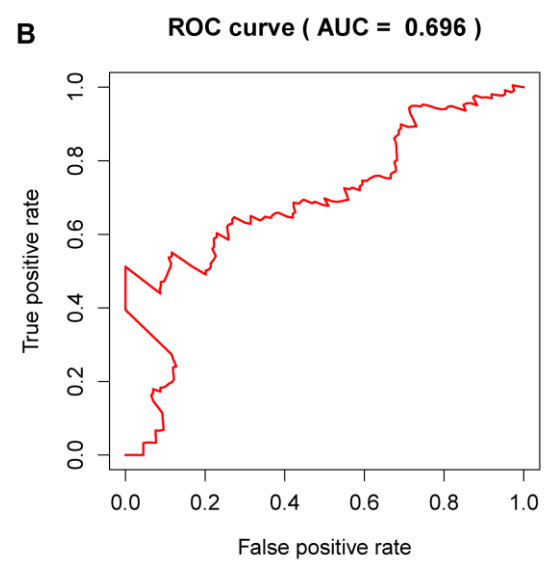
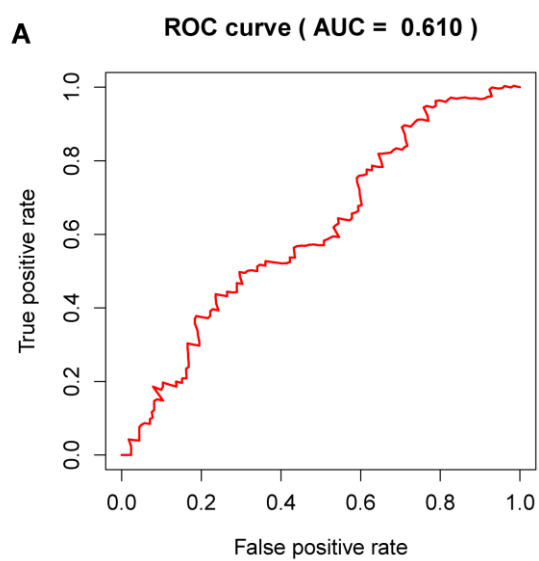


Supplementary Figure 1 Box plot of CpG methylation levels of the 3 clusters.



Supplementary Figure 2 ROC curve of the prognostic score. A: ROC curve of the 3-year OS in the training set. B: ROC curve of the 3-year OS in the test set.

Supplementary Table 1 The accession number of the sample set from TCGA.

The accession number of 375 GC samples

TCGA-BR-8381-01A	TCGA-BR-A4J6-01A	TCGA-VQ-A8PE-01A
TCGA-D7-8572-01A	TCGA-BR-8080-01A	TCGA-BR-4280-01A
TCGA-MX-A666-01A	TCGA-CG-5726-01A	TCGA-CD-A489-01A
TCGA-RD-A8N9-01A	TCGA-BR-8485-01A	TCGA-IN-7808-01A
TCGA-HF-7131-01A	TCGA-HU-A4H0-01A	TCGA-CD-A486-01A
TCGA-IN-8663-01A	TCGA-BR-8589-01A	TCGA-CD-5800-01A
TCGA-BR-8487-01A	TCGA-IN-A7NU-01A	TCGA-FP-8209-01A
TCGA-CG-5721-01A	TCGA-F1-6874-01A	TCGA-BR-6710-01A
TCGA-VQ-AA6K-01A	TCGA-CD-A4MH-01A	TCGA-IN-A7NR-01A
TCGA-BR-A4PF-01A	TCGA-IN-8462-01A	TCGA-BR-4357-01A
TCGA-CD-A487-01A	TCGA-ZQ-A9CR-01A	TCGA-D7-8570-01A
TCGA-BR-8483-01A	TCGA-BR-8368-01A	TCGA-B7-5818-01A
TCGA-D7-8576-01A	TCGA-CG-4469-01A	TCGA-CG-4443-01A
TCGA-BR-8591-01A	TCGA-VQ-A8P3-01A	TCGA-BR-8296-01A
TCGA-CG-4306-01A	TCGA-CD-A4MG-01A	TCGA-3M-AB47-01A
TCGA-BR-8677-01A	TCGA-VQ-A8PP-01A	TCGA-BR-6705-01A
TCGA-F1-6177-01A	TCGA-ZA-A8F6-01A	TCGA-BR-8680-01A
TCGA-RD-A7BT-01A	TCGA-VQ-A8DU-01A	TCGA-D7-A4Z0-01A
TCGA-BR-8679-01A	TCGA-R5-A7ZF-01A	TCGA-FP-7829-01A
TCGA-FP-8211-01A	TCGA-HU-A4GF-01A	TCGA-BR-7704-01A
TCGA-HF-7133-01A	TCGA-VQ-A8PQ-01A	TCGA-CD-8532-01A
TCGA-D7-A6EX-01A	TCGA-D7-6528-01A	TCGA-CG-4475-01A
TCGA-VQ-A91D-01A	TCGA-HU-A4H5-01A	TCGA-BR-6707-01A
TCGA-CD-8526-01A	TCGA-VQ-A8DV-01A	TCGA-CD-8533-01A
TCGA-BR-7196-01A	TCGA-VQ-A924-01A	TCGA-VQ-A8P8-01A
TCGA-HU-8610-01A	TCGA-VQ-A91K-01A	TCGA-BR-8289-01A
TCGA-D7-5577-01A	TCGA-FP-7916-01A	TCGA-BR-8687-01A
TCGA-HJ-7597-01A	TCGA-CG-5732-01A	TCGA-BR-8291-01A
TCGA-SW-A7EA-01A	TCGA-D7-6527-01A	TCGA-BR-6565-01A
TCGA-VQ-A94P-01A	TCGA-CG-5722-01A	TCGA-BR-6454-01A
TCGA-BR-4257-01A	TCGA-D7-A6F0-01A	TCGA-VQ-A91Y-01A
TCGA-CD-5801-01A	TCGA-HU-A4GJ-01A	TCGA-BR-7715-01A
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TCGA-BR-4363-01A	TCGA-BR-8366-01A	TCGA-BR-8690-01A
TCGA-D7-8579-01A	TCGA-3M-AB46-01A	TCGA-BR-6457-01A
TCGA-RD-A7C1-01A	TCGA-MX-A5UG-01A	TCGA-CG-4465-01A
TCGA-HU-A4HB-01A	TCGA-BR-6564-01A	TCGA-HU-A4G2-01A
TCGA-RD-A8MW-01A	TCGA-BR-6452-01A	TCGA-R5-A7O7-01A
TCGA-BR-8367-01A	TCGA-VQ-A8PB-01A	TCGA-VQ-A925-01A
TCGA-VQ-A94R-01A	TCGA-VQ-A91E-01A	TCGA-D7-A6EV-01A
TCGA-HU-A4GC-01A	TCGA-VQ-A8PC-01A	TCGA-BR-4201-01A
TCGA-CG-4477-01A	TCGA-RD-A7BS-01A	TCGA-FP-8099-01A

TCGA-CD-5799-01A	TCGA-VQ-AA6J-01A	TCGA-RD-A8N2-01A
TCGA-VQ-A8E0-01A	TCGA-CG-4476-01A	TCGA-HU-A4GT-01A
TCGA-D7-5578-01A	TCGA-VQ-A91U-01A	TCGA-BR-8058-01A
TCGA-D7-6525-01A	TCGA-BR-8295-01A	TCGA-VQ-AA64-01A
TCGA-IN-7806-01A	TCGA-HU-A4H8-01A	TCGA-BR-8284-01A
TCGA-RD-A8MV-01A	TCGA-HU-A4G3-01A	TCGA-HU-A4GU-01A
TCGA-HU-A4G8-01A	TCGA-IN-A6RJ-01A	TCGA-CG-5719-01A
TCGA-BR-8286-01A	TCGA-CD-8527-01A	TCGA-R5-A805-01A
TCGA-D7-8578-01A	TCGA-VQ-A92D-01A	TCGA-CG-5716-01A
TCGA-D7-6526-01A	TCGA-D7-A6EZ-01A	TCGA-D7-8573-01A
TCGA-VQ-AA6G-01A	TCGA-CD-5804-01A	TCGA-CG-4305-01A
TCGA-D7-A4YX-01A	TCGA-D7-6815-01A	TCGA-EQ-8122-01A
TCGA-HU-A4H3-01A	TCGA-BR-8590-01A	TCGA-CD-8531-01A
TCGA-HU-A4GX-01A	TCGA-BR-4368-01A	TCGA-B7-A5TN-01A
TCGA-HU-A4GQ-01A	TCGA-BR-4279-01A	TCGA-KB-A93J-01A
TCGA-VQ-AA6D-01A	TCGA-B7-A5TK-01A	TCGA-VQ-AA69-01A
TCGA-B7-A5TI-01A	TCGA-F1-6875-01A	TCGA-FP-A8CX-01A
TCGA-BR-A44U-01A	TCGA-CG-4466-01A	TCGA-CD-8535-01A
TCGA-VQ-A8PU-01A	TCGA-IN-A6RN-01A	TCGA-CD-8534-01A
TCGA-BR-4256-01A	TCGA-VQ-A91V-01A	TCGA-VQ-A94T-01A
TCGA-BR-4371-01A	TCGA-BR-4253-01A	TCGA-F1-A448-01A
TCGA-CG-5734-01A	TCGA-VQ-A8DT-01A	TCGA-R5-A7ZI-01A
TCGA-RD-A8N4-01A	TCGA-CG-5725-01A	TCGA-HU-8238-01A
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TCGA-VQ-A922-01A	TCGA-VQ-A91Z-01A	TCGA-BR-8382-01A
TCGA-BR-A4CS-01A	TCGA-IN-A6RS-01A	TCGA-BR-8682-01A
TCGA-VQ-A8P2-01A	TCGA-D7-6822-01A	TCGA-RD-A7BW-01A
TCGA-BR-8592-01A	TCGA-BR-8371-01A	TCGA-B7-A5TJ-01A
TCGA-BR-6563-01A	TCGA-CG-4441-01A	TCGA-HU-A4GH-01A
TCGA-VQ-A8PO-01A	TCGA-BR-A4CR-01A	TCGA-IN-AB1V-01A
TCGA-RD-A8NB-01A	TCGA-IN-A7NT-01A	TCGA-BR-7197-01A
TCGA-BR-8059-01A	TCGA-CG-5723-01A	TCGA-BR-7707-01A
TCGA-HU-A4H6-01A	TCGA-CG-4304-01A	TCGA-BR-8678-01A
TCGA-IN-AB1X-01A	TCGA-CG-4437-01A	TCGA-BR-6458-01A
TCGA-IP-7968-01A	TCGA-IN-A6RI-01A	TCGA-BR-7958-01A
TCGA-BR-A4QL-01A	TCGA-HU-8604-01A	TCGA-BR-8686-01A
TCGA-BR-6802-01A	TCGA-BR-A4J7-01A	TCGA-BR-4191-01A
TCGA-BR-4366-01A	TCGA-HU-8244-01A	TCGA-BR-7722-01A
TCGA-FP-8631-01A	TCGA-BR-4369-01A	TCGA-VQ-A923-01A
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TCGA-CG-5724-01A	TCGA-BR-7851-01A	TCGA-D7-8574-01A
TCGA-CD-8530-01A	TCGA-HU-A4GP-01A	TCGA-BR-6709-01A
TCGA-FP-7998-01A	TCGA-BR-7723-01A	TCGA-KB-A6F7-01A
TCGA-BR-8683-01A	TCGA-BR-6453-01A	TCGA-BR-7717-01A
TCGA-D7-6521-01A	TCGA-VQ-A8PK-01A	TCGA-BR-4370-01A
TCGA-BR-A4J9-01A	TCGA-BR-6803-01A	TCGA-CG-4301-01A
TCGA-CD-A48C-01A	TCGA-BR-8365-01A	TCGA-BR-8369-01A
TCGA-BR-4187-01A	TCGA-HU-A4GD-01A	TCGA-BR-8297-01A
TCGA-BR-8077-01A	TCGA-BR-A4J5-01A	TCGA-BR-8676-01A
TCGA-VQ-A8E3-01A	TCGA-VQ-A91Q-01A	TCGA-HF-7134-01A
TCGA-HU-A4H2-01A	TCGA-BR-8373-01A	TCGA-MX-A5UJ-01A

TCGA-BR-7959-01A	TCGA-D7-A4YU-01A	TCGA-HU-A4HD-01A
TCGA-BR-4361-01A	TCGA-VQ-A927-01A	TCGA-BR-8384-01A
TCGA-VQ-A91X-01A	TCGA-D7-6522-01A	TCGA-VQ-AA6A-01A
TCGA-HF-7132-01A	TCGA-D7-A748-01A	TCGA-HU-8608-01A
TCGA-VQ-A8PJ-01A	TCGA-D7-6524-01A	TCGA-MX-A663-01A
TCGA-BR-6566-01A	TCGA-FP-A4BF-01A	TCGA-CG-4438-01A
TCGA-BR-6456-01A	TCGA-CG-4460-01A	TCGA-VQ-AA68-01A
TCGA-D7-8575-01A	TCGA-BR-4367-01A	TCGA-VQ-A8P5-01A
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TCGA-BR-A4IV-01A	TCGA-BR-7901-01A	TCGA-BR-6801-01A
TCGA-RD-A8N5-01A	TCGA-BR-6455-01A	TCGA-BR-4294-01A
TCGA-BR-8081-01A	TCGA-D7-6519-01A	TCGA-VQ-A91S-01A
TCGA-BR-A4J8-01A	TCGA-CD-8528-01A	TCGA-SW-A7EB-01A
TCGA-VQ-A91N-01A	TCGA-CG-4442-01A	TCGA-HF-A5NB-01A
TCGA-FP-8210-01A	TCGA-VQ-A8PM-01A	TCGA-VQ-A928-01A
TCGA-HU-A4GY-01A	TCGA-HU-A4H4-01A	TCGA-CD-5803-01A
TCGA-BR-8486-01A	TCGA-CG-4436-01A	TCGA-VQ-A8PD-01A
TCGA-RD-A8N6-01A	TCGA-BR-4267-01A	TCGA-BR-8588-01A
TCGA-RD-A8N1-01A	TCGA-BR-A4J4-01A	TCGA-BR-7957-01A
TCGA-HU-A4G9-01A	TCGA-R5-A7ZR-01A	TCGA-HU-8249-01A
TCGA-BR-6852-01A	TCGA-BR-8380-01A	TCGA-IN-A6RR-01A
TCGA-IN-A6RL-01A	TCGA-CG-5717-01A	TCGA-HU-8602-01A
TCGA-KB-A93G-01A	TCGA-VQ-A91A-01A	TCGA-CG-4440-01A
TCGA-CD-A48A-01A	TCGA-CG-5718-01A	TCGA-CD-8525-01A
TCGA-BR-8364-01A	TCGA-CD-8524-01A	TCGA-BR-A44T-01A
TCGA-BR-8372-01A	TCGA-VQ-A8PH-01A	TCGA-KB-A93H-01A
TCGA-IN-A6RO-01A	TCGA-CD-5798-01A	TCGA-D7-A6EY-01A
TCGA-CG-4444-01A	TCGA-VQ-A8PX-01A	TCGA-BR-8361-01A
TCGA-FP-7735-01A	TCGA-CG-5720-01A	TCGA-D7-A6F2-01A
TCGA-VQ-A8PF-01A	TCGA-CG-4462-01A	TCGA-BR-8060-01A
TCGA-D7-6818-01A	TCGA-FP-A9TM-01A	TCGA-D7-A74A-01A
TCGA-BR-7716-01A	TCGA-R5-A7ZE-01B	TCGA-VQ-A8E7-01B
The accession number of 32 non-tumor samples		
TCGA-CG-5734-11A	TCGA-HU-A4GC-11A	TCGA-HU-8238-11A
TCGA-IN-AB1X-11A	TCGA-BR-6802-11A	TCGA-IN-AB1V-11A
TCGA-CG-5721-11A	TCGA-BR-7851-11A	TCGA-BR-7717-11A
TCGA-BR-6453-11A	TCGA-BR-6457-11A	TCGA-BR-7703-11A
TCGA-HU-A4GP-11A	TCGA-CG-5720-11A	TCGA-BR-7704-11A
TCGA-BR-7716-11A	TCGA-BR-6454-11A	TCGA-CG-5733-11A
TCGA-IP-7968-11A	TCGA-IN-8663-11A	TCGA-CG-5722-11A
TCGA-BR-7715-11A	TCGA-IN-7806-11A	TCGA-FP-7735-11A
TCGA-CG-5728-11A	TCGA-HU-A4HB-11A	TCGA-BR-8060-11A
TCGA-FP-7829-11A	TCGA-HU-A4GN-11A	TCGA-HU-A4GH-11A
TCGA-HU-A4GY-11A	TCGA-CG-5730-11A	

Supplementary Table 2 Clinical information of the GC patients.

ID	Survival time (days)	Survival status (0, alive; 1,	Age (year)	gender	grade	stage	T	M	N
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dead)

TCGA-VQ-A8PS	406	1	76	MALE	G2	Stage IIIA	T3	M0	N1
TCGA-CG-4301	92	0	75	FEMALE	G3	Stage IV	T4	M1	N1
TCGA-R5-A7ZR	185	1	70	FEMALE	G2	Stage III	T3	M0	NX
TCGA-VQ-AA64	560	1	68	MALE	G2	Stage IIIB	T3	M0	N2
TCGA-BR-8686	635	1	69	MALE	G3	Stage IIIB	T4b	M0	N1
TCGA-B7-A5TJ	335	0	74	MALE	G1	Stage IIB	T4a	M0	NX
TCGA-BR-A4QL	491	1	75	FEMALE	G2	Stage IIIB	T3	M0	N3a
TCGA-D7-6817	389	0	63	MALE	G3	Stage IIIA	T2b	M0	N3
TCGA-BR-4366	0	0	87	MALE	G2	unknow	TX	M0	NX
TCGA-MX-A5UG	113	1	78	MALE	G3	Stage IIIA	T3	M0	N1
TCGA-IN-A6RJ	379	0	64	MALE	G3	Stage IA	T1b	M0	N0
TCGA-CG-4475	699	0	76	MALE	G3	Stage IIB	T3	M0	N1
TCGA-BR-8591	856	0	79	MALE	G3	Stage IIIC	T4a	M0	N3a
TCGA-BR-8676	229	0	59	MALE	G3	Stage IIIB	T3	M0	N3a
TCGA-D7-A4YV	180	0	69	FEMALE	G3	Stage IIB	T3	M0	N1
TCGA-BR-8285	17	1	57	FEMALE	G3	Stage IIIC	T4a	M0	N3a
TCGA-CD-5798	408	0	82	MALE	G2	Stage II	T3	M0	N0
TCGA-FP-A4BF	168	1	68	MALE	G3	Stage IIIA	T3	M0	N2
TCGA-VQ-A91D	356	1	70	MALE	G2	Stage IIIC	T4b	M0	N2
TCGA-BR-4184	212	1	70	MALE	G2	Stage IIIA	T3	MX	N1
TCGA-BR-8380	21	0	55	MALE	G3	Stage IIIC	T4a	M0	N3a
TCGA-VQ-A8PH	389	1	62	MALE	G2	Stage IIIB	T3	M0	N3
TCGA-BR-8382	762	1	67	FEMALE	G3	Stage IIIC	T4b	M0	N3a
TCGA-FP-A9TM	189	0	77	MALE	G2	unknow	T1b	M0	N1
TCGA-BR-8058	1133	0	53	FEMALE	G3	Stage IIIB	T4a	M0	N2
TCGA-CG-4469	215	1	70	MALE	G3	Stage IV	T3	M0	N3
TCGA-BR-6801	1223	0	70	MALE	G2	Stage IIA	T3	M0	N0
TCGA-BR-8361	946	0	71	FEMALE	G3	Stage IIIC	T4b	M0	N2
TCGA-D7-6522	566	0	58	MALE	G3	Stage IB	T2	M0	N0
TCGA-BR-4256	284	1	80	MALE	G2	unknow	TX	M0	N1
TCGA-VQ-A91Z	1690	0	67	FEMALE	G2	Stage IIIA	T3	M0	N1
TCGA-VQ-A91V	1297	0	58	MALE	G2	Stage IIIA	T3	M0	N2
TCGA-CG-4455	366	0	72	MALE	G3	Stage II	T2b	M0	N1
TCGA-CD-8529	374	0	65	MALE	G2	Stage IV	T4	M1	N0
TCGA-D7-A74A	607	0	61	FEMALE	G2	Stage IIIA	T3	M0	N2
TCGA-CG-4443	912	0	68	MALE	G2	Stage IA	T1	M0	N0
TCGA-BR-4368	0	0	78	FEMALE	G3	Stage IV	T4	M0	N2
TCGA-SW-A7EA	579	0	61	FEMALE	GX	Stage IB	T2	M0	N0
TCGA-D7-6518	582	0	75	MALE	G3	Stage IIIA	T2	M0	N3
TCGA-CG-5725	457	1	72	MALE	G3	Stage IB	T2	M0	N0
TCGA-VQ-A8PK	543	1	58	MALE	G2	Stage IIIB	T3	M0	N3a
TCGA-BR-A4PE	621	0	68	FEMALE	G2	Stage IB	T2	M0	N0
TCGA-BR-6563	1190	0	60	MALE	G3	Stage IIB	T3	M0	N1
TCGA-D7-A6EX	344	0	72	FEMALE	G3	Stage IIIA	T3	M0	N2
TCGA-VQ-A91S	1000	0	63	MALE	GX	Stage IIIB	T4b	M0	N1
TCGA-BR-4370	0	0	74	FEMALE	G2	unknow	TX	M0	NX
TCGA-BR-8373	450	0	65	FEMALE	G2	Stage IIIA	T4a	M0	N1

TCGA-CG-5718	1095	1	78	FEMALE	G2	Stage II	T2b	M0	N1
TCGA-RD-A7BS	336	1	46	MALE	G3	Stage IIIA	T3	M0	N1
TCGA-D7-A6EY	348	1	72	FEMALE	G3	Stage IIIB	T3	M0	N3a
TCGA-VQ-AA68	1328	0	52	FEMALE	G2	Stage IIIC	T4a	M0	N3
TCGA-BR-6802	940	0	65	MALE	G3	Stage IIIA	T3	M0	N2
TCGA-CG-4460	669	1	66	FEMALE	G2	Stage IV	T4	M1	N1
TCGA-CG-4474	0	0	67	FEMALE	G3	Stage IV	T4a	M1	N2
TCGA-VQ-A8DU	166	1	63	MALE	G2	Stage IIIA	T3	M0	N2
TCGA-BR-4267	188	1	51	MALE	G2	Stage IB	T2a	M0	N0
TCGA-RD-A8N4	2171	0	58	FEMALE	G3	Stage IIIA	T3	M0	N1
TCGA-VQ-A91E	664	0	67	FEMALE	G3	Stage IIIB	T4b	M0	N0
TCGA-IN-AB1X	411	0	78	FEMALE	G3	Stage IIA	T3	M0	N0
TCGA-BR-8381	224	0	51	MALE	G3	Stage IIB	T3	M0	N1
TCGA-HU-A4GH	358	0	75	MALE	G2	Stage IA	T1b	M0	N0
TCGA-CG-5730	122	0	80	FEMALE	G2	Stage IV	T2	M1	N1
TCGA-BR-8286	895	0	49	MALE	G3	Stage II	T3	M0	N0
TCGA-BR-A4PF	35	0	72	MALE	G3	Stage IIIB	T4a	M0	N2
TCGA-HU-A4H8	270	0	77	MALE	G2	Stage IB	T1b	M0	N1
TCGA-CD-8524	388	0	61	FEMALE	G3	Stage II	T3	M0	N0
TCGA-IN-A6RP	196	0	63	MALE	G3	unknow	T1b	M0	N3
TCGA-B7-A5TK	288	0	51	MALE	G3	Stage IIIA	T4	M0	unknow
TCGA-CG-4438	1645	0	56	MALE	G3	Stage IV	T4	M0	N2
TCGA-VQ-A8PP	712	1	76	MALE	G2	Stage IV	T4	M0	N1
TCGA-BR-4371	0	0	71	FEMALE	G1	unknow	T2	M0	NX
TCGA-BR-8296	474	1	58	FEMALE	G3	Stage IIIC	T4b	M0	N2
TCGA-VQ-A928	174	1	49	MALE	G2	Stage IV	T3	M0	N3
TCGA-D7-8574	523	0	72	MALE	G3	Stage IIIA	T2	M0	N3a
TCGA-HU-A4H3	882	0	56	FEMALE	G3	Stage IIIC	T4a	M0	N3b
TCGA-D7-6524	543	0	53	MALE	G3	Stage II	T2	M0	N1
TCGA-MX-A666	427	0	61	MALE	G2	Stage IIA	T2	MX	NX
TCGA-BR-8592	191	1	63	FEMALE	G3	Stage IIIB	T4b	M0	N1
TCGA-BR-6455	422	1	59	MALE	G3	Stage IIB	T3	M0	N1
TCGA-BR-6707	605	1	75	MALE	G3	Stage IIA	T3	M0	N0
TCGA-BR-A4PD	628	0	72	FEMALE	G3	Stage IIB	T4a	M0	N0
TCGA-D7-A74B	217	1	52	FEMALE	G3	Stage IIIB	T3	M0	N3
TCGA-CD-8533	468	0	48	MALE	G3	Stage II	T3	M0	N0
TCGA-CD-A4MI	358	1	62	MALE	G1	Stage IIIA	T3	M0	N1
TCGA-CG-4465	274	1	69	FEMALE	G3	Stage IV	T4	M1	N3
TCGA-CD-5803	341	1	78	FEMALE	G3	Stage II	T3	M0	N0
TCGA-D7-A6F0	678	0	79	FEMALE	G3	Stage IB	T2	M0	N0
TCGA-BR-7197	280	0	69	MALE	GX	Stage II	T3	M0	N0
TCGA-BR-8384	113	0	69	MALE	G3	Stage IIIC	T4b	M0	N2
TCGA-F1-6874	440	0	79	MALE	G3	Stage IB	T2	M0	N0
TCGA-CG-4449	580	0	81	MALE	G2	Stage II	T2	M0	N1
TCGA-D7-6527	312	1	62	MALE	G2	Stage II	T2	M0	N1
TCGA-VQ-AA6D	521	0	52	FEMALE	G2	Stage IIIA	T4a	M0	N1
TCGA-CG-4477	942	0	58	FEMALE	G3	Stage IB	T2a	M0	N0
TCGA-D7-6525	406	1	58	MALE	G3	Stage IIIA	T2	M0	N2

TCGA-IN-8462	572	0	80	MALE	G2	Stage IIB	T2	M0	N1
TCGA-CD-A486	192	1	68	MALE	G2	Stage IIA	T3	M0	N0
TCGA-HU-8610	23	0	75	MALE	G2	Stage IA	T1b	M0	N0
TCGA-BR-4363	0	0	60	FEMALE	G3	unknow	T3	MX	NX
TCGA-VQ-A923	0	1	90	MALE	G3	Stage IIIA	T3	M0	N1
TCGA-HU-A4GU	200	0	73	MALE	G3	Stage IIB	T3	M0	N1
TCGA-CG-5727	2405	0	66	MALE	G3	Stage II	T3	M0	N0
TCGA-RD-A8N5	1747	1	78	MALE	G2	Stage IIIA	T3	M0	N1
TCGA-B7-5816	812	0	51	FEMALE	G3	Stage IIB	T4a	M0	N0
TCGA-IN-7806	1106	0	50	MALE	G3	Stage IIB	T3	M0	N1
TCGA-CG-4466	577	0	81	FEMALE	G2	Stage IB	T2a	M0	N0
TCGA-HU-8249	881	0	76	MALE	G2	Stage IIIA	T3	M0	N2
TCGA-HU-A4GF	785	0	69	MALE	G2	Stage IIA	T3	M0	N0
TCGA-D7-A747	255	1	57	MALE	G3	Stage IIB	T3	M0	N1
TCGA-HU-A4H4	725	0	53	FEMALE	G3	Stage IIB	T2	M0	N2
TCGA-CG-4472	365	0	49	MALE	G3	Stage IV	T4	M0	N1
TCGA-VQ-A8PB	1043	1	65	FEMALE	G2	Stage II	T3	M0	N0
TCGA-R5-A7O7	1389	0	51	MALE	G2	Stage IV	T3	M1	N1
TCGA-BR-8363	8	1	73	FEMALE	G3	Stage IB	T2	M0	N0
TCGA-CD-8536	378	0	74	MALE	G3	Stage II	T3	M0	N0
TCGA-BR-7715	1023	0	65	MALE	G2	Stage IIA	T3	M0	N0
TCGA-BR-4361	0	0	66	FEMALE	G3	Stage IIIA	T4	M0	N0
TCGA-BR-4367	0	0	78	MALE	G3	unknow	TX	M0	N1
TCGA-BR-8483	164	0	59	MALE	G2	Stage IIIA	T3	M0	N2
TCGA-CG-4476	0	0	69	MALE	G3	Stage IIIC	T4b	M0	N3a
TCGA-VQ-A91N	570	1	59	FEMALE	G2	Stage IV	T4	M0	N3
TCGA-BR-4188	226	1	53	FEMALE	G3	unknow	TX	M0	N1
TCGA-CG-5726	881	1	73	MALE	G2	Stage IA	T1	M0	N0
TCGA-BR-7704	1072	0	69	FEMALE	G3	Stage II	T3	M0	N0
TCGA-D7-8573	593	0	57	MALE	G3	Stage IIA	T3	M0	N0
TCGA-HU-A4HD	1016	0	73	MALE	G2	Stage IIIA	T3	M0	N2
TCGA-FP-7829	594	0	69	MALE	G2	Stage IIB	T3	M0	N1
TCGA-BR-8680	972	0	45	MALE	G2	Stage IV	T4b	M1	N2
TCGA-D7-A6EV	342	0	71	FEMALE	G3	Stage IIB	T2	M0	N2
TCGA-IN-A6RI	559	0	45	MALE	G2	Stage I	T1b	M0	N0
TCGA-BR-6706	549	1	63	MALE	G3	Stage IIIA	T3	M0	N1
TCGA-HF-7132	2351	0	unknow	MALE	G2	Stage II	T2b	M0	N1
TCGA-BR-8364	675	0	42	FEMALE	G3	Stage IIIC	T4b	M0	N2
TCGA-VQ-A927	200	1	81	MALE	G1	Stage IIIB	T3	M0	N3
TCGA-BR-8485	280	0	68	FEMALE	G3	Stage IIIC	T4	M0	N3a
TCGA-VQ-A94T	342	1	73	MALE	G3	Stage IIIB	T3	M0	N2
TCGA-BR-A4J4	16	0	39	MALE	G3	Stage IIIB	T4a	M0	N2
TCGA-BR-8284	245	1	72	FEMALE	G3	Stage IIIC	T4a	M0	N3a
TCGA-BR-7717	552	1	63	MALE	G2	Stage IV	T4	M0	N1
TCGA-BR-8077	21	0	58	FEMALE	G2	Stage IIIB	T4b	M0	N1
TCGA-BR-6458	588	1	57	FEMALE	G3	Stage IIB	T3	M0	N1
TCGA-BR-A4J7	989	0	49	MALE	G3	Stage IIB	T4a	M0	NX
TCGA-VQ-AA6G	792	1	68	MALE	G2	Stage IIA	T3	M0	N0

TCGA-BR-8060	348	1	75	FEMALE	G3	Stage IIB	T2	M0	N2
TCGA-BR-A4J1	22	1	63	MALE	G3	Stage IIIA	T4a	M0	N1
TCGA-HU-8602	679	0	58	FEMALE	G3	Stage IIB	T4a	M0	N0
TCGA-CG-5722	30	0	67	FEMALE	G3	Stage IV	T3	M1	N2
TCGA-KB-A6F7	1935	0	54	FEMALE	G3	Stage IB	T1	M0	N1
TCGA-KB-A6F5	169	0	73	MALE	G3	Stage IIIA	T3	M0	N2
TCGA-CG-4300	609	1	79	MALE	G2	Stage IIIB	T3	M0	N2
TCGA-HU-A4GY	8	0	76	FEMALE	G3	Stage IIIA	T4	M0	N1
TCGA-BR-A4J9	14	0	55	MALE	G3	Stage IIA	T3	M0	N0
TCGA-HU-A4GQ	3	1	71	MALE	G2	Stage IIIC	T4b	M0	N2
TCGA-IN-A7NU	356	0	69	MALE	G3	Stage IIIB	T3	M0	N3
TCGA-RD-A7C1	507	1	82	MALE	G3	Stage IB	T2	M0	N0
TCGA-IN-A6RN	594	0	72	FEMALE	G2	Stage IIA	T1b	M0	N2
TCGA-RD-A8MW	1153	1	72	MALE	G3	Stage IIIB	T3	M0	N2
TCGA-BR-8367	801	1	55	MALE	G3	Stage IIIB	T3	M0	N3a
TCGA-CD-5799	396	0	45	MALE	G3	Stage II	T2	M0	N1
TCGA-VQ-A8PM	57	1	56	MALE	G3	Stage IV	T4	M0	N3
TCGA-VQ-A922	275	1	70	MALE	G2	Stage IV	T4	M0	N1
TCGA-BR-8362	398	1	65	MALE	G3	Stage IIIC	T4b	M0	N3a
TCGA-BR-8370	101	0	64	MALE	G3	Stage IIIB	T3	M0	N3a
TCGA-BR-6452	1055	0	78	FEMALE	G3	Stage IIA	T3	M0	N0
TCGA-HU-A4GJ	650	0	60	FEMALE	G3	Stage IIIC	T4	M0	N3a
TCGA-BR-7851	378	0	74	MALE	G3	Stage IIB	T4a	M0	N0
TCGA-FP-7735	106	1	77	MALE	G2	Stage IB	T2	MX	N0
TCGA-HU-8245	552	0	72	MALE	G3	Stage IIA	T3	M0	N0
TCGA-CD-5801	401	1	69	MALE	G3	Stage IIIA	T3	M0	N1
TCGA-CG-5723	2496	0	83	MALE	G3	Stage II	T2	M0	N1
TCGA-BR-A4IZ	273	1	45	FEMALE	G3	Stage IIIB	T4a	M0	N2
TCGA-CG-4441	426	1	83	MALE	G2	Stage IIIA	T2	M0	N2
TCGA-HU-A4GC	99	0	74	MALE	G3	Stage IIIB	T4a	M0	N2
TCGA-D7-A4YY	419	0	61	MALE	G3	Stage IIIB	T3	M0	N3a
TCGA-D7-A4Z0	449	0	60	FEMALE	G3	Stage IIB	T2	M0	N2
TCGA-D7-8570	752	0	44	MALE	G3	Stage IIIB	T3	M0	N3a
TCGA-VQ-A8PQ	476	1	50	FEMALE	G2	Stage IV	T4	M1	N1
TCGA-RD-A7BT	262	1	66	MALE	G3	Stage IV	T3	M0	N3
TCGA-CD-8535	390	0	59	MALE	G3	Stage IIIA	T3	M0	N1
TCGA-VQ-A8PU	832	1	72	FEMALE	G3	Stage IIIA	T4a	M0	N1
TCGA-VQ-A8P8	942	0	72	FEMALE	G2	Stage IIB	T4a	M0	N0
TCGA-HU-A4G3	170	0	54	MALE	G2	Stage IIB	T2	M0	N2
TCGA-BR-8687	250	1	67	FEMALE	G3	Stage IIIC	T4b	M0	N2
TCGA-HF-7133	1918	0	unknow	FEMALE	G2	Stage IV	T2b	M0	N3
TCGA-D7-A748	132	1	41	FEMALE	G3	Stage IV	T4a	M1	N3
TCGA-D7-5579	636	0	74	MALE	G3	Stage IIIA	T3	M0	N2
TCGA-BR-6564	794	1	46	FEMALE	G3	Stage IIIA	T3	M0	N2
TCGA-CG-4304	unknow	0	84	MALE	G2	Stage IB	T2a	M0	N0
TCGA-VQ-A8E0	562	1	68	MALE	G3	Stage IIIA	T3	M0	N2
TCGA-BR-8677	813	0	74	FEMALE	G3	Stage IIIB	T3	M0	N3a
TCGA-CD-5802	406	0	58	MALE	G2	Stage II	T3	M0	N0

TCGA-RD-A8N1	3519	0	70	MALE	G3	Stage IIIB	T3	M0	N2
TCGA-HU-A4GP	273	0	62	FEMALE	G2	Stage IIA	T2	M0	N1
TCGA-VQ-A94R	1294	1	63	MALE	G2	unknow	T4a	M0	N2
TCGA-BR-8080	292	1	72	FEMALE	G3	Stage IIIC	T4	M0	N3a
TCGA-BR-4369	0	0	75	MALE	G3	unknow	TX	M0	NX
TCGA-BR-A4J2	431	0	70	MALE	G3	Stage IIB	T4a	M0	N0
TCGA-BR-A4J5	862	0	56	MALE	G3	Stage IIIA	T4a	M0	N1
TCGA-CD-8528	375	0	43	FEMALE	G3	Stage IIIA	T4	M0	N0
TCGA-VQ-A94P	81	1	57	MALE	GX	unknow	T4	MX	NX
TCGA-BR-A4IY	392	0	58	MALE	G3	Stage IIB	T4a	M0	N0
TCGA-CG-5720	30	1	71	MALE	G3	Stage IB	T2	M0	N0
TCGA-MX-A663	300	1	66	MALE	G3	Stage IIA	T3	M0	N0
TCGA-CG-4442	0	0	85	MALE	G3	Stage IB	T2	M0	N0
TCGA-D7-6528	463	0	70	FEMALE	G2	Stage IB	T2	M0	N0
TCGA-VQ-A8E7	1138	0	59	MALE	G2	Stage IV	T3	M1	N1
TCGA-IN-AB1V	479	0	63	MALE	G2	Stage IA	T1b	M0	N0
TCGA-BR-4255	124	1	76	FEMALE	G3	Stage IIIA	T3	M0	N1
TCGA-BR-6453	485	0	54	MALE	G3	Stage IIA	T2	M0	N1
TCGA-BR-8295	67	1	60	FEMALE	G3	Stage IIB	T4a	M0	N0
TCGA-VQ-A91W	1851	0	30	MALE	G2	Stage IIIA	T3	M0	N1
TCGA-CD-8530	377	0	51	MALE	G3	Stage II	T3	M0	N0
TCGA-CG-4436	243	0	57	MALE	G2	Stage IB	T2	M0	N0
TCGA-HU-8244	742	0	77	FEMALE	G1	Stage IA	T1a	M0	N0
TCGA-CG-5728	579	0	88	FEMALE	G3	Stage IB	T2	M0	N0
TCGA-BR-4187	141	1	56	MALE	G3	unknow	TX	M0	NX
TCGA-D7-6520	573	0	53	MALE	G3	Stage IIIA	T2b	M0	N2
TCGA-KB-A93H	1145	0	79	FEMALE	G1	Stage IIB	T3	M0	N1
TCGA-IN-A6RS	383	0	76	MALE	G2	Stage IA	T1b	M0	N0
TCGA-VQ-AA6B	1002	0	48	MALE	G2	Stage IIIB	T3	M0	N2
TCGA-VQ-A94U	819	0	70	MALE	G3	Stage IIB	T4a	M0	N0
TCGA-BR-A452	229	1	57	MALE	G3	Stage IIIA	T4a	M0	N1
TCGA-VQ-AA6K	378	1	59	MALE	G3	Stage IIIC	T4a	M0	N3a
TCGA-VQ-A925	138	1	66	MALE	G2	Stage IIIA	T3	M0	N2
TCGA-BR-6852	1367	0	64	FEMALE	G3	Stage IIA	T3	M0	N0
TCGA-VQ-A8DZ	396	1	70	MALE	G3	Stage IV	T4	M1	N3
TCGA-RD-A8N0	1236	0	53	FEMALE	G3	Stage IIIB	T3	M0	N2
TCGA-BR-8078	900	0	70	FEMALE	G3	Stage IIB	T4a	M0	N0
TCGA-CD-5800	400	0	51	FEMALE	G1	Stage II	T3	M0	N0
TCGA-CD-8531	383	0	66	FEMALE	G3	Stage IIIA	T3	M0	N1
TCGA-R5-A804	140	1	54	MALE	G3	Stage IV	T3	M1	N2
TCGA-KB-A93J	1124	0	78	MALE	G3	Stage II	T2b	M0	N1
TCGA-CG-4306	1	1	90	MALE	G3	Stage IV	T3	M1	N2
TCGA-D7-8572	511	0	57	MALE	G2	Stage IIB	T2	M0	N2
TCGA-CD-8534	367	0	41	MALE	G3	Stage II	T3	M0	N0
TCGA-R5-A7ZF	259	1	65	FEMALE	G2	Stage IV	T4a	M1	N1
TCGA-HF-7134	1588	0	unknow	MALE	G2	Stage IA	T1	M0	N0
TCGA-D7-5578	385	0	80	MALE	G3	Stage IIIA	T3	M0	N2
TCGA-VQ-A8PE	675	1	78	MALE	G3	Stage IIIB	T3	M0	N3a

TCGA-HU-A4GT	198	0	71	FEMALE	G3	Stage IIA	T3	M0	N0
TCGA-CG-5734	243	1	68	MALE	G3	Stage IIIA	T3	M0	N1
TCGA-VQ-A8DT	1484	0	43	MALE	G3	Stage IIIB	T3	M0	N3a
TCGA-FP-7916	428	1	77	MALE	G3	Stage IIIC	T4a	MX	N3a
TCGA-CD-A4MG	200	1	76	MALE	G3	Stage IIA	T3	M0	N0
TCGA-RD-A8N2	3540	0	59	FEMALE	G3	Stage IB	T2	M0	N0
TCGA-BR-A4CQ	1064	0	58	MALE	G3	Stage IIIA	T4a	M0	N1
TCGA-D7-6519	625	0	64	FEMALE	G3	unknow	T2	M0	N1
TCGA-CG-5732	2100	1	66	MALE	G2	Stage IV	T2	M0	N3
TCGA-CD-8527	218	1	72	FEMALE	G2	Stage II	T2	M0	N1
TCGA-BR-7703	1100	0	81	MALE	G2	Stage IA	T1b	M0	N0
TCGA-HF-A5NB	928	0	75	FEMALE	G3	Stage IIIC	T4a	M0	N3a
TCGA-HU-A4GD	692	0	56	MALE	G3	Stage IIB	T3	M0	N1
TCGA-RD-A8N9	1083	0	63	FEMALE	G3	Stage II	T2	M0	N1
TCGA-BR-6709	370	1	57	FEMALE	G3	Stage IIIB	T3	M0	N3a
TCGA-D7-6818	376	1	53	MALE	G3	Stage IIIA	T2	M0	N3
TCGA-CG-4444	1431	0	76	MALE	G3	Stage IIIA	T2b	M0	N2
TCGA-BR-8366	29	0	80	FEMALE	G3	Stage IIA	T3	M0	N0
TCGA-CD-A4MH	371	0	86	FEMALE	G2	Stage IIA	T3	M0	N0
TCGA-BR-8683	300	1	75	MALE	G3	Stage IIIB	T4a	M0	N2
TCGA-BR-8484	766	1	61	MALE	G2	Stage IIIA	T4a	M0	N1
TCGA-D7-8575	554	1	75	MALE	G3	Stage IIIA	T3	M0	N2
TCGA-BR-8679	0	0	63	FEMALE	G2	Stage IB	T2	M0	N0
TCGA-BR-8371	359	1	62	MALE	G3	Stage IIIB	T3	M0	N3a
TCGA-BR-4357	0	0	58	MALE	G2	unknow	T3	MX	NX
TCGA-CG-4437	245	0	83	MALE	G2	Stage II	T2	M0	N1
TCGA-BR-A4J8	411	0	71	FEMALE	G3	Stage IIIB	T3	M0	N3a
TCGA-FP-8099	519	0	79	MALE	G2	Stage IIA	T3	MX	N0
TCGA-RD-A8MV	3720	0	56	MALE	G3	Stage IIIB	T3	M0	N2
TCGA-BR-8486	0	0	90	FEMALE	G2	Stage IA	T1b	M0	N0
TCGA-BR-4253	124	1	80	FEMALE	G3	Stage IIIA	T3	M0	N1
TCGA-F1-6177	0	0	90	MALE	G2	Stage I	T1b	MX	N1
TCGA-D7-A6EZ	618	1	66	MALE	G3	Stage IIIA	T3	M0	N2
TCGA-VQ-A924	1686	1	69	MALE	G2	Stage II	T3	M0	N0
TCGA-BR-7723	874	1	59	MALE	G3	Stage IIIB	T3	M0	N3a
TCGA-VQ-AA69	864	0	35	MALE	G2	Stage IIIA	T3	M0	N2
TCGA-HU-A4H0	64	0	72	MALE	G3	Stage IIIC	T4a	M0	N3b
TCGA-BR-8291	607	1	61	MALE	GX	Stage IIB	T3	M0	N1
TCGA-CG-5717	212	1	58	MALE	G3	Stage II	T2b	M0	N1
TCGA-HU-A4G9	736	0	67	FEMALE	G2	Stage IA	T1a	M0	N0
TCGA-HF-7136	unknow	0	unknow	MALE	G2	Stage IIIA	T3	M0	N1
TCGA-HJ-7597	805	1	71	FEMALE	G3	Stage IB	T2b	MX	N0
TCGA-CD-5804	0	0	90	MALE	G2	unknow	T3	M0	N1
TCGA-BR-4201	940	1	66	FEMALE	G1	unknow	T2a	M0	NX
TCGA-BR-6454	0	0	58	MALE	G3	Stage IIA	T3	M0	N0
TCGA-3M-AB46	1765	0	70	MALE	G2	Stage IB	T2b	MX	N0
TCGA-CD-A48C	353	1	79	FEMALE	G3	Stage IIB	T3	M0	N1
TCGA-D7-6820	344	0	64	MALE	G2	Stage IIB	T2	M0	N1

TCGA-BR-A44U	422	1	70	MALE	G3	Stage IIIB	T3	M0	N3a
TCGA-BR-7196	666	0	64	MALE	G3	Stage IV	T3	M1	N3a
TCGA-FP-8210	153	1	48	MALE	G3	Stage IIIA	T3	M0	N1
TCGA-BR-8690	325	0	54	FEMALE	G2	Stage IIIB	T3	M0	N3a
TCGA-BR-8368	131	0	84	FEMALE	G3	Stage IB	T2	M0	N0
TCGA-CG-5716	0	0	86	MALE	G2	Stage IV	T4a	M1	N2
TCGA-BR-8081	981	0	71	FEMALE	G2	Stage IIB	T4a	M0	N0
TCGA-HU-A4GN	912	0	61	MALE	G2	Stage IIA	T2	M0	N1
TCGA-CD-A489	344	1	58	MALE	G3	Stage IIA	T3	M0	N0
TCGA-RD-A8N6	272	1	78	FEMALE	G3	Stage IIIA	T2	M0	N2
TCGA-BR-8289	81	1	57	MALE	G3	Stage IV	T4	M1	N3a
TCGA-RD-A8NB	513	1	80	FEMALE	G3	Stage IIIA	T3	M0	N1
TCGA-VQ-A8PJ	82	1	53	MALE	GX	Stage IV	T4	M1	N2
TCGA-D7-6526	523	0	67	FEMALE	G2	Stage IIIA	T3	M0	N2
TCGA-CG-5721	183	0	58	MALE	G3	Stage IV	T4	M0	N1
TCGA-BR-6710	273	0	41	MALE	G2	Stage IB	T2	M0	N0
TCGA-EQ-5647	19	1	86	FEMALE	G2	Stage IV	T4	M1	N3
TCGA-B7-A5TI	595	0	52	MALE	G3	Stage IIIC	T4	M0	N3
TCGA-FP-8209	1811	1	49	MALE	G3	Stage IB	T2a	M0	N0
TCGA-RD-A7BW	156	1	68	FEMALE	G3	Stage IB	T2	M0	N0
TCGA-R5-A7ZI	2267	0	44	FEMALE	G3	Stage IV	T4	M1	N1
TCGA-BR-4280	201	1	78	FEMALE	G2	Stage III	T2b	M0	N1
TCGA-HU-A4H2	394	0	58	FEMALE	G2	Stage IIIB	T3	M0	N3b
TCGA-HU-A4G6	738	0	74	MALE	G3	Stage IA	T1b	M0	N0
TCGA-IN-A6RO	unknow	1	70	MALE	G2	Stage IA	T1b	M0	N0
TCGA-CD-A48A	378	0	57	MALE	G2	Stage IIA	T3	M0	N0
TCGA-CD-8526	381	0	73	FEMALE	G3	Stage IIIA	T3	M0	N1
TCGA-FP-8211	413	0	62	MALE	G2	Stage IIB	T3	MX	N1
TCGA-BR-8369	427	0	76	FEMALE	G3	Stage IIIB	T3	M0	N3a
TCGA-ZA-A8F6	525	0	71	MALE	G2	Stage IB	T2	MX	N0
TCGA-CD-5813	377	1	60	MALE	G3	Stage II	T3	M0	N0
TCGA-EQ-8122	243	1	71	FEMALE	G3	Stage IIB	T3	MX	N1
TCGA-BR-4292	0	0	73	FEMALE	G1	unknow	T1	M0	NX
TCGA-R5-A805	281	1	71	MALE	G3	Stage IIIB	T3	M0	N2
TCGA-VQ-A91A	1200	0	67	MALE	G1	Stage IIIB	T3	M0	N3a
TCGA-VQ-A91Q	633	1	61	MALE	G3	Stage IV	T3	M0	N3
TCGA-BR-A4QM	156	0	65	MALE	G3	Stage IIIA	T3	M0	N2
TCGA-FP-A8CX	7	0	60	MALE	G3	Stage IIIC	T4b	MX	N3a
TCGA-BR-8487	34	0	64	FEMALE	G3	Stage IIA	T3	M0	N0
TCGA-HU-A4G2	739	0	45	MALE	G3	Stage IIB	T3	M0	N1
TCGA-IN-A6RL	406	1	84	MALE	G2	unknow	T2	M0	N1
TCGA-BR-7959	1010	0	59	MALE	G3	Stage IIIA	T4a	M0	N1
TCGA-D7-8578	643	0	72	MALE	G2	Stage IB	T2	M0	N0
TCGA-CG-5724	366	1	59	MALE	G3	Stage IV	T3	M1	N3
TCGA-F1-A448	647	0	70	MALE	G3	Stage IIIB	T3	M0	N3b
TCGA-BR-6456	526	1	74	FEMALE	G2	Stage IIB	T3	M0	N1
TCGA-CG-4462	0	1	72	FEMALE	G3	Stage IV	T3	M1	N3
TCGA-VQ-AA6F	1646	0	57	MALE	G2	Stage IIB	T3	M0	N1

TCGA-VQ-A8PY	436	1	47	FEMALE	G2	Stage IIIB	T3	M0	N2
TCGA-VQ-A91U	52	1	78	MALE	G2	Stage IIIA	T3	M0	N1
TCGA-D7-5577	782	1	53	FEMALE	G2	Stage IIIA	T2	M0	N3
TCGA-BR-8678	754	0	76	MALE	G2	Stage IB	T2	M0	N0
TCGA-D7-6822	375	0	77	MALE	G2	Stage IB	T2	M0	N0
TCGA-BR-A4CS	45	1	77	MALE	G3	Stage IIIC	T4b	M0	N3a
TCGA-BR-8588	389	0	55	FEMALE	G3	Stage IIB	T4a	M0	N0
TCGA-VQ-A8PD	496	1	69	MALE	G2	Stage IIIC	T4a	M0	N3
TCGA-FP-A4BE	337	0	55	MALE	G3	Stage IIA	T3	M0	N0
TCGA-D7-A6F2	476	0	62	MALE	G3	Stage IB	T2	M0	N0
TCGA-VQ-A8DL	28	1	69	FEMALE	G2	Stage IIA	T3	M0	N0
TCGA-HU-A4H6	644	0	72	FEMALE	G2	Stage IIIA	T3	M0	N2
TCGA-BR-4191	558	1	72	MALE	G2	unknow	TX	M0	N1
TCGA-BR-A4J6	20	0	69	FEMALE	G2	Stage IIA	T3	M0	N0
TCGA-IN-8663	103	1	68	MALE	G3	Stage IIB	T2	M0	N2
TCGA-VQ-A92D	2032	0	67	MALE	G2	Stage IB	T2b	M0	N0
TCGA-FP-8631	17	0	68	MALE	G2	Stage IIIA	T3	MX	N2
TCGA-IN-7808	105	1	59	MALE	G3	unknow	T3	M1	N3
TCGA-HU-A4H5	724	0	71	MALE	GX	Stage IB	T2	M0	N0
TCGA-D7-A4YT	434	0	56	MALE	G2	Stage IIIA	T2	M0	N3a
TCGA-SW-A7EB	176	0	45	MALE	G2	Stage IIIA	T3	M0	N2
TCGA-D7-8579	636	0	66	FEMALE	G2	Stage IIB	T2	M0	N2
TCGA-D7-A4YU	500	0	73	MALE	G3	Stage IIIB	T3	M0	N3a
TCGA-CD-A4MJ	384	0	60	MALE	G2	Stage IB	T2	M0	N0
TCGA-IN-A6RR	205	1	84	MALE	G3	unknow	T3	M0	N1
TCGA-VQ-A91X	289	1	74	MALE	G3	Stage IIIB	T3	M0	N2
TCGA-VQ-A8P5	235	1	67	MALE	G3	Stage IIA	T3	M0	N0
TCGA-BR-6566	997	0	64	FEMALE	G3	Stage IIA	T3	M0	N0
TCGA-BR-8372	951	0	63	MALE	G3	Stage IIIC	T4b	M0	N3a
TCGA-F1-A72C	346	0	68	MALE	G2	Stage IIA	T3	M0	N0
TCGA-CG-5719	31	0	54	FEMALE	G1	Stage IV	T4	M1	N0
TCGA-BR-A4QI	652	1	70	FEMALE	G3	Stage IIA	T3	M0	N0
TCGA-BR-8590	284	1	62	MALE	G3	Stage IIIC	T4b	M0	N2
TCGA-CG-4440	122	1	68	FEMALE	G3	Stage IV	T3	M1	N3
TCGA-BR-A4IU	838	0	34	FEMALE	G3	Stage IIIA	T4a	M0	N1
TCGA-VQ-A8E2	1319	0	57	MALE	G2	Stage IIIB	T3	M0	N2
TCGA-VQ-AA6A	1184	0	56	MALE	G2	Stage IIIC	T4	M0	N3a
TCGA-BR-6705	779	1	68	FEMALE	G3	Stage IIIB	T3	M0	N3a
TCGA-BR-8059	439	1	72	MALE	G3	Stage III	T4	M0	N1
TCGA-CD-8532	354	1	52	MALE	G2	Stage II	T3	M0	N0
TCGA-BR-7707	1090	0	69	FEMALE	G3	Stage IB	T2	M0	N0
TCGA-VQ-A8PT	900	0	65	MALE	G3	Stage IIIB	T4b	M0	N0
TCGA-BR-A4CR	0	0	70	FEMALE	G3	Stage IIIC	T4b	M0	N3a
TCGA-HU-8243	180	1	66	MALE	G2	Stage IIIC	T4a	M0	N3b
TCGA-CG-5733	641	1	83	FEMALE	G3	Stage IIIA	T2	M0	N2
TCGA-D7-8576	446	1	54	FEMALE	G3	Stage IIIB	T3	M0	N3a
TCGA-VQ-A8E3	661	1	79	MALE	G3	Stage IIA	T3	M0	N0
TCGA-BR-A4IV	869	1	47	MALE	G3	Stage IIIB	T4a	M0	N2

TCGA-D7-6815	486	0	70	FEMALE	G2	Stage IIB	T2	M0	N2
TCGA-VQ-A91K	1862	0	69	MALE	G2	Stage IIIA	T3	M0	N1
TCGA-VQ-A8PX	1964	0	51	MALE	G2	Stage IA	T1	M0	N0
TCGA-BR-A453	185	1	51	MALE	G3	Stage IV	T4a	M1	N3a
TCGA-BR-8365	533	1	70	FEMALE	G3	Stage IIA	T3	M0	N0
TCGA-HU-8238	46	0	56	MALE	G2	unknow	T3	M0	unknow
TCGA-BR-8589	825	0	56	MALE	G3	Stage IIIB	T4b	M0	N1
TCGA-BR-4183	201	1	55	FEMALE	G3	Stage IIIA	T3	M0	N1
TCGA-BR-7722	466	1	62	MALE	G3	Stage IIB	T3	M0	N1
TCGA-B7-A5TN	287	0	60	MALE	G2	Stage IIB	T4a	M0	NX
TCGA-BR-6457	416	0	69	MALE	G3	Stage IIA	T3	M0	N0
TCGA-BR-4257	294	1	79	FEMALE	G2	unknow	TX	M0	NX
TCGA-BR-8360	188	0	66	MALE	G2	Stage IIA	T3	M0	N0
TCGA-KB-A93G	613	0	68	MALE	G1	Stage IB	T2	M0	N0
TCGA-IN-A7NR	198	0	64	FEMALE	G3	Stage IV	T3	M1	N3
TCGA-BR-7716	1210	0	62	FEMALE	G2	Stage IIB	T3	M0	N1
TCGA-HF-7131	unknow	0	unknow	FEMALE	G2	Stage IB	T2b	MX	N0
TCGA-EQ-A4SO	494	0	70	MALE	G2	Stage IIIB	T4b	MX	N1
TCGA-D7-A6ET	804	0	76	MALE	G2	Stage IIIB	T3	M0	N3a
TCGA-HU-8604	694	0	82	FEMALE	G2	Stage IIA	T3	M0	N0
TCGA-VQ-A8P2	1160	0	68	MALE	G2	Stage IIIA	T4a	M0	N1
TCGA-VQ-A94O	640	1	74	MALE	G2	Stage IIIC	T4a	M0	N3
TCGA-HU-A4GX	616	0	70	FEMALE	G3	Stage IIIC	T4b	M0	N2
TCGA-VQ-A8P3	1132	0	72	MALE	G2	Stage IIIA	T4	M0	N1
TCGA-B7-5818	356	0	62	MALE	G3	Stage IB	T2	M0	N0
TCGA-BR-4362	0	0	74	FEMALE	G3	unknow	TX	M0	N1
TCGA-IP-7968	77	0	74	MALE	G2	Stage IIIB	T3	MX	N2
TCGA-3M-AB47	unknow	1	51	MALE	G3	Stage IIIB	T3	MX	N2
TCGA-VQ-A8PO	282	1	74	MALE	G3	Stage IIB	T4a	M0	N0
TCGA-BR-8682	991	0	52	MALE	G3	Stage IIB	T4a	M0	N0
TCGA-ZQ-A9CR	24	1	79	FEMALE	G3	Stage IIIC	T4a	MX	N3
TCGA-VQ-A8PZ	2233	0	56	FEMALE	G3	Stage II	T3	M0	N0
TCGA-BR-7958	899	0	60	MALE	G3	Stage IIIB	T4b	M0	N0
TCGA-BR-A44T	1038	0	53	FEMALE	G3	Stage IIA	T3	M0	N0
TCGA-BR-6565	279	1	67	MALE	G2	Stage IIB	T4a	M0	N0
TCGA-F1-6875	2197	1	79	MALE	G2	Stage IA	T2	M0	N0
TCGA-VQ-AA6I	491	1	68	MALE	G3	Stage IIIB	T3	M0	N3
TCGA-VQ-A8DV	403	1	48	MALE	G2	Stage IB	T2	M0	N0
TCGA-VQ-A8PC	1407	1	65	MALE	G3	Stage IIIA	T3	M0	N1
TCGA-BR-4294	0	0	65	MALE	G2	unknow	T2a	M0	NX
TCGA-HU-A4HB	477	1	68	MALE	G3	Stage IIB	T2	M0	N2
TCGA-BR-8297	225	0	58	MALE	GX	Stage IIIC	T4b	M0	N3a
TCGA-CD-A487	374	0	51	MALE	G3	Stage IIB	T3	M0	N1
TCGA-CD-8525	383	0	82	FEMALE	G3	Stage IIIA	T3	M0	N1
TCGA-HU-8608	641	0	70	MALE	G3	Stage IIIB	T4a	M0	N2
TCGA-D7-A4YX	1108	0	63	MALE	G3	Stage IIB	T3	M0	N1
TCGA-D7-6521	564	0	65	MALE	G3	unknow	T2b	M0	N2
TCGA-VQ-A91Y	296	1	67	MALE	G3	Stage IIIC	T4a	M0	N3b

TCGA-FP-7998	678	0	77	MALE	G3	Stage IIIC	T4a	MX	N3a
TCGA-BR-6803	949	0	54	FEMALE	G3	Stage IIA	T3	M0	N0
TCGA-BR-7901	105	1	74	MALE	G2	Stage IIB	T3	M0	N1
TCGA-BR-4279	291	1	43	MALE	G3	Stage II	T2a	M0	N1
TCGA-HU-A4G8	690	0	71	FEMALE	G3	Stage IIB	T3	M0	N1
TCGA-BR-7957	276	1	50	FEMALE	GX	Stage IV	T3	M1	N3a
TCGA-R5-A7ZE	554	1	66	FEMALE	G2	Stage IIIA	T3	M0	N2
TCGA-VQ-AA6J	838	0	75	MALE	G3	Stage IIIB	T4a	M0	N2
TCGA-CG-4305	485	0	69	MALE	G3	Stage II	T2a	M0	N1
TCGA-IN-A7NT	323	0	73	FEMALE	G3	Stage IIB	T3	M0	N1
TCGA-MX-A5UJ	600	0	86	FEMALE	G3	Stage IIIA	T3	M0	N2
TCGA-VQ-A8PF	76	1	76	MALE	G3	Stage IIIB	T3	M0	N3b

Supplementary Table 3 **Univariate Cox regression analysis of methylation sites and clinical features.**

Parameters	HR	HR.95L	HR.95H	P value
age	1.034818777	1.010124512	1.060116737	0.005479152
gender	1.771360121	1.047203726	2.996281049	0.033010898
grade	0.924185263	0.582902542	1.465285086	0.737412488
stage	1.482978392	1.077499398	2.041045142	0.015606546
T	1.183306698	0.865020657	1.618706709	0.292389762
M	2.309476248	0.987957787	5.398692751	0.053359555
N	1.288662494	1.038110753	1.599685793	0.02150307
cg19215261	1.95E-09	3.39E-13	1.12E-05	5.60E-06
cg08418747	1.25348E+11	596701.0456	2.63318E+16	4.37E-05
cg23850377	2.72E+23	6.01878E+11	1.23E+35	8.12E-05
cg04211745	3.59806E+18	1350213407	9.59E+27	0.000114071
cg23376526	2575491.306	1261.215617	5259335024	0.000147045
cg17592292	279703704.9	11819.34857	6.61916E+12	0.000153816
cg21566550	1.95E+44	1.14E+21	3.33E+67	0.000186595
cg23968678	2.17E+22	40934486097	1.15E+34	0.000188483
cg08996502	12242.73299	79.99361649	1873705.899	0.00024526
cg02770814	5308063.541	1212.072013	23245762839	0.000294998
cg06544198	1.39194E+12	368009.628	5.26482E+18	0.000296415
cg03640568	2.15E+25	3.2155E+11	1.43E+39	0.00032894

cg16090392	1.31604E+11	103591.0314	1.67192E+17	0.000356473
cg07314414	6.97E+19	859736326.1	5.65E+30	0.000363588
cg24823993	5.78E+24	1.22718E+11	2.72E+38	0.000385925
cg15790852	4.2129E+18	200145395.5	8.87E+28	0.000406153
cg20862496	0.016323609	0.001665172	0.160019646	0.000410322
cg20116574	57902879.96	2843.793304	1.17897E+12	0.000413907
cg07437033	5979523573	21571.46454	1.6575E+15	0.00043056
cg27514224	2.77E-19	1.27E-29	6.04E-09	0.000434685
cg03878377	3.95E+22	9512334425	1.64E+35	0.000448448
cg08934443	47665.38554	112.8014508	20141487.21	0.000479755
cg21434440	7757.606186	50.86411461	1183161.335	0.000479759
cg02537909	56178737235	50522.43158	6.24683E+16	0.000492698
cg18130076	2.27E+20	740909947.3	6.96E+31	0.000513858
cg21116410	4.03E+36	6.54274E+15	2.49E+57	0.000558536
cg19317638	2447897.285	556.222671	10773025682	0.000588826
cg03070588	1692164898	9121.030904	3.13936E+14	0.000596523
cg13376158	6685423.059	826.7580097	54060415442	0.000618888
cg16482226	7.92E+23	14595287890	4.30E+37	0.000648653
cg06386533	10813.18673	51.08267793	2288936.525	0.000674822
cg10905613	1.10431E+12	112565.4534	1.08337E+19	0.000735444
cg26840318	6.64503E+11	78710.37893	5.60999E+18	0.000821694
cg01244871	1.71749E+19	84139344.48	3.51E+30	0.000858107
cg25495394	2116.665992	23.12626009	193731.0618	0.000890649
cg16222698	6.62E+50	4.38E+20	1.00E+81	0.000965079
cg03752689	1433333.101	314.9618334	6522834071	0.000972018
cg11691938	1.21083E+19	47581354.17	3.08E+30	0.001040772
cg02171008	1.56935E+17	7443119.631	3.31E+27	0.001096421
cg08778586	1217036.364	261.5996211	5662001746	0.001146263
cg22234344	1.14185E+15	935340.7958	1.39E+24	0.001162658
cg21796234	6278608120	7648.911779	5.15379E+15	0.001166391
cg26007077	2.30606E+13	187247.9639	2.84E+21	0.001206916
cg00426056	7556834.513	502.5057641	1.13642E+11	0.001249409
cg09976774	1.65133E+15	907670.5934	3.00E+24	0.001277322
cg16161425	8.22856E+17	9889695.567	6.85E+28	0.001302309
cg05646865	0.000793433	1.02E-05	0.061655189	0.001306799
cg13219107	26058211380	10657.93637	6.37112E+16	0.001395014
cg04001333	0.148211199	0.045947349	0.478081108	0.001398302
cg04703844	4330163889	4988.124368	3.75899E+15	0.001470563
cg21666675	411.2440607	10.01068214	16894.12121	0.001497575
cg19234089	0.008665559	0.000459245	0.163511797	0.001533838
cg21644628	0.010384352	0.000608956	0.177081259	0.001598218
cg19864851	1.58918E+11	17374.07085	1.45359E+18	0.00161204
cg04739149	2.44E-05	3.27E-08	0.018182001	0.001646385
cg23749163	15631318.37	511.9906284	4.77232E+11	0.001666593
cg03522403	3.64E+26	9500678025	1.40E+43	0.00169412
cg07924819	3.90356E+13	127121.6693	1.20E+22	0.00169708
cg11226328	33221.05683	49.11504861	22470477.95	0.001741168
cg22194305	4458957710	3791.924541	5.24333E+15	0.001836435

cg24229963	7.14878E+11	24155.48739	2.11567E+19	0.001872243
cg12903171	0.013558938	0.000900802	0.204090191	0.001879252
cg22111003	6.16986E+16	1517826.056	2.51E+27	0.00192276
cg09830278	0.005624376	0.00020918	0.151226959	0.002037454
cg05287690	115269619.6	817.4067541	1.62552E+13	0.002151202
cg07807709	22355.41477	37.11088809	13466790.89	0.002165476
cg13315147	0.14169882	0.040608118	0.494446847	0.002180021
cg04025889	2.69922E+11	12839.84387	5.67438E+18	0.002215977
cg21011830	3.73E+20	24339861.25	5.73E+33	0.002229121
cg06433995	4.25E+28	18368000652	9.86E+46	0.002247721
cg14550007	2631.2601	16.81777255	411679.3526	0.002252247
cg15239703	2.42E-10	1.63E-16	0.000358616	0.002256398
cg10185638	2.77E+21	46113112.38	1.66E+35	0.002287241
cg25363317	4.63285E+17	2032655.72	1.06E+29	0.002299721
cg19459675	1.26509E+11	9142.031353	1.75066E+18	0.002310419
cg05915281	2.14817E+12	24389.21299	1.89E+20	0.002348042
cg08552121	19526844.02	386.9665559	9.8535E+11	0.002378537
cg23182539	97195769392	7919.041356	1.19295E+18	0.002382557
cg15781794	14009022503	3972.857131	4.93984E+16	0.002386515
cg03274654	5.15827E+12	31673.78812	8.40E+20	0.002411945
cg05368762	3.33E+39	7.99113E+13	1.39E+65	0.002498434
cg19401923	2.96E+20	14931628.69	5.87E+33	0.0025495
cg03301801	0.001841253	3.05E-05	0.111188936	0.002614288
cg03804985	529517.4831	98.74659772	2839477728	0.002628131
cg00093177	0.005778841	0.000200782	0.166324741	0.002643462
cg20109151	622550.515	103.5014286	3744577720	0.002656288
cg04249030	5.91303E+14	136158.0928	2.57E+24	0.002664222
cg20770803	1.58474E+11	7692.762157	3.26464E+18	0.002687839
cg22688260	2.6834E+13	43571.17497	1.65E+22	0.002749336
cg17319849	9.43913E+16	676344.4378	1.32E+28	0.002833177
cg04595372	0.063167614	0.01030177	0.387326417	0.002835154
cg02071439	6.41949E+15	261809.3355	1.57E+26	0.002863183
cg27127056	1.93411E+11	7367.264374	5.07756E+18	0.002867356
cg24905739	1.36E+23	73255631.35	2.52E+38	0.002982397
cg25461905	5.88E-05	9.44E-08	0.036572467	0.002998901
cg12288365	2.84E+49	5.82422E+16	1.38E+82	0.003024851
cg23377693	82071362.58	479.0875082	1.40595E+13	0.003039293
cg06417705	5.0557E+12	19940.30743	1.28E+21	0.00304921
cg07209631	113639.0072	51.40973449	251194138.4	0.003049671
cg09311052	360001.3416	75.36501433	1719643619	0.003076612
cg21743830	0.022537116	0.001826118	0.278142872	0.003096525
cg12836863	0.092764454	0.019150148	0.44935653	0.003140014
cg14817542	8034.186133	20.48353752	3151220.669	0.003167398
cg16208491	23257390386	2915.021399	1.85558E+17	0.003241766
cg13853761	0.109291368	0.025015169	0.477494401	0.003255544
cg14424111	3.07763E+15	148401.4018	6.38E+25	0.003256527
cg17889103	1319393.221	110.3472634	15775637919	0.00326261
cg15119375	9.29177E+15	208794.6265	4.14E+26	0.003291422

cg22374901	4204.445972	16.04130808	1101990.302	0.003317156
cg22458065	0.01637497	0.001050611	0.25522255	0.003340398
cg03984733	1703426225	1134.060442	2.55865E+15	0.003397809
cg20011794	75798.99001	40.41976576	142145477	0.003477727
cg22091798	42376866326	3089.093543	5.81335E+17	0.003519434
cg27378424	2.13412E+15	106662.7918	4.27E+25	0.00353845
cg07684150	1.10E+20	3744376.946	3.25E+33	0.003539833
cg23318804	3.27573E+18	1175725.671	9.13E+30	0.003545769
cg14086033	43062996.15	304.5410519	6.08923E+12	0.00367142
cg01241375	6.1221E+11	6822.605867	5.49352E+19	0.003674627
cg14712964	266457531.8	477.7761863	1.48604E+14	0.004055851
cg15425811	0.125805499	0.030592656	0.517347154	0.004059711
cg03085312	0.045482856	0.005523975	0.374493032	0.004065059
cg11304524	6.08E-07	3.42E-11	0.010827692	0.004152983
cg09455096	2.75038E+14	36292.26718	2.08E+24	0.004175831
cg20950277	0.020949984	0.001478636	0.296828811	0.004263902
cg19350340	3295.957149	12.71963577	854060.1098	0.004278177
cg17597195	1.7229E+15	58814.67398	5.05E+25	0.004329802
cg16522484	0.054997851	0.007486646	0.404021165	0.004362242
cg15118204	1778505341	773.1233303	4.0913E+15	0.004374891
cg16917279	1.39E+21	3713172.442	5.19E+35	0.004461042
cg22816171	311624.7838	49.91306573	1945582874	0.004555011
cg19175383	1.00E+21	3058103.883	3.29E+35	0.004573496
cg07478100	158020.821	40.29673275	619667604.6	0.004575079
cg07399355	16576254.39	165.4751854	1.6605E+12	0.004661202
cg21306212	4.73438E+16	132825.9096	1.69E+28	0.004666387
cg17398595	0.136780884	0.034449551	0.543084306	0.00468803
cg01663570	41110153332	1763.558773	9.58315E+17	0.004748926
cg03759077	2.19053E+16	96732.98315	4.96E+27	0.004794648
cg27533013	1.92E-05	1.01E-08	0.03659196	0.004825988
cg09128050	7.45203E+17	276804.7378	2.01E+30	0.004831183
cg22190090	5.49631E+12	7130.118527	4.24E+21	0.004958166
cg05358404	0.095660682	0.018553714	0.493214796	0.005037867
cg03415518	0.001012115	8.08E-06	0.126744941	0.005139925
cg02809263	1.44943E+12	4290.53032	4.90E+20	0.005194059
cg07190917	2.51E+21	2458909.785	2.57E+36	0.005198216
cg11286618	1.30275E+11	2085.637763	8.13741E+18	0.005198293
cg04433306	28113.54536	21.11725096	37427761.52	0.005255307
cg27447599	0.05500974	0.007153669	0.423009703	0.005326155
cg19584823	10719121.01	120.4233378	9.5413E+11	0.005370661
cg03764352	1779795870	538.1592631	5.88613E+15	0.005419748
cg01783386	133194420.8	249.8514345	7.10052E+13	0.005426589
cg06976977	34036969481	1246.191226	9.29645E+17	0.005505744
cg03373442	2133892.861	71.5972685	63598777415	0.005562677
cg05401645	7.45E+18	314507.6042	1.77E+32	0.005681749
cg01139966	46.70938408	3.059059902	713.2147231	0.005711171
cg13052755	0.00039692	1.54E-06	0.102634785	0.005724154
cg17176395	2.45901E+13	7737.590063	7.81E+22	0.005744002

cg23873703	0.125927746	0.02891504	0.54842729	0.005777475
cg06462703	0.001596049	1.64E-05	0.155442811	0.005837322
cg25959506	0.042518684	0.004502174	0.401547928	0.005843968
cg14206730	1.54864E+13	6269.690299	3.83E+22	0.005917274
cg10906135	2.46E-13	2.51E-22	0.000242176	0.0059948
cg17158059	4.50799E+12	4232.871864	4.80E+21	0.006007762
cg09326702	0.099210926	0.019064241	0.51629688	0.006041985
cg09659887	1.68806E+15	21887.3838	1.30E+26	0.006119545
cg21039822	3.44E-61	1.79E-104	6.62E-18	0.006183713
cg19032144	4.30239E+13	7376.769621	2.51E+23	0.006214784
cg25848060	1492303869	398.3657771	5.59027E+15	0.006233124
cg10624768	3304.775985	9.885660927	1104786.457	0.006284137
cg12259537	0.120488636	0.026404259	0.549817034	0.006289865
cg22334665	0.143560797	0.035644519	0.578201155	0.006320372
cg09498106	65203.31419	22.73967066	186962786.1	0.006350903
cg05886626	0.114101171	0.024001716	0.542422773	0.006352273
cg10391629	1.02868E+12	2408.078051	4.39E+20	0.006373451
cg14534967	4.82529E+12	3707.137962	6.28E+21	0.006382703
cg27556566	59497232.49	153.5518083	2.30536E+13	0.006396164
cg14916213	1961294490	405.9738542	9.47518E+15	0.006432983
cg09546332	55222035.65	148.431801	2.05446E+13	0.006449697
cg02290509	9.95538E+14	15716.78684	6.31E+25	0.006500745
cg03276813	76752394639	1095.506449	5.37736E+18	0.006541564
cg02675652	0.092743298	0.016705877	0.514867875	0.006547179
cg14596431	7.53874E+17	97619.63781	5.82E+30	0.006552512
cg24705286	476345.3232	38.33298329	5919311450	0.006567391
cg05719902	0.102799776	0.019920223	0.530505799	0.006586002
cg18909638	0.112701407	0.023319279	0.544682681	0.00661172
cg16954341	0.139270328	0.03351587	0.578717614	0.006676741
cg03738331	3.72428E+14	11028.19102	1.26E+25	0.006677665
cg18979762	0.002729458	3.83E-05	0.194520778	0.006686103
cg03959219	3151.300148	9.272129108	1071026.137	0.006751894
cg26705561	0.155886342	0.04061972	0.598245183	0.006754961
cg20821095	4.2657E+17	71536.18688	2.54E+30	0.006836051
cg06305312	1.23775E+12	2128.943713	7.20E+20	0.00684632
cg10872447	7.78E+53	6.22904E+14	9.73E+92	0.006900185
cg02218260	0.0386082	0.003641076	0.409382623	0.006906708
cg05291178	5.32E-06	7.80E-10	0.0362945	0.007012998
cg09650667	4699507.055	65.99070271	3.34674E+11	0.007041879
cg26760212	0.133809325	0.03091124	0.579237055	0.007137802
cg21703572	1189103676	290.7564309	4.86307E+15	0.007139839
cg22464182	360.3893356	4.916517841	26417.16707	0.007214109
cg24642516	2.38486E+11	1189.443722	4.7817E+19	0.007231503
cg18757066	7.76E+22	1486844.106	4.05E+39	0.007283236
cg12820608	44096232.61	114.1329514	1.7037E+13	0.007324444
cg17291001	0.035327795	0.003059645	0.407907803	0.007397787
cg19275050	0.119345698	0.025169268	0.565904231	0.007430289
cg24394865	7.05099E+19	204862.523	2.43E+34	0.007448506

cg22156632	0.109992036	0.021824928	0.554331626	0.007474355
cg08632701	0.058610629	0.007328691	0.468733862	0.007489461
cg03036064	49535505.51	112.5910915	2.17936E+13	0.007529874
cg11044823	149699622.2	150.0912312	1.49309E+14	0.007561931
cg11603096	3.76E+27	21423651.68	6.60E+47	0.00759182
cg21943652	1.41662E+15	10485.04105	1.91E+26	0.007631961
cg00155485	1.90E+21	432320.1593	8.31E+36	0.007672838
cg19786920	0.076624721	0.011586222	0.506752571	0.007694406
cg17997329	1.81703E+19	122809.4083	2.69E+33	0.007724302
cg15309223	7.09085E+11	1347.518628	3.73E+20	0.00773819
cg16978263	51.49537045	2.829240466	937.2738761	0.0077564
cg13634678	3.18642E+19	138820.214	7.31E+33	0.007772307
cg08115510	27612758.15	90.84162283	8.39334E+12	0.007814095
cg17324707	1.48624E+12	1561.639365	1.41E+21	0.007881446
cg10239941	40049.58623	16.11852654	99510917.05	0.007886102
cg23337289	16.18469389	2.070005596	126.5428059	0.007969536
cg13575604	1.17807E+16	15735.68613	8.82E+27	0.007985082
cg13581941	3.30E+28	27415215.28	3.97E+49	0.008013141
cg08388746	0.002503035	2.99E-05	0.20971484	0.008017874
cg11787828	54514.99237	16.93926649	175443511.4	0.008129655
cg11050527	419246.0656	28.73591569	6116640424	0.008134715
cg01360768	11516902810	404.6072562	3.27822E+17	0.008158647
cg21548788	7.05695E+18	75242.72167	6.62E+32	0.008192851
cg09194650	7.94069E+15	12867.32125	4.90E+27	0.008215031
cg16072462	0.109203444	0.021099557	0.565196319	0.008285127
cg22621736	2.5312E+14	5136.391063	1.25E+25	0.0082875
cg20377673	79250.91027	18.25445631	344064302.5	0.008300598
cg15663121	8.49626E+12	2072.654393	3.48E+22	0.008384496
cg23599056	0.000808738	4.06E-06	0.161186057	0.008399178
cg11879514	0.168957943	0.04499711	0.634413786	0.00843658
cg27072323	26454.30539	13.47107217	51950599.4	0.00848452
cg02161046	1.34062E+14	4032.523845	4.46E+24	0.008498319
cg16104446	23157604.7	75.2491363	7.12666E+12	0.008535792
cg15198335	1515684769	217.4763429	1.05634E+16	0.008552977
cg20273774	263494469.7	138.0038402	5.03097E+14	0.008595867
cg16370389	1.45E-10	6.64E-18	0.003173386	0.008610696
cg18338021	0.04564794	0.004558931	0.457066417	0.00863896
cg09189322	52676342.43	90.47083401	3.06706E+13	0.008661884
cg25492727	3843269.67	46.32231988	3.18868E+11	0.008697876
cg02668984	81541.85734	17.46472094	380714614.3	0.00870361
cg18333824	1.18481E+13	2006.659811	7.00E+22	0.008731415
cg27662379	4.17E-14	4.15E-24	0.000418618	0.008743094
cg19185384	1303404779	195.2689833	8.70012E+15	0.008849135
cg12675800	9.50104E+18	58345.86148	1.55E+33	0.00886411
cg21693780	5.52215E+12	1577.841196	1.93E+22	0.008877968
cg21515243	18681.25406	11.7480952	29706028.68	0.008922418
cg25898500	29261706.13	73.48487261	1.1652E+13	0.008972258
cg02005336	8751231.286	54.18827783	1.4133E+12	0.008988887

cg17229388	0.104297291	0.019096211	0.569637875	0.009063952
cg20126158	169261.7061	19.93025341	1437489256	0.009101642
cg25047001	0.142902696	0.033092952	0.617085491	0.009140218
cg02595263	14844663.88	59.92090232	3.67758E+12	0.009164235
cg03386722	7653892114	277.9617684	2.10756E+17	0.009219477
cg16358738	0.042234751	0.003900919	0.457270229	0.009219692
cg09892131	5.12285E+12	1335.605632	1.96E+22	0.009344457
cg17055959	2.16E-17	5.72E-30	8.12E-05	0.009390279
cg19219437	0.14696811	0.034560401	0.624981907	0.009420608
cg03552688	0.017058956	0.000788482	0.369073816	0.009447405
cg22478328	142340945.9	98.71039681	2.05256E+14	0.009469313
cg20451680	0.146949923	0.034510156	0.625736952	0.009481605
cg04177705	1.59E+24	822901.8287	3.06E+42	0.009486045
cg02197293	0.13526303	0.029681673	0.616410251	0.009731809
cg08942800	0.174810861	0.046591614	0.655887064	0.009734219
cg27305662	0.014943407	0.00061409	0.363636224	0.009847639
cg11451801	1542605118	162.2928898	1.46626E+16	0.009857407
cg06171242	1.01E+21	112732.4746	8.98E+36	0.00985883
cg13859541	64796123729	394.5448237	1.06415E+19	0.009899625
cg13685294	0.092344182	0.015097482	0.564825842	0.009931913
cg01994513	2.24E+24	682599.1674	7.35E+42	0.009951102
cg04478795	0.144983617	0.033376037	0.62980064	0.00996813
cg11783451	6.20307E+12	1148.043604	3.35E+22	0.009989879
cg08532057	0.215669129	0.067126954	0.692913506	0.009995051
cg05477027	3693649.013	36.92777071	3.69452E+11	0.01004308
cg18023724	0.158952658	0.039080597	0.646508744	0.010190666
cg10780112	11440303.16	47.05719643	2.78131E+12	0.010209449
cg23104823	324175.3714	20.15054641	5215226888	0.010238148
cg14489649	1.17171E+11	416.3086866	3.29778E+19	0.01024123
cg12477119	198264.8003	17.89610078	2196508140	0.010256711
cg10698549	1.35079E+13	1274.119688	1.43E+23	0.010257271
cg05723825	0.076880434	0.010825445	0.54599151	0.010317698
cg20123891	0.186818804	0.051817496	0.673542103	0.01034818
cg02453653	3.49349E+11	522.0306403	2.34E+20	0.010362132
cg20732367	4838662421	189.3875994	1.23623E+17	0.010390876
cg26637901	0.031652541	0.002255431	0.444209216	0.010405235
cg01320361	2.13288E+19	34332.72764	1.33E+34	0.010440093
cg13614181	0.12861776	0.026753174	0.618338886	0.010466841
cg19819891	310446433.7	96.66671555	9.97003E+14	0.010528425
cg17021265	2809.640072	6.3737952	1238520.706	0.010582312
cg21369679	24812790521	264.3997054	2.32858E+18	0.010604743
cg26706070	831978.3668	23.67180898	29241026886	0.01069633
cg17676129	0.038028339	0.003081016	0.469375848	0.010776983
cg26129270	3.27E+30	11203882.97	9.54E+53	0.010810218
cg04466273	3.15E+24	449646.7122	2.21E+43	0.010838732
cg24532476	0.076684254	0.010630458	0.553172304	0.010857478
cg27614038	1.63203E+16	5365.954681	4.96E+28	0.010910433
cg14791831	1.06E+61	1.06364E+14	1.06E+108	0.010930542

cg26525091	0.142364002	0.031713155	0.639088397	0.010949096
cg25264554	19403266.15	46.28902291	8.13339E+12	0.011067872
cg19432434	2.27E+20	44120.8883	1.17E+36	0.011104507
cg17301902	0.085145463	0.012695459	0.571050654	0.011181425
cg27462969	77819334.17	61.51453773	9.84458E+13	0.011258422
cg19885761	0.239648201	0.079375285	0.72354084	0.011278626
cg23142935	1.56882E+13	970.6842107	2.54E+23	0.011294154
cg17414107	0.158614033	0.038126544	0.659866041	0.011356843
cg16438432	8.49352E+14	2319.221462	3.11E+26	0.011394456
cg10387901	37475.62919	10.73060412	130880122.6	0.011403706
cg04946535	6.4626E+18	17315.72836	2.41E+33	0.011404812
cg06901392	9.99784E+12	843.3547718	1.19E+23	0.01143083
cg20951821	143149.7083	14.46075459	1417065676	0.011436417
cg21989500	858991180.9	102.2409599	7.21693E+15	0.011445488
cg00290506	0.214508862	0.065023133	0.707656643	0.011478666
cg09755102	13192.98233	8.408890619	20698899.61	0.011499724
cg01843018	0.165941603	0.041115247	0.669742193	0.011633563
cg01182585	5665529.642	31.95356726	1.00453E+12	0.011676346
cg19948393	0.134563689	0.028286067	0.640152152	0.011719027
cg14838256	5.15355E+12	669.9015312	3.96E+22	0.011727695
cg24595957	11518964.61	36.90704445	3.59516E+12	0.011769086
cg08351143	1.87844E+19	18469.09535	1.91E+34	0.011830411
cg21273125	120648.8898	13.32705705	1092225730	0.011832788
cg10490196	87775817.52	56.8656001	1.35488E+14	0.011878233
cg09059181	2.99079E+12	548.8835438	1.63E+22	0.01202417
cg03821311	0.01931396	0.000886953	0.420573661	0.012039328
cg26023204	4641.109168	6.371605199	3380607.184	0.012050553
cg19187486	8012410755	145.4102626	4.41501E+17	0.01215868
cg05815893	2.98922E+11	319.9238749	2.79E+20	0.012166058
cg27413543	59585719286	223.0306299	1.59191E+19	0.012204884
cg25955816	0.043736467	0.003774395	0.506804068	0.012291211
cg25201980	3.34128E+13	850.6467042	1.31E+24	0.012350101
cg07027513	0.111519713	0.01999659	0.621938373	0.012364617
cg12578480	5.23E-10	2.78E-17	0.009864662	0.012407026
cg19570574	0.189075706	0.051231839	0.697800879	0.012417571
cg06790275	65119546.95	48.64964608	8.71652E+13	0.012430701
cg13449778	0.183967515	0.048753186	0.694191485	0.012465876
cg21607066	1343892337	92.18076834	1.95924E+16	0.012507914
cg11108432	3.56556E+19	15908.83038	7.99E+34	0.012544942
cg00622677	0.177612704	0.045710791	0.690127474	0.012576881
cg21092462	0.076163032	0.010070876	0.575998306	0.012618274
cg09765256	1.03193E+18	7183.613124	1.48E+32	0.012636833
cg18788872	83814810515	216.6024285	3.24323E+19	0.0126657
cg02735133	6.63916E+11	334.7648101	1.32E+21	0.012695445
cg14242091	8.84E+22	79440.19971	9.84E+40	0.012697546
cg11011602	1934451.334	21.99815209	1.7011E+11	0.012698617
cg23759710	0.013385793	0.000449765	0.398384679	0.012718313
cg21584983	12219613680	139.8138409	1.06798E+18	0.012792804

cg07028533	0.242466739	0.07944879	0.739975016	0.012811964
cg06585027	2.57133E+19	13259.62829	4.99E+34	0.012828438
cg01305547	0.006741325	0.00013129	0.346145141	0.012850074
cg01934797	1.53E-07	6.55E-13	0.035827542	0.012855055
cg09386615	0.016661092	0.000660674	0.420164908	0.012899893
cg20910436	6.62359E+11	318.0764528	1.38E+21	0.012907222
cg04025590	4368459217	109.6418522	1.74052E+17	0.012917739
cg10891157	8.8242E+11	334.3501562	2.33E+21	0.01295232
cg00425792	8618939934	125.3516276	5.92622E+17	0.012967306
cg16328820	3.9399E+11	277.1223008	5.60E+20	0.013026923
cg09664442	6.99008E+19	14300.53349	3.42E+35	0.013172501
cg17498523	1656.211164	4.719124317	581259.4111	0.013179986
cg05603623	1802431.57	20.31812109	1.59895E+11	0.013210803
cg24892074	1.78E+21	27001.18123	1.17E+38	0.013271617
cg17237881	0.040268834	0.003165976	0.51218936	0.013301064
cg20300655	0.055321028	0.005586237	0.547849287	0.013347727
cg19313758	74282526.01	43.06082189	1.28142E+14	0.013380168
cg21908116	6.40726E+13	729.8068217	5.63E+24	0.013407348
cg04532952	0.134581739	0.027443254	0.659988951	0.0134297
cg01817393	0.158106628	0.03655939	0.683756094	0.013557123
cg11081833	0.154051734	0.034883069	0.680328229	0.013577847
cg20009671	1.7511E+12	331.2449813	9.26E+21	0.013588258
cg16538604	24056.10725	7.957543067	72722986.4	0.013616481
cg18652121	5838052.399	24.60074322	1.38544E+12	0.013619885
cg00676660	0.06473189	0.007352614	0.569894956	0.013639206
cg19846131	14808658378	119.8085225	1.83039E+18	0.0137629
cg10313675	3210539.888	21.34329531	4.82942E+11	0.013771106
cg24576270	1.90779E+17	3386.025991	1.07E+31	0.013775483
cg19921776	3.31E+22	39300.32986	2.79E+40	0.013804576
cg08211967	100002667.9	42.72657264	2.34059E+14	0.013825634
cg21339926	2.67E-06	9.72E-11	0.073589641	0.01388454
cg24670715	0.1206022	0.022344767	0.650930513	0.013928142
cg13887370	3684312.144	21.4638879	6.32418E+11	0.013948613
cg18075299	0.000237919	3.06E-07	0.185043354	0.014020201
cg20645649	8096685654	100.5814898	6.51773E+17	0.01403297
cg25889160	0.003548582	3.94E-05	0.319919259	0.014042123
cg09433780	7417074668	98.3287894	5.5948E+17	0.014059081
cg05780311	4.5947E+13	571.4264552	3.69E+24	0.014070398
cg20496643	0.041555723	0.003280445	0.526415744	0.01407744
cg02930996	0.119620599	0.021947898	0.651957089	0.014111196
cg11688219	10008884052	103.0371279	9.72249E+17	0.014130965
cg26055770	0.181232987	0.046273548	0.709809319	0.014204697
cg23855566	135.0353197	2.669946324	6829.552117	0.01426386
cg20203792	4533730526	85.26415355	2.41071E+17	0.014294011
cg15883761	2.89197E+15	1223.914487	6.83E+27	0.014322705
cg20239949	6.20025E+15	1411.648346	2.72E+28	0.014354869
cg15105703	0.07286857	0.008940693	0.593894491	0.014416076
cg10201668	0.02867755	0.001666343	0.49353701	0.014430523

cg27182555	76293155.52	36.23239721	1.60648E+14	0.014557125
cg24527001	73560.52782	9.105356041	594282225.6	0.0146403
cg03621406	212.1245525	2.87258754	15664.21394	0.014658142
cg16121444	235591680.6	44.49606601	1.24738E+15	0.014669335
cg19307060	2.19E-10	3.81E-18	0.012634687	0.014710344
cg12687990	0.119556869	0.021686858	0.659101701	0.014744469
cg14795305	0.050176903	0.004525388	0.556354843	0.014783398
cg17608500	2461349.945	17.82231137	3.39925E+11	0.014811437
cg01929105	9923844.689	23.34875943	4.2179E+12	0.014833049
cg17002259	3.96E-16	1.62E-28	0.000973128	0.014834082
cg10539418	199847.9699	10.81908692	3691550996	0.014889563
cg20301340	5.90E+20	11234.34173	3.10E+37	0.01490144
cg19434303	1135.225939	3.94120702	326990.6721	0.01490714
cg25107978	3.31124E+14	668.3287882	1.64E+26	0.014957609
cg03442064	450014.6526	12.57414188	16105527474	0.014966574
cg14766198	29158985.53	28.26616287	3.008E+13	0.014975497
cg17729667	0.094006014	0.013984626	0.631917536	0.015011381
cg24608308	9.45837E+14	805.7715187	1.11E+27	0.015019889
cg23088430	187646762.2	40.25563035	8.74693E+14	0.015030488
cg27243140	0.02268139	0.001069804	0.480878156	0.015106351
cg20337385	6.06126E+19	6676.874311	5.50E+35	0.015111369
cg17138359	271.7053231	2.949894866	25025.90295	0.015151583
cg17194182	0.206494193	0.057809843	0.737588086	0.01515964
cg06665941	108773810.1	35.50959574	3.33198E+14	0.015163917
cg09283635	1.14E+24	43721.93884	2.98E+43	0.01516518
cg13975369	0.120649694	0.021876652	0.665382832	0.015199097
cg05122605	795103070.1	51.49289178	1.22772E+16	0.015238316
cg24353217	0.059765782	0.006140145	0.581736847	0.015242613
cg23850272	0.004823047	6.47E-05	0.359362556	0.015297265
cg18362489	7243929581	77.42600486	6.77738E+17	0.015333228
cg25683012	11126.43168	5.951899015	20799661.02	0.015349182
cg23473849	50805.12092	7.946268776	324826706	0.015369662
cg01135200	103.0824672	2.426415113	4379.298076	0.015377492
cg08817171	3.93286E+12	255.9706042	6.04E+22	0.01537945
cg06534422	28599.974	7.105966646	115108690.1	0.015392631
cg25437385	0.208791811	0.05880274	0.741360356	0.015398957
cg05257479	5.78694E+13	424.6295044	7.89E+24	0.015411358
cg16175263	0.174592088	0.04253049	0.716718695	0.015426113
cg05412136	3324.602325	4.671107348	2366244.189	0.015522468
cg21950493	403.6820812	3.117371829	52274.55422	0.015599562
cg18275051	0.15540975	0.034365365	0.702806179	0.0156048
cg27308387	1631385198	55.45312339	4.7994E+16	0.015622563
cg17306637	2.55E-05	4.81E-09	0.1351859	0.0156349
cg00846036	0.188298261	0.048623291	0.729202702	0.01564358
cg07265622	9.62E+27	194314.3951	4.76E+50	0.015662305
cg12388309	0.261789784	0.088274195	0.776375142	0.015678153
cg14932684	363319.9716	11.18076433	11806116101	0.01571677
cg15863254	5504271237	68.62480653	4.41488E+17	0.01572028

cg12045676	19200099.15	23.43251652	1.57321E+13	0.015779482
cg05382565	1.5018E+16	1102.083418	2.05E+29	0.015781296
cg21885650	6.19959E+12	251.9612902	1.53E+23	0.015825925
cg21024145	5.30601E+11	155.338123	1.81E+21	0.015932295
cg24792749	9376547.525	19.97871172	4.40067E+12	0.015978002
cg25106358	6.80E-09	1.54E-15	0.030059356	0.016002123
cg08400019	244638420.6	36.37394443	1.64535E+15	0.016040039
cg06358566	5492032.561	17.92613245	1.6826E+12	0.016050174
cg07965714	4.00E+29	319927.8028	5.01E+53	0.016052631
cg12645220	0.201415328	0.054641509	0.742441693	0.016067076
cg23685580	2.53E-05	4.56E-09	0.139955876	0.016080838
cg20908993	682958.3069	12.11542225	38499033648	0.016089625
cg15765896	10532461.38	20.13333969	5.5099E+12	0.01609032
cg12468056	1.80E+22	13352.49424	2.43E+40	0.016130255
cg22496859	20375315209	80.44221746	5.16089E+18	0.016200047
cg06062132	1056.241014	3.613165319	308772.2205	0.01624373
cg00594118	897867.9834	12.30343433	65523730540	0.016427931
cg17891123	91489692.87	28.61284352	2.92539E+14	0.016447089
cg15876417	52.35700125	2.062071395	1329.369869	0.016461574
cg17178888	0.1308846	0.024838813	0.689677827	0.016479152
cg07815386	6.8992E+14	506.6963317	9.39E+26	0.016536651
cg13782957	88884.01245	7.973888102	990779851.5	0.016546772
cg07770222	0.150906563	0.032131448	0.708738386	0.016566825
cg08095532	2.44E-06	6.25E-11	0.095255387	0.016581834
cg06779945	5.32352E+14	473.2096144	5.99E+26	0.016619138
cg11828669	46156.8502	7.027651343	303153175.4	0.016632246
cg12588476	312245.1453	9.849294887	9898884322	0.016732463
cg09068198	4845900.609	16.1619628	1.45296E+12	0.016736885
cg02489552	0.131190293	0.024845022	0.692730032	0.016739626
cg07054788	14840.60319	5.656570709	38935870.21	0.01678504
cg03079681	0.039566371	0.002800948	0.558917053	0.016822877
cg22580173	0.157601644	0.034634816	0.717147687	0.016847142
cg02298612	0.051466963	0.004513385	0.586887311	0.016888991
cg09564133	66332.14857	7.342744065	599224744.2	0.016896134
cg19564877	0.115453136	0.01962842	0.679088119	0.016938169
cg12739647	1.19921E+17	1148.659615	1.25E+31	0.016949041
cg14473924	0.247467839	0.078568873	0.779447752	0.017050108
cg27250759	1646045690	43.98388678	6.16013E+16	0.01706726
cg00798206	2.47514E+18	1900.07351	3.22E+33	0.017073209
cg02959669	0.12939151	0.024097655	0.694763164	0.017095204
cg17260124	0.004389462	5.06E-05	0.38079216	0.017127108
cg06058597	660269026.6	36.78462411	1.18516E+16	0.017172688
cg20524216	920260386.5	39.00234985	2.17135E+16	0.017175281
cg11392765	0.094207944	0.013487283	0.658037427	0.017221386
cg09903430	5.49E-05	1.71E-08	0.175932629	0.017224003
cg22238923	427986.0694	9.888748062	18523282668	0.017281926
cg14196211	4.89E+24	22392.6781	1.07E+45	0.017352451
cg06659073	22760.1185	5.857341922	88439944.47	0.017352506

cg06190732	0.137134549	0.026683178	0.704784291	0.017365789
cg13463367	63949.28539	7.011742622	583237480.7	0.017378692
cg24655310	0.102523786	0.015686414	0.670078371	0.017409003
cg00034039	1363435.525	11.9674337	1.55335E+11	0.017416273
cg10423227	74059927.06	24.12125861	2.27388E+14	0.017424459
cg12082568	41470.75287	6.428472421	267532196	0.017514949
cg22967284	0.057273296	0.00541041	0.606281271	0.017518615
cg08492707	1.35E+29	123855.5477	1.48E+53	0.017538815
cg10883621	0.144165596	0.029145385	0.713104972	0.017572397
cg14047244	6.24725E+17	1276.940139	3.06E+32	0.017577117
cg15120942	0.099025827	0.014678679	0.668051542	0.017590525
cg16011258	5.16E+36	2496925.353	1.07E+67	0.017616812
cg26898336	0.215831522	0.06083971	0.76567173	0.017632771
cg14049461	0.132194495	0.024845292	0.703368048	0.017666315
cg17127132	73857073.37	23.34233079	2.3369E+14	0.0176687
cg26387998	6.52502E+13	252.0709434	1.69E+25	0.01767403
cg02244695	0.133690388	0.025357994	0.704831778	0.017674652
cg01092036	0.000453945	7.85E-07	0.262408537	0.017679107
cg03970351	1.29321E+17	926.9994749	1.80E+31	0.017735167
cg21686900	13215098501	56.66733947	3.08183E+18	0.017757088
cg20506766	1.01341E+19	1951.566295	5.26E+34	0.01777232
cg05072008	0.286026463	0.101600853	0.805220972	0.017778643
cg09886641	0.070784925	0.007923379	0.632369787	0.01778137
cg16085042	1.57406E+11	86.51772908	2.86E+20	0.017789346
cg15448599	0.009862755	0.000215916	0.450517661	0.017841202
cg06090630	7.37633E+12	165.6220923	3.29E+23	0.017864891
cg07331806	0.068712358	0.007483597	0.630898217	0.017926511
cg23508052	5.83523E+13	233.2582761	1.46E+25	0.017927029
cg01837574	0.076773292	0.00916264	0.643279503	0.017945624
cg27268486	0.228388159	0.067168975	0.776566129	0.018033031
cg14538332	0.172072653	0.040010581	0.740029192	0.018056042
cg04743872	0.212253322	0.058730256	0.767091369	0.018057272
cg14203179	0.143860917	0.028802818	0.718539526	0.018139738
cg09721659	0.079461314	0.00971351	0.650032833	0.018194385
cg09299307	5726258.668	14.0862034	2.32781E+12	0.018206876
cg00424946	19530094118	54.65669635	6.97855E+18	0.018366217
cg19273182	1.40821E+11	76.19364993	2.60E+20	0.018373727
cg02523617	1287.379337	3.348114641	495008.6045	0.018379362
cg04322344	1.43279E+16	531.7062673	3.86E+29	0.018386996
cg26124016	0.097875902	0.014148092	0.677101348	0.018517296
cg16823737	2.61086E+12	121.0375656	5.63E+22	0.018521738
cg00704909	1161886401	32.65858696	4.13361E+16	0.01862595
cg18943599	0.094712021	0.013295852	0.674674086	0.018632498
cg17163751	0.25599972	0.08225511	0.796739033	0.018661262
cg19744122	5.05E+43	19169119.25	1.33E+80	0.018679243
cg11038843	0.133596636	0.024959665	0.715076144	0.018683542
cg18485154	3.86E+27	38417.38916	3.88E+50	0.018743049
cg05284724	20729392.39	16.33359662	2.63082E+13	0.018798133

cg22068038	2.91834E+15	365.0614684	2.33E+28	0.018814103
cg01926595	4849.435329	4.079465553	5764731.362	0.018816667
cg07295678	0.205381957	0.054790747	0.769869922	0.018879691
cg01522975	984351.9234	9.774750314	99127719685	0.018882525
cg02755525	0.208921464	0.056530516	0.772117102	0.018888018
cg04735745	1.45502E+18	988.0264265	2.14E+33	0.01892848
cg17977409	0.217792805	0.060960437	0.778106391	0.01896842
cg14329157	0.163072547	0.035809249	0.742619754	0.019043299
cg11141013	7.83E+37	1638577.946	3.74E+69	0.019055361
cg05428978	9.27E+21	3997.237051	2.15E+40	0.019060437
cg23414431	0.001066391	3.49E-06	0.325855773	0.019076498
cg21692936	1000.029495	3.094422393	323181.1512	0.019122947
cg00930078	160477.4043	7.095205219	3629633887	0.019129973
cg15334028	3.74E+30	98702.34573	1.42E+56	0.019147271
cg06237414	1.39138E+16	431.2381303	4.49E+29	0.01916881
cg06207460	110.1663238	2.151789278	5640.245084	0.01920235
cg04051458	0.138249623	0.026384887	0.724390384	0.019205973
cg02162950	56747923.86	18.32090295	1.75773E+14	0.019216107
cg21123573	148.6918685	2.258223465	9790.559747	0.019219461
cg09416313	0.238195146	0.07166064	0.791744634	0.019232048
cg08351105	4.34E+21	3312.657531	5.69E+39	0.019243707
cg25094927	3.95833E+13	162.4798873	9.64E+24	0.019257788
cg17801256	544793.432	8.562963603	34660883464	0.019258326
cg08495878	0.184717831	0.044897759	0.75996392	0.01926766
cg16393207	0.111384139	0.01771435	0.70036023	0.01930274
cg04613791	28.00660651	1.716957046	456.8372926	0.019312462
cg08359956	0.097694628	0.013913459	0.685971804	0.019335173
cg03439703	0.126979354	0.022520851	0.715947901	0.019355084
cg03431064	33231645541	50.44911445	2.18902E+19	0.019365223
cg13650689	6.85998E+16	524.5988196	8.97E+30	0.019408499
cg16273788	22346100589	46.87362058	1.06531E+19	0.019421587
cg11473104	21667093.09	15.21487592	3.08555E+13	0.0194637
cg19531713	95413.94771	6.326835827	1438921708	0.019502989
cg17067528	83289.07232	6.189178361	1120838529	0.019504671
cg02772367	10883982.18	13.45445149	8.8046E+12	0.019571263
cg10045881	0.159760968	0.034213594	0.746006594	0.019667191
cg19784449	1.15E-07	1.69E-13	0.077923543	0.019677479
cg23964386	0.110482243	0.017343169	0.703811731	0.019713662
cg15188491	26781149.83	15.1377308	4.73803E+13	0.019797885
cg15410903	20.50348465	1.614893531	260.3223523	0.019827625
cg10235741	0.001191697	4.13E-06	0.343941895	0.019847739
cg26666286	0.037205503	0.00233143	0.59373409	0.019867574
cg04337944	0.124858526	0.021673601	0.719292183	0.01987208
cg00777555	11899735885	39.27600635	3.60535E+18	0.019893531
cg03048535	0.100034332	0.014399203	0.694959829	0.019916099
cg17775713	0.040990114	0.00277611	0.605231671	0.020044077
cg04223844	983374.0829	8.667246318	1.11572E+11	0.020145963
cg01161597	2.69E+20	1571.860055	4.59E+37	0.020151725

cg06392241	0.025740756	0.001173738	0.56450969	0.020184536
cg07520161	454081737.2	22.4553197	9.18224E+15	0.020206646
cg20103201	4.56E+20	1619.346919	1.28E+38	0.020317086
cg22468803	4925.083827	3.743824802	6479056.041	0.020328911
cg18349835	0.19229119	0.047748842	0.774383211	0.020356813
cg19028804	2998.229272	3.445986868	2608651.487	0.020437304
cg19238398	2574.544008	3.353791706	1976353.165	0.020505162
cg18695917	0.204156466	0.053240491	0.782860219	0.020506939
cg06235991	600550.5515	7.752140163	46524051076	0.020530046
cg16957313	0.009758365	0.000194141	0.490497115	0.020538001
cg09419116	1.11057E+16	294.0156392	4.19E+29	0.020542374
cg02548238	0.178533456	0.04154035	0.767306843	0.020558539
cg03802231	5579.251153	3.76575619	8266080.397	0.020562441
cg01692572	135.2762681	2.124211465	8614.805553	0.020588604
cg27320127	0.187115658	0.045285579	0.773143904	0.020590719
cg18591973	2079.460568	3.227688717	1339706.717	0.020611137
cg20162159	3.45936E+13	118.324223	1.01E+25	0.020649547
cg05670275	1.50306E+12	72.8758257	3.10E+22	0.020673412
cg08623787	0.245682421	0.074806379	0.806881085	0.020687571
cg22753607	4806945604	30.16482353	7.66016E+17	0.020695596
cg08909157	0.117139058	0.019035526	0.720839505	0.020720024
cg14634336	369356210.7	19.91404434	6.85064E+15	0.020871829
cg00314943	5.85E-05	1.50E-08	0.228228467	0.020878191
cg14135551	0.279121939	0.094500796	0.824427518	0.020923998
cg12814525	23789.75828	4.578130717	123620891.1	0.020973299
cg13114389	33798848960	38.56997816	2.96179E+19	0.021020127
cg09660171	0.200439991	0.051162641	0.785264185	0.021058392
cg14126210	94456427477	44.55647683	2.00E+20	0.021083309
cg02269221	1.37751E+12	66.31680393	2.86E+22	0.021110089
cg08197201	1.53372E+14	133.2336169	1.77E+26	0.021154312
cg21552947	8251265.02	10.85040024	6.27473E+12	0.021164157
cg19987840	1.8555E+16	271.9833558	1.27E+30	0.02117299
cg11822964	0.040141922	0.002603627	0.61889577	0.021236789
cg10337772	21.38403035	1.578561175	289.6794633	0.021262572
cg23668257	4.00198E+12	75.58934664	2.12E+23	0.021262791
cg19016517	1.76328E+15	186.954175	1.66E+28	0.021271173
cg10479325	4.87E+30	36871.98712	6.43E+56	0.021300046
cg22986077	0.173532738	0.039045261	0.77124882	0.021377056
cg22572159	0.286136764	0.098562653	0.830682261	0.02138525
cg15817236	0.28832866	0.099928908	0.831925593	0.021429996
cg10857774	0.047665755	0.003562479	0.637764961	0.021457119
cg26267341	4.62479E+11	52.92575129	4.04E+21	0.02146029
cg00177013	1365429.873	7.984053754	2.33515E+11	0.02156867
cg04281268	26286728706	33.8936247	2.04E+19	0.021600458
cg10601939	285478.671	6.324587136	12885911739	0.021603502
cg27583102	0.134509764	0.024286757	0.744968808	0.02161436
cg04794887	676476.6994	7.166640585	63854287017	0.021622728
cg08810065	1.73882E+15	169.505433	1.78E+28	0.02168937

cg11021744	0.242790221	0.072485372	0.813227405	0.021722892
cg10971750	1.70094E+11	43.58426784	6.64E+20	0.021735654
cg15473335	154468173.3	15.62639041	1.52693E+15	0.021763049
cg05668720	1.13804E+18	428.6320858	3.02E+33	0.021765948
cg02899772	0.216417017	0.058533355	0.800164722	0.021783435
cg12483860	3.01774E+14	122.4709888	7.44E+26	0.022008316
cg01488147	0.00696387	9.92E-05	0.488975017	0.022033986
cg16491909	4.67E-36	2.53E-66	8.64E-06	0.022146009
cg15810744	1.00841E+14	100.887893	1.01E+26	0.022180815
cg04367351	0.007079965	0.000101787	0.492458617	0.022182104
cg15042806	1014.576866	2.69121145	382491.7646	0.022192941
cg17704839	0.095774749	0.012823215	0.715327839	0.022223967
cg25162921	0.229081513	0.064738864	0.810615692	0.022277443
cg22262549	556273.5618	6.563469987	47145835386	0.022316107
cg03944089	0.018936813	0.000630405	0.568845282	0.022316755
cg16652259	0.136262095	0.024651978	0.753179253	0.022318515
cg05602212	1005931630	19.04921363	5.31202E+16	0.022325282
cg09329496	6.41E+36	163739.6831	2.51E+68	0.02240442
cg05522288	118816.9379	5.229473405	2699595856	0.022418593
cg10557828	0.145368766	0.02774039	0.761780129	0.02249342
cg06834261	2264125929	20.76404875	2.46882E+17	0.022537194
cg16722536	0.133914398	0.023788823	0.753844205	0.022579945
cg04065065	1036364462	18.43810792	5.82517E+16	0.022603521
cg12946690	14171.79611	3.818437575	52597378.11	0.022639378
cg21540749	8.5572E+11	46.66263654	1.57E+22	0.022685969
cg00107632	8.96527E+13	89.26466765	9.00E+25	0.022695667
cg00893242	0.015346821	0.000422197	0.55785491	0.022706995
cg14319409	0.19825126	0.049259112	0.797894251	0.022740583
cg08783491	2.26288E+17	257.315702	1.99E+32	0.022839911
cg08704884	1.67364E+11	36.15371633	7.75E+20	0.0228505
cg16353836	19117736.25	10.15894845	3.59769E+13	0.022937822
cg18123596	14813806774	25.31746964	8.66788E+18	0.022983671
cg11847459	98.46501418	1.88123419	5153.722524	0.023031804
cg06971096	0.291759881	0.100848329	0.844077723	0.023043629
cg01888601	0.24811586	0.074553206	0.825738874	0.023081453
cg24014661	0.043595355	0.002919424	0.65100337	0.023138247
cg07355551	133860.5551	5.022917614	3567378482	0.023183968
cg05668853	0.138265313	0.025053986	0.763044128	0.023191031
cg05531055	1.11155E+11	32.20546647	3.84E+20	0.023217993
cg21289924	2.12988E+17	231.5887307	1.96E+32	0.023225859
cg26159933	0.103890195	0.014696435	0.734407538	0.02324866
cg10019507	0.028733767	0.001338077	0.617026822	0.023296287
cg17902858	41788695459	27.79921192	6.28E+19	0.023306654
cg19709625	0.127682644	0.021566805	0.755923647	0.023308028
cg25432696	0.140853581	0.02589722	0.76609501	0.023309588
cg17976829	115542.1925	4.869243522	2741698620	0.023333996
cg15501381	0.102237993	0.014240634	0.733998736	0.023362835
cg05807768	11970556.26	9.107041479	1.57344E+13	0.023373534

cg26911140	5126532.682	8.108407071	3.24125E+12	0.023386021
cg14663792	1.04965E+15	108.0720718	1.02E+28	0.023397624
cg01372689	3.4648E+11	36.42422839	3.30E+21	0.023411201
cg09504352	4.98842E+13	71.25754067	3.49E+25	0.023418091
cg25124433	0.200159426	0.049797737	0.804530457	0.023427414
cg06141123	2.09233E+13	63.239511	6.92E+24	0.023427757
cg02631957	422967812.8	14.5955693	1.22573E+16	0.023466451
cg09149294	10.20799563	1.367234416	76.21456393	0.023518221
cg22777952	0.229652947	0.064272714	0.820573344	0.023553984
cg10971346	11544943690	22.45172454	5.93655E+18	0.023574822
cg08555772	0.240266112	0.069897992	0.825886453	0.023596999
cg04603184	0.248857864	0.074615771	0.829988562	0.023624929
cg19552482	4.19E-07	1.26E-12	0.139816965	0.023625146
cg05727959	13085110728	22.55418942	7.5915E+18	0.023659579
cg24058132	0.044140501	0.002948919	0.660711208	0.023811958
cg19836283	0.152452564	0.029834961	0.779011715	0.02381936
cg11675413	0.02170749	0.000783399	0.601500574	0.023827726
cg14026602	305332.3063	5.322003902	17517427457	0.02388261
cg08583049	0.112705136	0.016947525	0.749516382	0.023931321
cg00658626	0.172113132	0.037373227	0.79262437	0.023931487
cg01703884	0.05749318	0.004818902	0.685937534	0.023946213
cg25047102	3.58506E+11	33.48912396	3.84E+21	0.023948291
cg16348491	135028.0595	4.740159931	3846405422	0.023989228
cg19528976	0.207622475	0.052952905	0.814064724	0.024129579
cg19523029	18.99485748	1.468822395	245.6420953	0.024174461
cg23739862	0.184170132	0.042295609	0.801942286	0.024195242
cg04658354	8.52E-23	5.44E-42	0.001333754	0.024226468
cg24625388	0.226978664	0.062448057	0.824994663	0.024313651
cg06469542	0.10751856	0.015435371	0.748944809	0.024329972
cg08717396	10.30751586	1.352621851	78.54736571	0.02435584
cg13393195	55971779	10.06145752	3.1137E+14	0.02436628
cg06712026	8.543303819	1.319087625	55.33221505	0.024416834
cg02214188	7.155348829	1.288875125	39.72379936	0.024440361
cg12263485	158155713	11.36844707	2.20023E+15	0.02447297
cg12441964	1.54E-05	9.87E-10	0.24020236	0.024481087
cg20114394	0.047362671	0.003320985	0.675468975	0.024492064
cg06806080	0.126185649	0.020780726	0.766230097	0.024493364
cg25219047	9.06296E+11	34.09337454	2.41E+22	0.024568131
cg01667702	0.040216838	0.002441034	0.662585538	0.024583144
cg10544564	0.099696114	0.013336507	0.745271255	0.024677052
cg18342900	114915.9406	4.406452381	2996894612	0.024716004
cg21926138	0.193545824	0.046167243	0.811397515	0.024718866
cg20684399	86654818148	24.59052818	3.05E+20	0.024737157
cg22255355	3.29E+40	136315.9618	7.92E+75	0.02480741
cg21686523	135347.9213	4.460243529	4107188247	0.024837518
cg05028306	2.17827E+11	26.89850226	1.76E+21	0.024911227
cg15677132	17620382.49	8.17741382	3.79677E+13	0.024936405
cg22631938	0.208327337	0.052872914	0.820841443	0.024951323

cg14685339	508721514.8	12.4668406	2.07589E+16	0.024951651
cg15442702	1657863.955	6.046135278	4.5459E+11	0.024985906
cg23303408	0.119838203	0.018742974	0.766217502	0.025008466
cg03072102	7850527228	17.44237411	3.53339E+18	0.025013987
cg17391474	8.19E-06	2.90E-10	0.230974401	0.025074253
cg01722994	0.1374238	0.024200089	0.780381453	0.025103082
cg21985356	15812186526	18.76201983	1.33261E+19	0.025119585
cg01999523	562.5765343	2.197928676	143995.7358	0.025200025
cg00008493	5.91E-06	1.56E-10	0.22383005	0.02520322
cg03887534	9.44275E+16	127.327094	7.00E+31	0.025260006
cg27665659	308796.0662	4.78650176	19921649520	0.025281394
cg00784357	2.97249E+15	81.42926439	1.09E+29	0.025345172
cg15077070	0.212835654	0.054828531	0.826194215	0.025360629
cg08680102	2.16335E+12	33.24793297	1.41E+23	0.025365546
cg20811273	956268762.9	12.79323104	7.14792E+16	0.025383033
cg04119538	26.43891898	1.496144157	467.211955	0.02542275
cg16420530	7.20443E+12	38.1561399	1.36E+24	0.025426121
cg23347400	2.02187E+13	43.26051229	9.45E+24	0.025433649
cg14334099	4.08812E+11	26.66471699	6.27E+21	0.025460035
cg19872681	0.145871307	0.026948813	0.789587232	0.025473585
cg09068528	0.185844416	0.04242655	0.814069178	0.025554621
cg26499611	0.145817864	0.026903944	0.790324624	0.025558784
cg11368509	848052235.2	12.28146588	5.85592E+16	0.025595123
cg15563993	8.64684E+14	65.09401242	1.15E+28	0.025693328
cg10869376	3529151163	14.37318572	8.66538E+17	0.025722699
cg16893574	0.094256608	0.011826508	0.751219896	0.025742534
cg26217633	12947995.01	7.256484075	2.31036E+13	0.025759459
cg15061008	37291772.17	8.205616663	1.69479E+14	0.025808735
cg10091705	1.27783E+14	50.03850488	3.26E+26	0.025853617
cg04419707	4.41337E+13	43.57244081	4.47E+25	0.025909
cg05876094	1073458943	12.14658804	9.48673E+16	0.025917559
cg05468303	0.163075737	0.03305264	0.804586144	0.025950212
cg22197787	0.094727548	0.011900262	0.754042899	0.025967956
cg05275752	0.00833902	0.000123276	0.564091994	0.025998201
cg23740844	336.7701617	2.000213219	56701.02606	0.026079419
cg12506373	19268.7838	3.235588259	114750703.6	0.026098933
cg26339797	3080078422	13.44177838	7.05776E+17	0.02611333
cg21017752	0.152650245	0.029114811	0.800351998	0.026188702
cg04726446	0.114072952	0.016828506	0.773249768	0.026193888
cg00449941	3.99014E+17	120.6026971	1.32E+33	0.02622813
cg06622725	3.78E-07	8.21E-13	0.174213312	0.026242434
cg23699324	0.228903776	0.062321247	0.840755626	0.026332414
cg26336164	1.13381E+14	44.91266066	2.86E+26	0.026344575
cg26406994	1.49507E+12	26.88666801	8.31E+22	0.026370028
cg14550570	5.10688E+11	23.62128956	1.10E+22	0.026391247
cg10613440	3.93979E+12	29.84221685	5.20E+23	0.026425798
cg06938406	3.58998E+11	22.38817371	5.76E+21	0.02647002
cg09911342	0.024940277	0.000956919	0.650021301	0.02649377

cg24283842	2.14E+24	678.8741218	6.72E+45	0.026545433
cg12939527	2.7978E+15	61.77798223	1.27E+29	0.026623641
cg06688396	0.049629085	0.003487289	0.706292478	0.026649267
cg26265187	0.000853586	1.65E-06	0.441516948	0.026664122
cg17839278	524214529.1	10.19426256	2.69564E+16	0.026673672
cg00677811	6.83755E+15	67.03679289	6.97E+29	0.026726697
cg00887547	1606060.215	5.182359805	4.97733E+11	0.026760242
cg19728382	0.112240153	0.016204636	0.777422706	0.026764323
cg22670349	9.14905E+11	23.75048472	3.52E+22	0.026782554
cg01656955	0.255534909	0.076386325	0.854840051	0.026792343
cg05670408	0.123892034	0.019507688	0.786830099	0.026818507
cg06910048	1.90689E+13	33.1909257	1.10E+25	0.026864742
cg09203961	46595219.03	7.525626598	2.88496E+14	0.02690351
cg08638395	2.65018E+13	33.8898499	2.07E+25	0.026958733
cg21379816	174706555.3	8.691490258	3.51175E+15	0.026967444
cg06392589	0.051057256	0.003658381	0.712567602	0.026970728
cg11766698	3.09066E+18	126.540717	7.55E+34	0.027008964
cg11141561	6272990.978	5.91728239	6.65008E+12	0.027027202
cg14106632	823617583.4	10.286228	6.5947E+16	0.027036449
cg25503559	23612429.39	6.871315338	8.11412E+13	0.02703826
cg06587969	25196899.52	6.909352693	9.18876E+13	0.027057042
cg25270252	348232306.6	9.281760222	1.3065E+16	0.027080541
cg13991233	0.210543922	0.052873301	0.838395599	0.02710643
cg15787039	0.191735739	0.044299226	0.82986988	0.027144689
cg17940740	0.099304713	0.012795746	0.770680014	0.027166475
cg21762107	2.06993E+18	116.3345382	3.68E+34	0.027166861
cg04988423	0.260163419	0.078779781	0.859167209	0.027174959
cg01994779	0.033125888	0.001610903	0.68118581	0.027186046
cg26069745	0.17107107	0.035697147	0.819822122	0.02721282
cg12489819	8.97E-19	8.57E-35	0.009389687	0.02724411
cg07496902	0.019969129	0.000618433	0.644801356	0.027280539
cg21625881	0.0592425	0.004817255	0.728562994	0.027292827
cg23859078	1.17358E+11	17.33045733	7.95E+20	0.027317717
cg09775312	0.243239274	0.069305678	0.853686821	0.027320178
cg00427635	0.113496174	0.016426698	0.784173492	0.027349143
cg21300561	1.35882E+11	17.48362534	1.06E+21	0.027369236
cg05442902	0.025535645	0.000981434	0.66440457	0.027393182
cg07175883	0.202772184	0.049118303	0.837092414	0.027399813
cg12460105	29657915.95	6.788850929	1.29564E+14	0.027420642
cg20923575	7.4709E+12	26.92886418	2.07E+24	0.027459058
cg16022344	32767296752	14.67439609	7.32E+19	0.02748711
cg15873301	0.352815055	0.139728673	0.890858409	0.027488199
cg23576473	1.77986E+13	29.41161126	1.08E+25	0.027506177
cg13896604	8.06218E+13	34.66180859	1.88E+26	0.027523452
cg09322949	2480.055069	2.375818872	2588864.503	0.027526167
cg05203877	0.286460291	0.094188269	0.871228432	0.027604056
cg23357981	0.201357371	0.048344315	0.838667191	0.027689183
cg01507173	0.141020897	0.024646098	0.806898265	0.027732422

cg01530101	0.186444859	0.041772323	0.832170269	0.027758988
cg17296078	0.133513984	0.022214038	0.802464799	0.027774325
cg18264687	0.006588413	7.51E-05	0.577984157	0.02779909
cg19850348	0.266322733	0.081940595	0.865600234	0.027809795
cg26974738	87.49286808	1.627225802	4704.326808	0.027846203
cg20906802	0.106185559	0.014392114	0.783441076	0.027855431
cg18508525	6.084455625	1.216827839	30.42386035	0.027881825
cg19448990	4829796191	11.26779624	2.07023E+18	0.027892867
cg20066677	0.042956973	0.002597282	0.710474151	0.02789595
cg13878641	6832411.068	5.520837824	8.45557E+12	0.027901744
cg00648153	189547.9429	3.737177803	9613784668	0.027916348
cg09201327	0.080362207	0.008480296	0.76153995	0.027992742
cg06638433	0.28301822	0.091747	0.873045576	0.028078576
cg13918581	1.63E+20	145.3296242	1.83E+38	0.028181103
cg13936125	0.291559855	0.096974796	0.876590127	0.028200642
cg05741384	427537674.6	8.327131881	2.1951E+16	0.028239063
cg05647859	0.375232406	0.156282253	0.900929924	0.028277229
cg24906202	8237.83246	2.609180809	26008885.02	0.028289508
cg18284523	142655.2101	3.525876724	5771758502	0.028322675
cg00293409	0.250204969	0.072499853	0.863484873	0.028364395
cg12802819	2.16E-11	6.30E-21	0.074205816	0.028369471
cg15368822	23746841060	12.53010529	4.50046E+19	0.028385714
cg05417985	44.64740637	1.494691731	1333.646835	0.028389051
cg19280968	0.133678207	0.022074179	0.809536929	0.028531269
cg13603099	15265991040	11.67181204	1.99669E+19	0.028568741
cg09072120	0.008920027	0.000130344	0.610439827	0.028605245
cg09874600	11106540126	11.19082286	1.10229E+19	0.028635967
cg22386774	6.313964731	1.21210667	32.88996884	0.02864018
cg00327185	6.35151E+19	114.520371	3.52E+37	0.028714517
cg05559445	0.154721013	0.029047785	0.824110743	0.028768859
cg10066332	332651.002	3.734194575	29633348475	0.028776398
cg22571530	0.240525765	0.067057064	0.862737499	0.028777452
cg11820497	4.83218E+11	16.21614547	1.44E+22	0.028788317
cg19490266	723524288.9	8.14169019	6.42971E+16	0.028923776
cg13135180	1.1802E+13	21.74382552	6.41E+24	0.029011425
cg26514942	0.000193274	8.94E-08	0.418019145	0.02906648
cg04211818	1.92E+52	214058.6865	1.73E+99	0.029074504
cg05702952	4978291003	9.723468032	2.55E+18	0.029089838
cg22088594	0.155137982	0.029093665	0.827252047	0.029107046
cg23213688	936524.8969	4.032034472	2.17528E+11	0.02917339
cg09712606	2.90109E+17	58.16140646	1.45E+33	0.029236164
cg00327483	0.017494628	0.000460416	0.664750595	0.029258413
cg21643860	2596372.861	4.438749075	1.51871E+12	0.029262136
cg08983259	0.000688014	9.87E-07	0.479722932	0.029267937
cg15649193	117021810.4	6.505377015	2.10504E+15	0.029281739
cg19370515	1.92364E+15	34.66265359	1.07E+29	0.029290695
cg03079549	69044487913	12.29974457	3.88E+20	0.029326152
cg26523389	8.83E-11	7.94E-20	0.098340099	0.029391746

cg19308222	0.242878274	0.067957901	0.868035288	0.02942513
cg06615667	36186335008	11.37271456	1.15E+20	0.029425401
cg01025762	638028548	7.570529116	5.37717E+16	0.029453368
cg07965839	17591097.5	5.272650969	5.8689E+13	0.029487801
cg07093046	26404961.47	5.47316691	1.27389E+14	0.029521087
cg15104484	1.08384E+17	48.77103776	2.41E+32	0.029588044
cg13756879	0.352372399	0.137687557	0.901797595	0.029588486
cg08605641	15952733295	10.17117032	2.50207E+19	0.029654127
cg21700166	0.115984571	0.01662773	0.809035322	0.029720572
cg02318535	0.207148365	0.050096352	0.856558283	0.029723892
cg23772500	1.73811E+11	12.66646384	2.39E+21	0.029768968
cg06039392	0.148745597	0.026670355	0.82958222	0.029778377
cg10887021	0.246785799	0.06985694	0.87182792	0.029782207
cg06606198	3.09094E+15	32.94618881	2.90E+29	0.029789781
cg26661257	2.70884E+19	80.06297639	9.17E+36	0.029796317
cg11206763	6.03872E+12	17.85427407	2.04E+24	0.029798377
cg20103758	0.267446701	0.081357897	0.879173877	0.029852269
cg22704775	230817993.1	6.540893082	8.14521E+15	0.029873163
cg01870826	0.234498564	0.063314979	0.868508165	0.029931339
cg19918758	0.236958879	0.064558207	0.869750156	0.029983685
cg27661264	0.102057088	0.012993621	0.801597137	0.029986835
cg26964415	189375629.6	6.293047813	5.69885E+15	0.03005761
cg15432938	31674226.64	5.282914377	1.89906E+14	0.030082739
cg20349695	249092651.5	6.44383855	9.62891E+15	0.030083755
cg11151811	3.50103E+12	15.90301531	7.71E+23	0.030191147
cg22685463	569973580.5	6.867676107	4.73042E+16	0.030229178
cg07006042	2048288.352	3.990329441	1.05141E+12	0.030292309
cg24743310	0.0094271	0.000138122	0.643418585	0.030417514
cg16286776	3.22E+37	3514.537398	2.94E+71	0.030418303
cg21134096	0.180779523	0.038394599	0.85119356	0.030481418
cg15100639	1.46266E+17	41.34796818	5.17E+32	0.030485582
cg16189954	235858.8913	3.202143758	17372554398	0.030502854
cg25932713	6.585085433	1.193551471	36.33136167	0.030540146
cg13739345	20796.577	2.542625266	170098842.6	0.030542794
cg24739326	0.153335678	0.027994995	0.839858343	0.030687423
cg06637893	0.10966105	0.014768041	0.814295273	0.030711645
cg07068998	82.90396477	1.507192264	4560.179573	0.030725545
cg06417962	0.143658765	0.024709883	0.835205928	0.030736033
cg00059225	0.159927259	0.030312002	0.843782218	0.030762143
cg25605045	1264744854	6.957438255	2.29909E+17	0.030782398
cg11154542	0.104848067	0.013543951	0.811662535	0.030787851
cg00686623	4559245183	7.799960548	2.66498E+18	0.030818677
cg25396537	1.64956E+12	13.28807896	2.05E+23	0.030893139
cg23311628	8.87E+58	260860.4178	3.01E+112	0.030906298
cg13966710	0.049645674	0.003244722	0.759600635	0.030964967
cg15843217	0.023724157	0.00079271	0.710014965	0.030970312
cg23131007	0.075768498	0.007266153	0.790083194	0.031010361
cg25682936	290804476.9	5.903943075	1.43239E+16	0.031049048

cg27014642	23756610.07	4.69923478	1.201E+14	0.031049074
cg25519930	0.268373546	0.081167654	0.887352979	0.031096215
cg10042178	93887647.2	5.283630216	1.66834E+15	0.031129752
cg18211447	20074232	4.573216034	8.81163E+13	0.031179507
cg27600136	0.120292253	0.017522901	0.825789412	0.031184303
cg18277754	0.280607536	0.088314006	0.891597979	0.03120158
cg06243556	0.296961471	0.098399353	0.896206249	0.031207807
cg22470827	1.44838E+13	15.26248588	1.37E+25	0.031267397
cg01852131	17778996992	8.348614847	3.78617E+19	0.031271238
cg15842276	0.084604911	0.008932878	0.801308491	0.031313216
cg23709121	2541577.064	3.745539401	1.72462E+12	0.031340776
cg21282997	5.143858537	1.157898345	22.85112572	0.031345624
cg13846555	163731920.7	5.431414055	4.93576E+15	0.031353961
cg05361811	8730159833	7.751115118	9.83287E+18	0.031354939
cg15158783	0.18574111	0.040088702	0.860585609	0.031405972
cg01618304	108964191.7	5.204081296	2.28152E+15	0.031417537
cg08961832	0.11204069	0.015255061	0.822882092	0.031430169
cg17810944	0.026110721	0.000942715	0.723198247	0.031460182
cg23173032	15866.64881	2.355533576	106876228.4	0.031519106
cg21256656	0.024675644	0.000845127	0.720468584	0.0315228
cg07312445	0.047073732	0.002903895	0.763091118	0.031539469
cg18022322	9.20692E+12	13.95888357	6.07E+24	0.031570073
cg03101664	0.089603131	0.009933334	0.808260434	0.031582689
cg10453365	0.11975409	0.017291565	0.829366334	0.031598797
cg13342120	174774302.3	5.314867328	5.74728E+15	0.031624298
cg06076054	1.57265E+16	26.62487841	9.29E+30	0.031627979
cg10458581	8.77E+22	102.5237846	7.51E+43	0.031694415
cg27493997	0.073920661	0.006864674	0.795997667	0.031703851
cg11047295	6.30969E+12	13.10404326	3.04E+24	0.031759178
cg25905459	1.83463E+13	14.38168038	2.34E+25	0.031760046
cg22886089	0.233618424	0.061922431	0.881386064	0.031846292
cg16394138	322879.2533	3.008465654	34652551895	0.031846842
cg05950276	0.000580009	6.42E-07	0.52404727	0.031869922
cg05595345	5.607054098	1.160834642	27.08314735	0.03190734
cg17642353	0.153873032	0.027828562	0.85081328	0.031941943
cg18226566	409.6330762	1.678917023	99944.93765	0.03197628
cg19614321	0.183531211	0.03897861	0.864158708	0.031980574
cg14800883	0.008831942	0.000117217	0.665461835	0.031980661
cg14707431	1.41E+26	176.2514044	1.13E+50	0.032022187
cg15205507	0.326302978	0.117217164	0.908345072	0.032033085
cg00755043	0.191049676	0.042048064	0.868053722	0.032098626
cg14174099	0.308095709	0.10497223	0.904267405	0.03210162
cg27560864	0.112185538	0.01516175	0.830088547	0.032166663
cg15361590	0.214822829	0.052579634	0.877694357	0.032223348
cg21085625	39.24358495	1.364958971	1128.282235	0.03223196
cg02887841	0.161118278	0.030271991	0.857528664	0.032343037
cg22432367	7.68E+19	46.32961502	1.27E+38	0.032422071
cg21430666	0.001004667	1.80E-06	0.561197838	0.032438767

cg27416067	0.25284903	0.071726454	0.891339649	0.032443335
cg26160573	0.11636246	0.016203052	0.835658729	0.032480442
cg25824330	2.21977E+16	22.96775255	2.15E+31	0.032517612
cg08233173	9.00369E+13	14.38236695	5.64E+26	0.032573539
cg16685860	4.47E+20	50.97341326	3.91E+39	0.032628851
cg08907850	9.25125E+11	9.739584812	8.79E+22	0.032642009
cg00666746	0.144768594	0.024578053	0.852709773	0.032673381
cg09507928	427.1233066	1.646794904	110781.445	0.032690562
cg13755535	240566.5861	2.770257737	20890576929	0.032713562
cg00901766	2.99946E+11	8.757734218	1.03E+22	0.032736899
cg06422693	13769.44397	2.186021865	86731789	0.0327459
cg03589001	0.197456833	0.044528282	0.87560533	0.032779473
cg20988728	4496491198	6.161935016	3.28118E+18	0.032793783
cg00032227	2.47E+38	1375.663297	4.44E+73	0.032805955
cg13322449	0.081562113	0.008162954	0.814947464	0.032825654
cg05602615	5.73398E+17	27.78886237	1.18E+34	0.032889928
cg06230736	0.299338351	0.098831995	0.906623896	0.032896597
cg09535168	1.98179E+15	17.48453052	2.25E+29	0.032903492
cg20193288	23468836.77	3.967594789	1.38821E+14	0.032909003
cg12661229	2.95E+21	55.14262477	1.58E+41	0.032926507
cg18220560	0.010722991	0.000165876	0.693184756	0.032986269
cg27508821	75123408.03	4.318825661	1.30673E+15	0.03301045
cg14797438	484389016.7	5.018017312	4.67581E+16	0.033013351
cg10805447	1.13485E+13	11.26631661	1.14E+25	0.033030966
cg15804973	0.028196748	0.001059716	0.750254479	0.033039531
cg26232187	0.227652355	0.058363116	0.887985391	0.033086692
cg16150435	0.112796628	0.015153929	0.839589469	0.033115445
cg13643796	0.338978784	0.125295531	0.917084709	0.033137196
cg20011352	0.198369328	0.044770767	0.878930448	0.033181542
cg20727114	0.162826146	0.030622024	0.865793634	0.033254516
cg09469394	2750.748814	1.874460932	4036690.713	0.033265686
cg02583151	0.08855798	0.009502221	0.825335005	0.033293733
cg14662756	0.006675365	6.62E-05	0.673052129	0.033322776
cg17232861	0.000532475	5.14E-07	0.551321736	0.033331852
cg03532005	3049.315438	1.881101675	4943020.765	0.033376422
cg24977709	1.9066E+11	7.715148501	4.71E+21	0.033394735
cg09656405	120976252.5	4.299399229	3.40402E+15	0.033451814
cg21972430	0.138330843	0.022342856	0.856444754	0.033456723
cg22517351	9.64104E+13	12.40519083	7.49E+26	0.03348303
cg13301933	0.229788554	0.059229495	0.89149468	0.033502547
cg25484319	0.018088396	0.000447496	0.731158136	0.033514788
cg26535072	0.077618108	0.007348987	0.819782508	0.033570779
cg12909005	2749.379004	1.850173844	4085607.918	0.033580588
cg17675882	482.9346957	1.615253515	144389.669	0.033601
cg13118748	3.17308E+19	32.52452982	3.10E+37	0.033609804
cg15014549	0.210802689	0.050139156	0.886288832	0.033611003
cg07833035	1.03275E+15	14.54985945	7.33E+28	0.033627447
cg18731014	2.14468E+18	26.24411021	1.75E+35	0.03363545

cg16793061	0.321948959	0.113146389	0.916079897	0.033649361
cg03000603	1.76808E+11	7.357110406	4.25E+21	0.033703256
cg26018901	0.159690418	0.029367174	0.868351491	0.033724795
cg09926892	2335811869	5.250366277	1.03917E+18	0.033738645
cg20864636	5.91E-11	2.13E-20	0.164010342	0.033760324
cg11453347	14543.05095	2.085957563	101392441.9	0.033770802
cg26952662	0.138963483	0.022436827	0.860676484	0.033902612
cg26620356	0.183220133	0.038192377	0.878961193	0.033902974
cg16169604	0.025307973	0.000846964	0.756222623	0.033907489
cg22407574	8.55122E+18	27.24520943	2.68E+36	0.033943394
cg08983975	2.32427E+13	10.22959963	5.28E+25	0.033993674
cg09916853	0.073452449	0.00656104	0.822318154	0.034115879
cg25619607	0.006183869	5.58E-05	0.685299575	0.034235391
cg20695562	12213.96646	2.011246459	74173394.27	0.034245217
cg17539235	66.99493776	1.366205862	3285.245519	0.034253155
cg07489134	20552353.66	3.4889519	1.21068E+14	0.034253547
cg24073161	1.13E+21	36.39900622	3.48E+40	0.034264338
cg12515638	0.289344374	0.091763202	0.912350107	0.03430057
cg04135543	1.42428E+12	7.864008558	2.58E+23	0.034353993
cg17484237	4.96398363	1.125209986	21.8991422	0.034366497
cg18697049	57130742822	6.179502885	5.28E+20	0.034385804
cg04270788	241723571.5	4.094323448	1.4271E+16	0.034484285
cg11109684	13706722	3.319067581	5.66045E+13	0.034488382
cg02862835	10265442577	5.373405296	1.96113E+19	0.034500225
cg02676865	0.138620074	0.022187098	0.866067525	0.034533958
cg24653181	0.2031907	0.04632875	0.891162837	0.034624093
cg03513163	0.306649736	0.102406686	0.918241418	0.034652923
cg21718857	0.005885906	5.01E-05	0.691226546	0.034700831
cg08032971	0.023470234	0.000720632	0.764401111	0.034761055
cg07803864	0.04990403	0.00308577	0.8070635	0.034780176
cg05027081	680066524	4.253517661	1.08731E+17	0.034843051
cg12830829	7661.136606	1.883606102	31159919.29	0.034919371
cg04600406	6746626.91	3.043879822	1.49536E+13	0.03492053
cg01809579	1386810400	4.432289262	4.33916E+17	0.034931895
cg18502522	65634.6562	2.190351625	1966765539	0.034940391
cg02735486	0.166798237	0.031571965	0.881213823	0.034956279
cg12839593	0.109497094	0.014007026	0.855971386	0.035014247
cg10497569	4.02091E+11	6.53247509	2.47E+22	0.035028376
cg14962548	6.47984E+17	17.54485148	2.39E+34	0.035104596
cg14211646	18872.56793	1.977538477	180109678.9	0.035221516
cg17703212	0.154624298	0.027208002	0.878736816	0.035222928
cg18847227	0.231771912	0.059417524	0.904080405	0.035277308
cg22136753	0.101872309	0.012145219	0.854489912	0.035301741
cg06058319	1075350.541	2.59401028	4.45788E+11	0.035343741
cg24754277	0.175925822	0.034867874	0.887633557	0.035351582
cg03347966	6.38015E+16	14.12731961	2.88E+32	0.035382766
cg06528936	348985294.3	3.827395106	3.18208E+16	0.035422781
cg16160720	4.54944E+15	11.67860383	1.77E+30	0.035435398

cg17168535	28548589.13	3.220044688	2.53109E+14	0.035445437
cg04964702	6293819142	4.648684081	8.52116E+18	0.035448567
cg02553486	0.253316688	0.070446834	0.91089039	0.03547439
cg05806233	0.151945734	0.026233437	0.880079334	0.03550904
cg15555727	3.53888E+14	9.621086641	1.30E+28	0.035551505
cg10994430	0.107834992	0.013514151	0.860459913	0.035571418
cg21219744	41205935.9	3.252056423	5.22109E+14	0.035615508
cg20191453	0.22212557	0.054576779	0.904043245	0.035656328
cg11494699	5.55800276	1.121644489	27.54116388	0.03568071
cg01993411	467478.361	2.383127998	91701334618	0.035761453
cg16854524	590.6133521	1.527070502	228426.9988	0.035796149
cg15615135	7337.655472	1.791657581	30051047.93	0.035960378
cg15881088	2.0986E+11	5.452113421	8.08E+21	0.036051615
cg20899053	904.4540739	1.552969327	526756.8119	0.036130263
cg26408937	31539339.49	3.038936012	3.27328E+14	0.036187638
cg13258606	1.9959E+18	14.94107618	2.67E+35	0.036227337
cg18690395	10.86495079	1.165192141	101.3113216	0.036244234
cg00231920	11646691479	4.413408578	3.07348E+19	0.036251251
cg08268266	142.7305094	1.373506695	14832.10704	0.036267278
cg16862838	6.65037E+14	8.847496272	5.00E+28	0.036286652
cg11086568	3.44064E+12	6.318206077	1.87E+24	0.036289728
cg04730731	6.07575E+11	5.637879949	6.55E+22	0.036313226
cg16004226	0.195667912	0.04247971	0.901275744	0.036318286
cg03999420	3.05489E+12	6.237244416	1.50E+24	0.036326513
cg08305742	3.0291E+16	11.17254634	8.21E+31	0.036342364
cg24783979	0.093229295	0.010105409	0.860103875	0.036358562
cg00466544	1.4795E+12	5.925470868	3.69E+23	0.0363629
cg17756392	8.89603E+15	10.27778975	7.70E+30	0.036372536
cg24602243	929.7665427	1.542223242	560532.2239	0.03638476
cg09130402	310.5664283	1.436098488	67162.18083	0.036447127
cg21046940	3028902.453	2.549665708	3.59822E+12	0.03651811
cg22748452	0.173118156	0.033420658	0.896747622	0.036633356
cg13298382	9.09829E+11	5.501891722	1.50E+23	0.036677297
cg23269225	4.75852E+13	6.99718123	3.24E+26	0.036706615
cg00568128	5949389519	4.004118587	8.83971E+18	0.036733464
cg25752527	1908131981	3.721534495	9.78351E+17	0.036762476
cg14764661	0.225985289	0.055955432	0.912679055	0.036774801
cg21872391	304299931.8	3.305549771	2.8013E+16	0.03682035
cg14086647	6.9796E+12	6.065862519	8.03E+24	0.036871142
cg07050831	5197.935668	1.683800142	16046165.18	0.036882332
cg19678067	6.04523E+13	6.902097057	5.29E+26	0.036886614
cg17384214	0.016295342	0.000341165	0.778327471	0.036887498
cg23442323	0.157787551	0.027853855	0.893840757	0.036906571
cg05764061	529170.3181	2.226931064	1.25743E+11	0.036912333
cg08897388	0.251680345	0.068868656	0.919765242	0.036937566
cg16551261	0.094735222	0.01035254	0.866914076	0.036942316
cg26568669	9.30882E+15	9.239606336	9.38E+30	0.036968377
cg20492933	74093.61551	1.961036922	2799469913	0.037050766

cg08332868	1.46184E+15	8.126418009	2.63E+29	0.037063053
cg13640200	0.115461327	0.01517196	0.878681337	0.037081421
cg21751787	90110631361	4.50092728	1.80E+21	0.037136381
cg15054260	67772024.71	2.926057185	1.56971E+15	0.037155214
cg23128146	2.06E-19	5.49E-37	0.077362073	0.03716761
cg04719491	0.118716586	0.015993987	0.881182877	0.037192734
cg10996143	95563.21712	1.972206837	4630512528	0.037219508
cg09001953	0.049871034	0.002969271	0.837619725	0.037245141
cg14047667	0.04131727	0.002060279	0.828585217	0.037262565
cg18491230	1427068.305	2.285693922	8.90987E+11	0.037399061
cg03349953	0.261028448	0.073684831	0.924693041	0.037407713
cg16893614	0.002879333	1.17E-05	0.711102794	0.037410518
cg26404725	0.00523464	3.71E-05	0.737740878	0.03748525
cg10806140	0.295048038	0.093425569	0.931793573	0.03749193
cg05492605	4696973106	3.612743966	6.10659E+18	0.037532227
cg09002165	2.67E+51	901.4409916	7.91E+99	0.037576232
cg11126134	0.188997293	0.03929639	0.908988761	0.037613442
cg13041032	8.85E-05	1.34E-08	0.586025567	0.037616241
cg15637528	6.34E-08	1.04E-14	0.387251133	0.037620283
cg13155059	293373201.1	3.049383103	2.82247E+16	0.037631759
cg23526055	104361.2699	1.928224581	5648343432	0.037705679
cg07845392	0.128960719	0.018677325	0.890430886	0.037738708
cg15309264	2719.15983	1.561564761	4734885.396	0.037799521
cg18453621	0.310507235	0.102959189	0.936436503	0.037841314
cg23397015	0.303356769	0.09836422	0.935556945	0.037904129
cg02131995	0.174412578	0.033528451	0.907281624	0.037929728
cg00949554	0.015562655	0.000305334	0.793216681	0.037943864
cg25255854	3.64123E+14	6.399028819	2.07E+28	0.038002583
cg03383661	19585816.48	2.526948017	1.51805E+14	0.038032951
cg01745657	82.14021921	1.275475003	5289.806227	0.038036445
cg03782453	0.17642204	0.034249393	0.908767533	0.038046868
cg17987231	7.25488E+11	4.49426471	1.17E+23	0.038070404
cg25346576	128.7661294	1.305045736	12705.0843	0.038115913
cg10075436	3.33049E+12	4.844278993	2.29E+24	0.0381331
cg14939691	5.49514E+14	6.405580041	4.71E+28	0.038133242
cg24399106	0.171621242	0.032399547	0.909082164	0.038263034
cg24046110	0.248190588	0.066415343	0.927474971	0.038274564
cg17651821	0.226122803	0.055391886	0.923086856	0.038314209
cg12359315	0.084571272	0.008168911	0.87555128	0.038320335
cg26683023	0.144482146	0.023160551	0.901320994	0.038340734
cg25985103	0.005613368	4.16E-05	0.757399118	0.038358748
cg15219393	3.75E-05	2.43E-09	0.579378421	0.038370148
cg23051655	5.05E+21	14.3381871	1.78E+42	0.038426085
cg26932976	1.79703E+17	8.288557011	3.90E+33	0.038437277
cg03986968	56606299408	3.714934268	8.63E+20	0.038483655
cg26332534	0.188108599	0.038651278	0.915489654	0.038515587
cg14217534	270214.7946	1.933071549	37772029310	0.038546177
cg20199629	0.104540875	0.012302967	0.888305628	0.038597492

cg10040059	3.63722E+13	5.131193598	2.58E+26	0.038613102
cg16306381	4724167.295	2.235018548	9.98549E+12	0.038621505
cg24194132	0.226722805	0.055500825	0.926170562	0.038755044
cg22068473	999791371.2	2.917226564	3.42648E+17	0.038758682
cg15065896	1.34882E+11	3.734992033	4.87E+21	0.038809037
cg12317676	4.44456E+17	8.059337882	2.45E+34	0.038822225
cg03402876	0.056916996	0.003752968	0.863195248	0.038827717
cg06533629	0.272377498	0.079301014	0.935542904	0.038847833
cg05120641	44128736751	3.484119565	5.59E+20	0.038910424
cg01129459	0.233509061	0.058701629	0.9288751	0.038951841
cg24362016	0.211297277	0.048290782	0.924535441	0.039003162
cg11553177	13966.10673	1.617335389	120600920.9	0.03902431
cg22062239	12927634927	3.226775143	5.17928E+19	0.03903612
cg15448245	0.052578403	0.003204261	0.862753722	0.039076476
cg01520924	0.037293082	0.001639616	0.848231637	0.039091562
cg06291867	0.203150242	0.044688963	0.923494712	0.039114208
cg20188282	536.1880151	1.368387252	210099.5805	0.039120644
cg24680602	0.144776968	0.023080934	0.908124866	0.039128416
cg08349573	0.093968682	0.00993148	0.889103475	0.039162141
cg00791249	10091698.06	2.22377237	4.57971E+13	0.039192812
cg12197254	2.58015E+13	4.608895448	1.44E+26	0.039208738
cg00461841	0.140301385	0.021686629	0.907678105	0.039241316
cg05482722	2.27E-10	1.54E-19	0.334729142	0.039249153
cg07404485	0.172691759	0.032517362	0.917123701	0.03925399
cg15824705	3.72E-07	2.85E-13	0.484634606	0.039322873
cg09000510	133478.0437	1.774842674	10038291514	0.039387882
cg04402875	0.26762889	0.07635805	0.938017965	0.039402455
cg16427670	0.156068585	0.026646634	0.914089289	0.03944016
cg25784394	4.90006E+11	3.67404569	6.54E+22	0.03944362
cg02254407	0.236366896	0.059893286	0.932814227	0.039469456
cg11572744	0.30540095	0.098747071	0.944531716	0.039491748
cg09022993	0.037962831	0.001684865	0.855366263	0.039564813
cg01880569	0.22375017	0.053765292	0.931160916	0.039590059
cg05976074	0.057402065	0.003774681	0.872920755	0.039606052
cg19572947	802743061.7	2.648763927	2.43282E+17	0.039616695
cg06377278	0.334449899	0.117737706	0.950050237	0.039767276
cg02233558	10845830512	2.941629585	3.99887E+19	0.039785839
cg20375690	5.69E-11	9.71E-21	0.333393614	0.039812956
cg09113613	848.0202338	1.3680039	525684.4057	0.039832144
cg11646704	2.35E+20	8.831271874	6.23E+39	0.039838365
cg07656362	11445119674	2.891370137	4.5304E+19	0.039963245
cg00822607	1667793194	2.624809025	1.05971E+18	0.040045965
cg04785227	0.082464778	0.007615237	0.893004265	0.040065863
cg27635983	4.99E+30	24.44285375	1.02E+60	0.040092859
cg17188169	0.235138812	0.059017379	0.936847117	0.04012517
cg24098951	0.31080316	0.10181747	0.948742924	0.040133271
cg16639185	0.184014173	0.036534624	0.926825356	0.04016134
cg27090216	0.198829316	0.042481235	0.930601394	0.040237592

cg11747771	0.36723016	0.140991483	0.956497429	0.040264316
cg23692497	1.42785E+11	3.110987509	6.55E+21	0.040308466
cg11668844	0.164182417	0.029193762	0.923343361	0.040318069
cg00642303	12.49217166	1.117800327	139.6084335	0.040326301
cg03292388	0.292111666	0.090058788	0.947483605	0.040381972
cg06484397	0.116259164	0.014849487	0.910212804	0.040406841
cg07322981	40440332771	2.900886228	5.64E+20	0.04042996
cg15301525	2.68E+28	17.16733275	4.19E+55	0.040466608
cg02784848	0.037128175	0.001589776	0.867103998	0.040494695
cg01017147	0.173445282	0.032447726	0.927130179	0.040517659
cg11078738	0.359247196	0.134843635	0.95709781	0.040592232
cg25484373	3.64959E+12	3.402942293	3.91E+24	0.040696143
cg15528736	0.095577846	0.010088979	0.905455805	0.040703646
cg24461814	0.156058425	0.026342509	0.924522112	0.040714768
cg03209127	4.31736E+12	3.414196682	5.46E+24	0.040723663
cg14917512	0.180590986	0.035042094	0.930683654	0.04077295
cg08157638	0.000139718	2.83E-08	0.690180302	0.040814058
cg12530270	0.000838173	9.44E-07	0.744379082	0.040836354
cg12477012	169067126.6	2.201221624	1.29854E+16	0.040841532
cg05660795	0.128946148	0.01810727	0.918255972	0.040844246
cg00825031	2.60228E+13	3.600168053	1.88E+26	0.040878694
cg03552103	0.125710392	0.017218067	0.91782093	0.040903516
cg09649610	0.318798685	0.106526777	0.954056848	0.040947792
cg14364739	2.16774E+14	3.86648518	1.22E+28	0.040984212
cg15947959	4055144.185	1.863450622	8.82459E+12	0.040996912
cg26710722	0.178103833	0.034028019	0.932201663	0.041042769
cg02385474	0.134745194	0.019690033	0.922104471	0.041091273
cg03322749	41970234.98	2.033662471	8.66172E+14	0.041095289
cg01585758	14821771.65	1.948959145	1.12719E+14	0.04110103
cg16530429	0.200220758	0.042779767	0.937086728	0.041103567
cg10741760	0.241465299	0.061740747	0.944359974	0.041127933
cg13516796	4513341725	2.444861781	8.33186E+18	0.041142982
cg17524886	0.122391513	0.016295622	0.919245847	0.041170195
cg03812067	1556025427	2.335268148	1.0368E+18	0.041173264
cg12437239	2964055.362	1.815001678	4.84056E+12	0.04118828
cg05923103	297452.5066	1.647082623	53718005673	0.04127405
cg12977318	1.91766E+13	3.350343858	1.10E+26	0.041287268
cg18997662	496621.8465	1.677870615	1.46992E+11	0.041302653
cg03989322	1574.912052	1.335818469	1856800.18	0.041329929
cg23948756	2.48E+35	24.63678234	2.49E+69	0.041332612
cg26170257	0.00421801	2.20E-05	0.807341232	0.041370996
cg25355803	0.072128942	0.005765116	0.90242494	0.041389461
cg03423524	1.80832E+12	3.000989876	1.09E+24	0.041412965
cg01291404	0.263740521	0.07324783	0.949639912	0.04144834
cg25014318	0.257428825	0.069848739	0.948758713	0.041450017
cg11011938	0.095914963	0.010069967	0.913576027	0.041493489
cg14617642	0.270540141	0.076972032	0.95089042	0.041501643
cg02292024	93593.62854	1.553276265	5639542366	0.04151169

cg15488251	0.27142143	0.077455457	0.951122037	0.041520857
cg09754413	0.200921234	0.042932488	0.940298228	0.041535673
cg19100810	1940650.984	1.742114699	2.16181E+12	0.041539547
cg01169624	0.271324023	0.077391603	0.95122368	0.041540456
cg20648149	0.225922985	0.05397161	0.94570451	0.041711675
cg16114640	0.282039793	0.083413543	0.953639447	0.041716669
cg23478284	0.305982062	0.097869511	0.956631148	0.041730373
cg10978355	0.312838161	0.10219344	0.957671207	0.041777338
cg20940661	0.147420571	0.023328849	0.931585816	0.041820297
cg20229788	0.218642892	0.050549137	0.945707823	0.041883962
cg00115714	63220024.72	1.933161534	2.06748E+15	0.041888237
cg22878324	103655744.3	1.959145875	5.48428E+15	0.041943487
cg23639989	0.065706018	0.00476488	0.906062939	0.041986992
cg15384392	1.71734E+15	3.497258112	8.43E+29	0.042102715
cg17853587	0.163037348	0.028337245	0.938029684	0.04219201
cg15951107	168544043.3	1.949731482	1.45697E+16	0.042196926
cg11538128	0.248837762	0.065019989	0.952326084	0.042224619
cg05755779	0.083407298	0.007585089	0.917164945	0.042290482
cg22201387	1.82412E+13	2.877059296	1.16E+26	0.042333401
cg22968727	1.42358E+15	3.337505085	6.07E+29	0.042347758
cg12100077	226.4967154	1.203965134	42609.84033	0.042414355
cg00185839	2.51E+20	4.972004177	1.27E+40	0.042432868
cg16386080	0.119908208	0.015454664	0.930332624	0.042453667
cg07039362	4.95392505	1.055975768	23.24047023	0.042455661
cg20278498	5199914011	2.141217666	1.26279E+19	0.042456585
cg05038053	7.08222E+13	2.953222806	1.70E+27	0.042472981
cg07621046	0.209436126	0.046211518	0.949189575	0.042601435
cg04488521	0.266799829	0.074376091	0.957056872	0.042630539
cg05093686	0.171426459	0.031159053	0.943129772	0.042634896
cg13169373	0.029701402	0.000990884	0.890289314	0.042667857
cg11591325	0.260262203	0.070806305	0.956643829	0.042693051
cg24273512	0.156691579	0.026078595	0.941471393	0.042776526
cg01305625	0.222458146	0.05191159	0.953305929	0.042932033
cg23422659	0.208367796	0.045632179	0.951458806	0.042951546
cg01171858	0.000588703	4.38E-07	0.790451322	0.04297483
cg10089324	355461501.5	1.859573613	6.79472E+16	0.042998314
cg04296434	47737396669	2.164223616	1.05E+21	0.043021706
cg08635242	95226539574	2.211048227	4.10E+21	0.043024065
cg25537962	0.038058524	0.001603139	0.903509492	0.04309823
cg11485602	3404773125	1.96474768	5.90024E+18	0.043156971
cg09039698	119339.1371	1.428046265	9972946954	0.043219492
cg16969623	0.342851149	0.121435858	0.967975297	0.043235461
cg22524514	0.138902014	0.020485602	0.941820955	0.043244372
cg05800321	0.134360506	0.019177067	0.941371558	0.043301558
cg26490839	160331.5625	1.431051752	17963158846	0.043343649
cg14061619	0.080083629	0.006913811	0.927619749	0.043375026
cg08596544	18014208609	2.016892316	1.61E+20	0.043385964
cg26677448	0.198744713	0.041428499	0.953436937	0.043428695

cg24776019	2.43E-06	8.64E-12	0.685743179	0.04349902
cg19586645	3885074.123	1.555431356	9.70393E+12	0.043514277
cg04431054	0.106057541	0.012007524	0.93676278	0.043514512
cg08047907	0.344928054	0.122712397	0.969546395	0.043527218
cg12768605	0.311026485	0.100049275	0.966898303	0.043577408
cg19615059	0.205153654	0.044051724	0.955422798	0.043584855
cg02226871	1.87E+21	4.034258939	8.70E+41	0.04365252
cg15687659	928985777.9	1.794829099	4.80834E+17	0.043685154
cg02239082	31760453.05	1.630377994	6.18707E+14	0.043691107
cg06276114	24986240.36	1.617744744	3.85915E+14	0.0437037
cg17918239	151.2702949	1.151359378	19874.50884	0.043737996
cg22721186	17.03988115	1.082669777	268.1866214	0.043753042
cg19167673	0.085302235	0.007789578	0.934129055	0.043824627
cg24341944	347.5107144	1.173711613	102890.4335	0.043891022
cg11296363	2460564511	1.799014495	3.36539E+18	0.043938496
cg27304754	0.064821296	0.004521782	0.929235489	0.04401093
cg03777405	5.53243E+15	2.63154025	1.16E+31	0.044039564
cg13560548	0.093180065	0.009245241	0.939134438	0.044089891
cg15765532	14.23042516	1.072342158	188.8436434	0.044124092
cg04006554	0.183654555	0.035256926	0.956662962	0.044159004
cg25608041	0.155010457	0.025226945	0.952483227	0.044165333
cg22792938	83.68541524	1.121346057	6245.394704	0.044218296
cg07036775	6.38702E+17	2.875266742	1.42E+35	0.044242161
cg16799583	2.93105E+19	3.168040654	2.71E+38	0.044249933
cg16731240	0.342328324	0.120440681	0.972999157	0.044291556
cg23513644	3.00912E+17	2.7877273	3.25E+34	0.044304573
cg16639637	17.9132745	1.075938449	298.2376953	0.044328271
cg03644378	106.2656138	1.124999536	10037.67585	0.044354964
cg15286372	2273412.843	1.434536364	3.60284E+12	0.044483667
cg18849169	0.185692825	0.035932546	0.95962657	0.044522093
cg19283196	0.23643136	0.057907246	0.965333221	0.044524569
cg22298208	0.057464144	0.003540084	0.932782357	0.044547903
cg08263357	0.125923932	0.016674688	0.950952502	0.044567118
cg22826936	0.083952676	0.007483581	0.941802065	0.0445822
cg03429582	7382371.016	1.458971231	3.73547E+13	0.044651454
cg14450605	0.156041607	0.025446956	0.956852481	0.044682467
cg06421707	5476981738	1.688923273	1.77612E+19	0.044763649
cg22809047	0.270442418	0.075407253	0.969921313	0.044767538
cg23035555	1448117.824	1.385054375	1.51405E+12	0.044853349
cg13462160	0.000969353	1.10E-06	0.85394866	0.044899105
cg27634151	0.156222408	0.025457327	0.958680437	0.044904288
cg07447922	0.365046957	0.136339002	0.977411298	0.04491687
cg10140638	0.254657014	0.066891806	0.969478902	0.044919389
cg15109571	1.78781E+13	1.9765184	1.62E+26	0.044992352
cg08952029	0.166303588	0.028786411	0.960761783	0.044995619
cg18915437	1142508504	1.591524769	8.20173E+17	0.045002826
cg08878352	2339803.733	1.385080956	3.95261E+12	0.045017746
cg18986713	1.53108E+16	2.285639556	1.03E+32	0.045024536

cg02471507	97345.47775	1.288681848	7353360375	0.045046647
cg14607813	9441.282622	1.223617542	72847776.78	0.0450536
cg24692716	166.447714	1.119271894	24752.55715	0.045057699
cg24794531	0.332069998	0.112980361	0.976014612	0.045059447
cg19192120	0.039972607	0.001715032	0.931650021	0.045066568
cg16025584	7377569.149	1.411836576	3.85516E+13	0.045106229
cg08835688	0.158529786	0.026125538	0.961958876	0.045271476
cg23418591	0.244370172	0.061484839	0.971244001	0.045348547
cg04856689	0.36098353	0.133038132	0.979486913	0.045429002
cg12800028	0.207482414	0.044439441	0.968710482	0.045457255
cg05394497	1167114850	1.517301169	8.9775E+17	0.045510807
cg02917064	0.093375674	0.009140679	0.953869635	0.045522286
cg22836370	1.23545E+11	1.652921172	9.23E+21	0.045575474
cg14173613	18451635924	1.568770772	2.17E+20	0.045713982
cg21255605	0.024518691	0.000644936	0.9321338	0.04573551
cg25454755	100880.7307	1.239171119	8212684806	0.045810539
cg02025407	2.11026E+16	2.009931121	2.22E+32	0.045819322
cg15310873	0.177129364	0.032396054	0.968476337	0.04583403
cg01015879	0.175708837	0.031866367	0.968845785	0.045901477
cg15729423	353132762.9	1.424890229	8.75174E+16	0.045948006
cg01064307	65919889.59	1.380950273	3.1467E+15	0.045961867
cg24959428	0.099100567	0.010234239	0.959614353	0.045982793
cg14037413	12.9611628	1.046609107	160.5104905	0.045994251
cg16257091	0.325760165	0.108248782	0.980331446	0.046009864
cg17847607	1285777.341	1.282912877	1.28865E+12	0.046009948
cg00821764	16347215116	1.50358295	1.78E+20	0.046091469
cg22036988	0.363125073	0.134188197	0.982648414	0.046105529
cg22757447	0.249777101	0.063900471	0.976340219	0.046109554
cg11251877	0.123468938	0.015794096	0.965207442	0.046183066
cg01968530	6.48602E+19	2.161161245	1.95E+39	0.046191089
cg26258845	0.298124607	0.090708701	0.979820908	0.046201972
cg08063013	1.30752E+12	1.593718625	1.07E+24	0.046232712
cg24762359	0.170526303	0.029950137	0.970921097	0.046237699
cg23628240	81.69162565	1.075910817	6202.671816	0.046252166
cg02497175	960.0807531	1.119797739	823144.2344	0.046283417
cg12219753	1.02E+22	2.286128757	4.56E+43	0.046319133
cg25924032	0.155783891	0.02497867	0.971573758	0.046498198
cg15786837	0.206472997	0.043686421	0.975843239	0.046500386
cg06953304	2621.16233	1.128825657	6086406.627	0.046523899
cg24881834	0.109888568	0.01248734	0.967019214	0.046570158
cg16833230	0.005152061	2.87E-05	0.923264403	0.046577342
cg21329628	630686.7498	1.223716175	3.25047E+11	0.046585511
cg08473533	0.001965873	4.25E-06	0.910375634	0.046596715
cg02019333	0.226137985	0.052286552	0.978040943	0.04662603
cg09745307	3.262432594	1.017794584	10.45738167	0.046630379
cg00954003	6.27E+22	2.183481177	1.80E+45	0.046639137
cg00512279	0.261663208	0.069838295	0.9803738	0.046659757
cg03283421	7.497498816	1.030188157	54.56526374	0.046664473

cg12421458	4918073685	1.38850631	1.74198E+19	0.046676743
cg24454435	5.46312E+11	1.485753087	2.01E+23	0.046689815
cg05488632	0.194077332	0.038565891	0.976666414	0.046745208
cg09671005	5.27E-17	4.74E-33	0.584926251	0.046766056
cg11951446	1.11841E+14	1.584305159	7.90E+27	0.046784442
cg17009433	0.382397414	0.148234964	0.986459455	0.046793996
cg07348311	0.009941189	0.000105452	0.937180835	0.046818903
cg19339841	258.5907786	1.080677198	61877.11824	0.04684203
cg25755261	3299389381	1.353310913	8.04395E+18	0.046878186
cg03000846	0.164051885	0.027592243	0.975383582	0.046881672
cg17044611	3.16328E+16	1.68437682	5.94E+32	0.046896276
cg27258787	575.1499634	1.090942474	303221.7447	0.046902094
cg25511429	0.242237883	0.059816585	0.980985326	0.046937186
cg03693099	0.109274194	0.012289188	0.971654871	0.047060483
cg25943131	4.7128E+18	1.742732427	1.27E+37	0.047076073
cg01685739	168.5418054	1.068143103	26594.1334	0.047089754
cg17058777	1364017.184	1.198795835	1.55201E+12	0.047094564
cg07708788	0.092954333	0.008906775	0.970105157	0.047107974
cg00171126	3.03E-11	1.24E-21	0.73786922	0.047158316
cg18809535	0.000607279	4.04E-07	0.91315486	0.04722198
cg18273566	7202.649742	1.114023306	46568292.6	0.047246494
cg21796825	1.08766E+12	1.393280043	8.49E+23	0.047289006
cg09375488	0.21622934	0.047602646	0.98219598	0.047341919
cg00854637	190081168.8	1.250252145	2.88989E+16	0.047345147
cg02330106	0.148705305	0.022611818	0.97795177	0.047349104
cg25722142	28332.30356	1.125456334	713239066.4	0.047387182
cg17049328	0.006042528	3.87E-05	0.943242867	0.047407692
cg05679521	53246858371	1.320895039	2.15E+21	0.04744552
cg23391785	0.382164004	0.147583035	0.989607821	0.047537085
cg12431699	8704.089697	1.096102006	69118728.95	0.047704434
cg07295092	54457726268	1.279239851	2.32E+21	0.04773888
cg09597496	503.9284609	1.061614076	239205.4698	0.047818291
cg00241355	7023.597569	1.088437402	45322700.91	0.047827507
cg09594067	15.97911344	1.02686645	248.6516784	0.047827787
cg17947053	2.02143E+11	1.281944952	3.19E+22	0.047833516
cg12090388	26562956.73	1.17572912	6.0013E+14	0.047849553
cg10432859	0.079560114	0.006483159	0.976346806	0.047852508
cg25324046	1.89727E+11	1.277944888	2.82E+22	0.047855356
cg18371284	8.41405E+11	1.295841079	5.46E+23	0.047856669
cg27486427	0.139199848	0.019731769	0.982000037	0.04790769
cg08568512	0.328407004	0.108930765	0.990089074	0.047967722
cg08810779	2781858354	1.213475952	6.37733E+18	0.047978438
cg10762132	4.67E-46	5.50E-91	0.395802897	0.047982477
cg10665018	51.77747166	1.035018894	2590.200612	0.048018311
cg16384137	0.217337287	0.047866536	0.986816685	0.048024107
cg13765303	0.159991692	0.026006619	0.984262578	0.04803295
cg02153871	1.34663E+19	1.434181999	1.26E+38	0.048138703
cg02064106	0.351579163	0.124667317	0.991502107	0.048143765

cg07017374	0.428147165	0.184579974	0.993119624	0.048149468
cg19923810	0.148572458	0.022408204	0.985075595	0.048206452
cg04511195	3.71E-22	2.02E-43	0.681641348	0.048233525
cg21948783	0.189706398	0.036455144	0.987199966	0.048237249
cg20673481	0.320530641	0.103644363	0.991273322	0.048247728
cg04959837	0.10161585	0.010508968	0.982568468	0.048250636
cg00025991	0.044966418	0.002070615	0.976511077	0.04825691
cg15741583	0.129282914	0.016971225	0.984847717	0.04830198
cg22082462	0.173028468	0.030329707	0.987113074	0.048317736
cg11523020	0.094720555	0.009124683	0.983265231	0.048370395
cg05532892	0.114712468	0.013361331	0.984853247	0.048395712
cg16614332	1.27123E+14	1.248661136	1.29E+28	0.04844335
cg20696985	0.16591459	0.02785469	0.988259106	0.048502874
cg15042080	0.369098018	0.137097243	0.993698665	0.048555533
cg27589921	0.024289485	0.000603289	0.977937133	0.048632821
cg01708236	84.7766906	1.026894835	6998.854236	0.048638175
cg03756121	1469143.651	1.084214369	1.99073E+12	0.048702388
cg12770741	0.186597564	0.035132404	0.991069404	0.048781855
cg19001226	0.366775411	0.13524296	0.994685435	0.048788831
cg14654926	0.231828114	0.054136632	0.992752462	0.048865214
cg08586737	0.241353643	0.058659283	0.993049659	0.048881015
cg09186685	18895464.51	1.085059833	3.2905E+14	0.048888754
cg10634217	19.73203032	1.013338228	384.2280985	0.048986295
cg09822001	53763077.17	1.082271036	2.67074E+15	0.0489866
cg04510262	7.99E+26	1.289183219	4.95E+53	0.049064123
cg02043083	2097906.754	1.060398843	4.15053E+12	0.049080438
cg22660578	0.263930375	0.070027204	0.994745453	0.049097211
cg20566118	0.092522959	0.008638669	0.990951008	0.049128172
cg22740783	0.234898306	0.055463848	0.994832058	0.049183266
cg03340261	3.59929E+18	1.16483499	1.11E+37	0.049184581
cg22927043	0.092856321	0.00869416	0.991734223	0.049202498
cg23843505	0.09744069	0.009569814	0.992149646	0.049226988
cg20083871	2.14191E+11	1.091517326	4.20E+22	0.049233434
cg03328804	345541.0669	1.043692344	1.144E+11	0.049234128
cg10441365	17.15964997	1.0093989	291.7118169	0.049248312
cg23828212	63971952.16	1.05968762	3.8619E+15	0.049263249
cg24914860	2.45827E+13	1.095865915	5.51E+26	0.049321655
cg03923277	0.16160217	0.026252138	0.994786078	0.049344644
cg23897067	2.61615E+18	1.097552667	6.24E+36	0.049498161
cg12724357	0.050019643	0.002517121	0.993978681	0.049538923
cg12911791	0.192330807	0.037095021	0.997199569	0.049610884
cg11944393	6.78183E+16	1.062942686	4.33E+33	0.049639684
cg19729279	1658141.712	1.021579083	2.69136E+12	0.049658935
cg22080282	4.56577E+12	1.04382283	2.00E+25	0.049663367
cg24844534	0.109195592	0.011960658	0.996908146	0.049680067
cg17197538	0.013672874	0.000188035	0.994214321	0.049690683
cg07512345	0.004409462	1.96E-05	0.992804478	0.049695349
cg08209133	0.180810344	0.032758488	0.997981962	0.0497297

cg22377237	320581004.2	1.018776513	1.00878E+17	0.049782591
cg23043245	0.243138432	0.059176379	0.998984706	0.049835539
cg16246410	8.1525E+18	1.029294893	6.46E+37	0.049848179
cg16672449	104827428.8	1.009490154	1.08855E+16	0.049882881
cg03792199	2.44E+21	1.024831982	5.83E+42	0.049885945
cg22836229	0.279598095	0.078201963	0.99965643	0.049938241
cg07899016	0.161435282	0.026070346	0.999654963	0.049956654

Supplementary Table 4 Multivariate Cox regression analysis.

id	HR	HR.95L	HR.95H	P value
cg00008493	9.08E-07	7.87E-12	0.104833363	0.019325432
cg00032227	2.21E+46	397055396.2	1.23E+84	0.016107994
cg00034039	691448704.3	2266.383586	2.10953E+14	0.00158281
cg00059225	0.141639334	0.021695319	0.924701808	0.041176979
cg00107632	1.30287E+19	93910.98188	1.81E+33	0.008069875
cg00115714	9009880081	27.19223455	2.98534E+18	0.02202497
cg00155485	1.49E+21	18.00909504	1.23E+41	0.037204745
cg00177013	8402312.175	48.91337709	1.44334E+12	0.009528597
cg00185839	1.59E+20	4.72346216	5.32E+39	0.042596545
cg00241355	47777.3605	4.661030929	489736329	0.022217019
cg00290506	0.103551098	0.027180577	0.394503397	0.000890858
cg00327185	9.76112E+19	7.968878611	1.20E+39	0.040119218
cg00424946	31656971840	40.2759809	2.48824E+19	0.020689115
cg00425792	1.36798E+12	11091.36953	1.69E+20	0.003284136
cg00426056	91222626.21	3316.892774	2.50884E+12	0.000440828
cg00449941	9.25292E+17	75.65757582	1.13E+34	0.028606406
cg00512279	0.206236834	0.046768871	0.909443207	0.03703776
cg00568128	22904950842	12.69350728	4.13311E+19	0.028261349
cg00594118	22570607.44	205.4414783	2.4797E+12	0.004247463
cg00622677	0.191618806	0.048787934	0.752599334	0.017924788

cg00642303	20.33479891	1.793175236	230.598794	0.015044264
cg00648153	16506152.15	70.66540956	3.85554E+12	0.00841147
cg00658626	0.119289016	0.022152085	0.642371556	0.013316227
cg00677811	3.64147E+17	6233.955731	2.13E+31	0.012411217
cg00686623	9.13166E+11	180.7362365	4.61E+21	0.01569837
cg00704909	2363633612	6.730066397	8.3012E+17	0.031565178
cg00755043	0.135733146	0.02609836	0.705925088	0.017600026
cg00777555	7.18001E+13	37045.39973	1.39E+23	0.003454242
cg00784357	1.32919E+13	1.667018664	1.06E+26	0.04618701
cg00791249	130693618.9	24.5609667	6.95446E+14	0.018026053
cg00798206	2.66772E+17	4.575814575	1.56E+34	0.04163251
cg00822607	89670015589	49.15514708	1.64E+20	0.020451582
cg00825031	3.64967E+18	17569.03729	7.58E+32	0.01105234
cg00846036	0.153178057	0.038066832	0.616376933	0.008261927
cg00854637	1.75468E+12	3801.261056	8.10E+20	0.005609287
cg00887547	186092865.7	64.08315396	5.404E+14	0.0121459
cg00930078	775205.1722	19.09961913	31463614793	0.012252483
cg01015879	0.164391886	0.028260316	0.956277061	0.044459921
cg01025762	2602218643	21.96139434	3.08338E+17	0.022273878
cg01064307	1451162960	13.23749887	1.59084E+17	0.025520135
cg01135200	56.35104809	1.134344153	2799.362621	0.04305012
cg01139966	59.52930911	3.495691991	1013.744533	0.004724766
cg01182585	12850377.73	83.93253627	1.96744E+12	0.007204855
cg01244871	4.42E+21	5640053658	3.46E+33	0.0003613
cg01305547	0.001618988	1.74E-05	0.150850051	0.00547749
cg01305625	0.175410384	0.03225402	0.953952513	0.043954621
cg01320361	5.45E+20	26499.48997	1.12E+37	0.012724099
cg01360768	1.19659E+13	409214.0738	3.50E+20	0.000596487
cg01488147	0.007715561	6.05E-05	0.983487854	0.049218328
cg01507173	0.104717345	0.014626835	0.749698921	0.024652049
cg01530101	0.176959361	0.038582627	0.811624754	0.025844301
cg01585758	1735817847	18.94133221	1.59073E+17	0.02294112
cg01618304	531162753.7	23.00601166	1.22635E+16	0.020208459
cg01656955	0.272589368	0.077712036	0.956157729	0.042358343
cg01663570	3.20896E+13	112121.2062	9.18E+21	0.001746242
cg01667702	0.030905875	0.001296914	0.736496989	0.031633655
cg01685739	312.1095507	1.519750694	64097.59972	0.034513287
cg01692572	88.58121485	1.374324101	5709.447733	0.034896615
cg01703884	0.052558272	0.003561084	0.775710942	0.031961999
cg01708236	668.6719666	2.826659712	158180.4124	0.019672148
cg01783386	25141821.13	26.79145134	2.35938E+13	0.01515767
cg01809579	5.37032E+11	164.4506016	1.75E+21	0.01567106
cg01817393	0.202913273	0.046404253	0.887284973	0.03410476
cg01837574	0.063916807	0.005894695	0.693056793	0.023731227
cg01843018	0.168786808	0.039036172	0.729809941	0.01723778
cg01852131	1.97184E+13	4078.763052	9.53E+22	0.007130653
cg01926595	4532.890251	2.162360961	9502157.317	0.030958719
cg01929105	8091047.937	3.58403413	1.82657E+13	0.033091095

cg01934797	1.28E-07	1.02E-13	0.160427007	0.026733405
cg01993411	87800685.83	94.78480776	8.13312E+13	0.009073188
cg01994513	1.50E+24	9591.673943	2.34E+44	0.018953937
cg01994779	0.013753781	0.000355618	0.531937165	0.02153697
cg01999523	1098.755281	2.926338144	412550.8082	0.020614805
cg02005336	59674547.2	184.3909137	1.93125E+13	0.005676529
cg02019333	0.174577922	0.038329552	0.795142369	0.024051819
cg02064106	0.25957711	0.087863726	0.766872509	0.014678429
cg02071439	1.11621E+19	645725247.6	1.93E+29	0.000265722
cg02161046	5.97037E+17	640540.2182	5.56E+29	0.003605401
cg02162950	261354758.8	19.50530254	3.50194E+15	0.020626116
cg02171008	3.35622E+14	7189.73512	1.57E+25	0.007620034
cg02197293	0.111812071	0.021636448	0.57781846	0.008935892
cg02214188	9.18068038	1.18997979	70.82884343	0.033435263
cg02218260	0.067125446	0.005620747	0.801641722	0.032786421
cg02226871	1.94E+35	2.26864E+11	1.66E+59	0.003852892
cg02233558	2.82734E+11	51.43769867	1.55E+21	0.02120475
cg02239082	33150062577	139.3855162	7.88408E+18	0.01382842
cg02244695	0.17299187	0.034021715	0.879620174	0.034468313
cg02269221	3.29077E+12	3.909869928	2.77E+24	0.039658412
cg02290509	5.89134E+17	7488047.991	4.64E+28	0.001390877
cg02292024	1475060.043	5.770249739	3.77072E+11	0.025361251
cg02318535	0.181563224	0.035779375	0.921346578	0.039511888
cg02453653	7.70337E+13	37569.18239	1.58E+23	0.003468129
cg02489552	0.065160836	0.009743862	0.435754797	0.004851137
cg02523617	4545.24558	2.973503257	6947783.676	0.024368709
cg02537909	2.30279E+12	2296763.07	2.30883E+18	5.40E-05
cg02548238	0.180724752	0.039478839	0.827314998	0.027509563
cg02595263	61853433	93.67373119	4.08423E+13	0.008691348
cg02631957	597374407.2	19.69956297	1.81149E+16	0.021501205
cg02668984	332123.7986	65.19951127	1691825835	0.003509576
cg02675652	0.088221582	0.013475649	0.577563836	0.011323193
cg02735133	9.76621E+13	11603.06471	8.22E+23	0.005734068
cg02735486	0.132234108	0.021829498	0.801019785	0.027709488
cg02755525	0.208512189	0.055554178	0.782611408	0.02016864
cg02770814	41035377.39	4870.859871	3.45709E+11	0.000144041
cg02772367	9805443889	6028.520528	1.59486E+16	0.001617066
cg02784848	0.027794126	0.000988302	0.781657537	0.03532031
cg02809263	2.3866E+14	253457.3656	2.25E+23	0.001688217
cg02862835	5.23629E+11	5.72010579	4.79E+22	0.036136368
cg02899772	0.211555147	0.054793391	0.816806176	0.024224707
cg02930996	0.173182496	0.030725931	0.976119382	0.046882592
cg02959669	0.120457273	0.019350333	0.749855551	0.023297432
cg03036064	2135580.742	10.67977595	4.27041E+11	0.019270192
cg03048535	0.113925615	0.014318176	0.906473375	0.040096068
cg03070588	2386096716	12097.36707	4.70636E+14	0.000518161
cg03072102	13214793928	9.987943766	1.74842E+19	0.029650924
cg03079549	7.76296E+12	1643.644651	3.67E+22	0.009015238

cg03079681	0.04716539	0.003006178	0.740000804	0.029680216
cg03085312	0.032624781	0.003362437	0.316549108	0.003156363
cg03101664	0.06884285	0.005958781	0.795353622	0.032083969
cg03274654	8.14322E+16	89086656.1	7.44E+25	0.000216653
cg03276813	2.49867E+12	15332.85345	4.07E+20	0.003087
cg03301801	0.005786731	7.90E-05	0.42386134	0.018684545
cg03322749	4252872485	54.88241655	3.29558E+17	0.01675229
cg03328804	695077.27	6.609122481	73100840939	0.022604537
cg03347966	1.46E+19	317.5595801	6.69E+35	0.024179982
cg03349953	0.248026841	0.061784618	0.995673621	0.049289586
cg03373442	1831637.802	29.26293869	1.14647E+11	0.010493339
cg03383661	1077439922	131.0511179	8.8582E+15	0.010463353
cg03386722	7353976745	107.0375865	5.05252E+17	0.013604735
cg03415518	0.000311363	4.50E-07	0.215643526	0.015533517
cg03423524	3.22662E+11	3.001071035	3.47E+22	0.040878351
cg03429582	1007524526	39.08705275	2.59704E+16	0.01726612
cg03431064	3.42454E+12	608.2651122	1.93E+22	0.011748876
cg03439703	0.145251375	0.023248037	0.907515859	0.039039263
cg03442064	2272820.367	47.5819325	1.08565E+11	0.007753925
cg03522403	3.01E+22	23783444.73	3.81E+37	0.003531152
cg03532005	12109.49557	6.043135322	24265530.25	0.015362614
cg03589001	0.156710343	0.03037725	0.808438281	0.026829199
cg03640568	5.92E+27	1.54E+13	2.28E+42	0.000189868
cg03644378	502.6053916	5.418061738	46624.08659	0.007122954
cg03738331	6.60322E+14	123.8608106	3.52E+27	0.022472738
cg03752689	113388042.7	11559.38848	1.11224E+12	7.66E-05
cg03756121	1110049480	290.4019233	4.24312E+15	0.007073822
cg03759077	1.18575E+18	4092910.512	3.44E+29	0.001997502
cg03764352	1.29633E+11	26181.03832	6.41869E+17	0.001140394
cg03802231	27649.09784	11.03948102	69248962.89	0.010424932
cg03804985	695636.4893	36.07808988	13412853253	0.00753499
cg03812067	3.67003E+13	11178.43502	1.20E+23	0.005209849
cg03821311	0.018553489	0.000414821	0.829833131	0.039767249
cg03878377	8.35E+23	45640117823	1.53E+37	0.000407409
cg03923277	0.062725875	0.00862021	0.456431513	0.006247145
cg03959219	9428.265214	9.134879205	9731073.936	0.009744895
cg03970351	4.14088E+17	5123.916725	3.35E+31	0.013037137
cg03984733	15469976998	5308.688907	4.50808E+16	0.002006031
cg03989322	31444.42592	5.015579175	197136140.6	0.02026312
cg04001333	0.206236025	0.054916748	0.774505038	0.019363212
cg04025889	4.82198E+11	27516.36359	8.45006E+18	0.001571113
cg04051458	0.155939121	0.028235781	0.861212561	0.033061835
cg04119538	41.61458355	2.130716408	812.7658646	0.013938996
cg04135543	1.28343E+17	21591.83449	7.63E+29	0.008665242
cg04177705	1.96E+20	2310.845621	1.66E+37	0.018802743
cg04211745	1.24363E+18	644237192.4	2.40E+27	0.000133815
cg04249030	1.4046E+17	613932.7278	3.21E+28	0.003089895
cg04270788	5.46978E+11	1771.864819	1.69E+20	0.006729881

cg04322344	3.09059E+17	9103.299516	1.05E+31	0.011294256
cg04367351	0.00822209	0.000108064	0.625578634	0.029840558
cg04402875	0.203291474	0.053938939	0.766189037	0.018603221
cg04433306	46023.14812	31.48461122	67275093.48	0.003880513
cg04466273	2.59E+30	33603369.95	2.00E+53	0.009201205
cg04478795	0.156747162	0.033222289	0.739553878	0.019225765
cg04488521	0.154240216	0.037281015	0.638127585	0.009880408
cg04532952	0.138149469	0.026656765	0.71596369	0.018374035
cg04595372	0.053798847	0.007329535	0.394884001	0.004058618
cg04600406	6.58744E+11	15958.57048	2.71919E+19	0.002352959
cg04603184	0.24208632	0.07213339	0.812464048	0.021667023
cg04613791	46.6394836	2.69520645	807.0778513	0.008252149
cg04658354	4.25E-21	2.58E-41	0.700553318	0.048274074
cg04703844	4465712733	15173.56966	1.3143E+15	0.000543346
cg04726446	0.107506875	0.014389773	0.803190439	0.029738085
cg04735745	6.59113E+18	88.02831887	4.94E+35	0.028827826
cg04739149	2.45E-05	1.30E-08	0.046187438	0.005797079
cg04743872	0.187877119	0.04768502	0.740228523	0.016851815
cg04794887	285363.5221	1.910066657	42633244993	0.038788761
cg04946535	2.19E+20	3792485.824	1.27E+34	0.003768587
cg04988423	0.188746015	0.052171664	0.682843051	0.011039474
cg05028306	1.07433E+14	446.4145858	2.59E+25	0.015680465
cg05038053	2.41741E+17	90.6516577	6.45E+32	0.027198264
cg05120641	1.59845E+15	26307.80197	9.71E+25	0.00572146
cg05122605	6780664587	32.77431216	1.40285E+18	0.020494739
cg05203877	0.297823012	0.092765317	0.956160654	0.041821563
cg05257479	1.07676E+18	2024438.386	5.73E+29	0.002577772
cg05284724	76577307476	33812.75896	1.73428E+17	0.00078854
cg05287690	1919742082	8962.341985	4.11211E+14	0.000642197
cg05291178	6.05E-07	3.99E-11	0.00917368	0.003555986
cg05358404	0.10903817	0.018480591	0.64334102	0.014404546
cg05361811	5812488063	5.826599525	5.79841E+18	0.033447442
cg05368762	7.22E+28	3.075361245	1.70E+57	0.046188178
cg05382565	1.1072E+14	1.374215542	8.92E+27	0.047768545
cg05401645	8.79238E+16	1282.025618	6.03E+30	0.016385573
cg05412136	7649.691522	7.5884432	7711434.195	0.01126664
cg05417985	46.31751366	1.442778414	1486.931085	0.030228966
cg05477027	7763025.386	175.9815134	3.42448E+11	0.003642945
cg05492605	5.93658E+12	4.26219386	8.27E+24	0.0392474
cg05522288	225628.224	3.651794319	13940570304	0.028517947
cg05531055	1.50275E+17	514388.9066	4.39E+28	0.003321854
cg05595345	5.486343528	1.055948448	28.50514659	0.042896575
cg05602212	7.947E+11	3492.639376	1.81E+20	0.005255626
cg05602615	8.71384E+19	4.449809552	1.71E+39	0.042781957
cg05603623	797373.7046	7.286323413	87260033463	0.021708258
cg05646865	0.000207778	1.36E-06	0.031751887	0.0009518
cg05647859	0.32461263	0.129312136	0.814876023	0.016579345
cg05668720	1.11E+20	31438.50885	3.94E+35	0.011508605

cg05670275	3.09043E+15	78467.20729	1.22E+26	0.004164805
cg05702952	31005495905	1.514987998	6.35E+20	0.046123984
cg05719902	0.083392434	0.015858055	0.438534118	0.003353719
cg05741384	4565499945	39.02822525	5.3407E+17	0.018947955
cg05755779	0.045964527	0.00333625	0.633267138	0.021372465
cg05807768	488999511.7	766.8207703	3.11834E+14	0.003346256
cg05876094	15099188726	52.04277491	4.38073E+18	0.018399515
cg05886626	0.144299997	0.03116141	0.668213954	0.013305363
cg05915281	5.94529E+15	1770916.7	2.00E+25	0.001172334
cg05923103	7381918.716	34.20608115	1.59307E+12	0.011614047
cg05950276	0.000383435	2.12E-07	0.693043511	0.039803006
cg05976074	0.033653724	0.001522654	0.743815159	0.031765654
cg06058319	47071212.75	34.36835354	6.44692E+13	0.01426196
cg06058597	19742203411	474.9099457	8.20692E+17	0.008084187
cg06062132	1324.66583	2.115878386	829319.6684	0.028663847
cg06090630	1.52782E+13	71.38481788	3.27E+24	0.022571892
cg06141123	8.04621E+14	12.09764007	5.35E+28	0.034559586
cg06171242	1.01E+22	645691.0896	1.59E+38	0.007742874
cg06190732	0.110416327	0.020397669	0.597703832	0.010550409
cg06207460	713.8225964	8.830994147	57699.35871	0.003368393
cg06230736	0.271944739	0.08429444	0.87732882	0.029334584
cg06235991	1789778.931	14.31509897	2.23771E+11	0.01619884
cg06237414	9.68792E+19	89183.03163	1.05E+35	0.009180924
cg06243556	0.259492414	0.079961431	0.842109908	0.024698962
cg06305312	5.91594E+13	80572.70006	4.34E+22	0.002330121
cg06358566	8773713.422	8.449247316	9.11064E+12	0.023703864
cg06377278	0.298997481	0.099938623	0.894543983	0.030828838
cg06386533	3149.126266	13.10790463	756566.0964	0.003976566
cg06392241	0.037071218	0.001705076	0.805990564	0.035971565
cg06417705	9.17822E+12	16392.10158	5.14E+21	0.003681608
cg06417962	0.104921759	0.015291991	0.719891591	0.021765575
cg06422693	115788.7493	9.341612831	1435194832	0.015323993
cg06433995	7.87E+26	334379342.4	1.85E+45	0.004113169
cg06528936	32064828556	60.70519332	1.69368E+19	0.018243203
cg06533629	0.238942187	0.063661813	0.896822855	0.033893696
cg06534422	47762.74019	14.66528372	155556441.6	0.009035843
cg06544198	1.31584E+16	340915986.6	5.08E+23	3.12E-05
cg06585027	5.06933E+19	23860.51052	1.08E+35	0.011743597
cg06587969	268171914.3	127.9431019	5.62095E+14	0.008968578
cg06615667	1.46087E+13	503.3016609	4.24E+23	0.013659703
cg06638433	0.243206406	0.072346941	0.817579223	0.022280658
cg06665941	951751139.2	137.1052041	6.60683E+15	0.010105643
cg06790275	3144330344	1101.886951	8.97262E+15	0.003931487
cg06806080	0.078570994	0.011454681	0.538941319	0.009621524
cg06901392	1.42455E+16	1057497.918	1.92E+26	0.001774321
cg06910048	8.62193E+15	4560.070886	1.63E+28	0.010955386
cg06938406	1.60E+20	22989801.26	1.11E+33	0.002045764
cg06971096	0.252369456	0.074592705	0.853841435	0.026825318

cg06976977	1.03624E+14	520511.9584	2.06E+22	0.000932956
cg07006042	3444153489	2195.847373	5.4021E+15	0.002552118
cg07017374	0.27312192	0.105116648	0.709645757	0.007721764
cg07027513	0.167222484	0.029446713	0.949625832	0.043560599
cg07028533	0.224220875	0.066222946	0.75917796	0.016272907
cg07036775	2.98E+22	5179.659212	1.72E+41	0.018874232
cg07039362	6.399499007	1.275832273	32.09950744	0.024068657
cg07054788	70457.68575	22.19913493	223625177.2	0.006656542
cg07068998	390.9652271	4.142966697	36894.7713	0.010092919
cg07093046	37467542769	1674.176697	8.38512E+17	0.004807671
cg07175883	0.087900567	0.018520875	0.417178427	0.002211535
cg07190917	1.96384E+19	6619.833894	5.83E+34	0.014526487
cg07209631	706083.2769	206.54307	2413799669	0.001178927
cg07265622	2.10E+30	1219381.33	3.62E+54	0.014200734
cg07295678	0.127675964	0.028681069	0.568359286	0.006901666
cg07312445	0.045605568	0.002776961	0.748972535	0.030587872
cg07314414	1.91E+22	29200952459	1.25E+34	0.000219049
cg07322981	2.00191E+15	14969.25542	2.68E+26	0.007029279
cg07355551	257736.6667	8.31749711	7986559956	0.018203571
cg07399355	361903516.2	2048.137404	6.39479E+13	0.00138945
cg07437033	59248952710	93933.00612	3.73717E+16	0.00027217
cg07478100	2446955.388	445.0712603	13453105621	0.000814521
cg07489134	4837392.354	1.116239991	2.09636E+13	0.048374065
cg07512345	0.002385237	6.87E-06	0.828043896	0.043054155
cg07520161	21111037048	317.4130133	1.40409E+18	0.009689234
cg07656362	1.24876E+11	2.526754872	6.17E+21	0.041977302
cg07684150	1.87725E+17	40.974757	8.60E+32	0.030635965
cg07807709	3047.429391	4.801280833	1934239.262	0.014831534
cg07815386	2.27456E+18	658371.4413	7.86E+30	0.004111377
cg07833035	7.88276E+16	41.79693506	1.49E+32	0.03016106
cg07899016	0.127028793	0.019066778	0.846305259	0.032971803
cg07924819	7.86189E+15	2068950.595	2.99E+25	0.001145444
cg07965714	4.44E+28	955.4519122	2.06E+54	0.02870357
cg07965839	13666962787	378.7721642	4.93135E+17	0.008572216
cg08032971	0.011480385	0.000201781	0.653179434	0.03027112
cg08115510	643024680.7	943.4477877	4.38266E+14	0.003082181
cg08209133	0.125804029	0.01860696	0.850577086	0.033508718
cg08211967	2327620901	142.9760584	3.78932E+16	0.010905385
cg08263357	0.11525227	0.015054106	0.882356334	0.037481498
cg08305742	1.19255E+19	33.03312346	4.31E+36	0.03321078
cg08332868	2.3182E+17	165.0464526	3.26E+32	0.024646198
cg08351105	1.00E+30	53357949383	1.88E+49	0.002282271
cg08351143	4.96E+21	4320477.168	5.69E+36	0.004749361
cg08388746	0.002068106	2.44E-05	0.175532482	0.006375406
cg08418747	31255416919	65628.42182	1.48853E+16	0.000291427
cg08495878	0.20195159	0.047133534	0.865295707	0.031173155
cg08552121	3004869941	4525.536621	1.99518E+15	0.001419754
cg08555772	0.150332066	0.039302031	0.57502703	0.005633882

cg08583049	0.035213258	0.004451621	0.278544283	0.001517701
cg08605641	1.47048E+15	20904.47572	1.03E+26	0.006133083
cg08623787	0.21521351	0.059537678	0.777941902	0.019131607
cg08632701	0.062586835	0.006800088	0.576038451	0.014404291
cg08635242	7.08901E+17	4810285.599	1.04E+29	0.00173248
cg08638395	3.12463E+14	18.28990047	5.34E+27	0.031799789
cg08704884	2.83159E+11	16.93430446	4.73E+21	0.028124994
cg08717396	17.13172126	1.540478808	190.5224999	0.020803105
cg08778586	17372004.54	186.553277	1.6177E+12	0.004294921
cg08783491	2.2487E+17	91.8246841	5.51E+32	0.02710727
cg08810065	3.33628E+14	3.559812833	3.13E+28	0.041618186
cg08810779	2.89047E+11	70.09959814	1.19E+21	0.01948119
cg08817171	1.80333E+15	60355.69439	5.39E+25	0.004311174
cg08897388	0.232864658	0.05962625	0.909430801	0.036033928
cg08907850	3.00801E+12	25.49062739	3.55E+23	0.027179958
cg08909157	0.146245913	0.024378485	0.877325527	0.035453434
cg08934443	5768.042124	9.877257268	3368375.354	0.007706736
cg08942800	0.128293081	0.027959814	0.588670399	0.008250631
cg08952029	0.146833552	0.023261768	0.926846662	0.041273224
cg08961832	0.06702465	0.007132939	0.629797053	0.018056445
cg08983975	1.14E+22	1916615553	6.82E+34	0.000714297
cg08996502	5682.219882	25.12198007	1285233.994	0.001775435
cg09000510	6498788.718	4.96376354	8.50851E+12	0.029042449
cg09002165	7.07E+55	7495.249676	6.68E+107	0.03519728
cg09022993	0.037581543	0.001595614	0.885159297	0.041786149
cg09039698	924499.0122	11.77258988	72600713355	0.016906288
cg09059181	3.60781E+11	28.81717726	4.52E+21	0.024878416
cg09068198	97155265.61	239.9734904	3.93341E+13	0.005239617
cg09068528	0.218874127	0.050206004	0.954186345	0.043135983
cg09072120	0.008190363	0.000108565	0.617899879	0.029389971
cg09128050	5.7907E+14	84.15759689	3.98E+27	0.024204079
cg09130402	6678.303126	21.44549408	2079678.485	0.002642702
cg09149294	16.93281682	1.849010506	155.0668774	0.012281851
cg09186685	1.52327E+12	2545.637899	9.11E+20	0.00651826
cg09189322	128762330.5	222.9197201	7.43754E+13	0.005802387
cg09194650	2.48174E+14	122.0028933	5.05E+26	0.021894473
cg09283635	1.91E+23	1.97340986	1.84E+46	0.047129156
cg09299307	4690610.49	20.23878108	1.08711E+12	0.01480392
cg09311052	1143062.464	157.1965783	8311833575	0.002106678
cg09322949	1050.742207	1.053122609	1048367.185	0.04830734
cg09329496	1.21E+43	1833364.032	7.95E+79	0.021826397
cg09375488	0.195356104	0.040553307	0.941082499	0.041783998
cg09386615	0.011859275	0.00024542	0.573067631	0.025002946
cg09416313	0.273653281	0.076739633	0.975846711	0.045754191
cg09419116	5.68915E+17	188.0257619	1.72E+33	0.024582997
cg09433780	6719445258	143.2525174	3.15184E+17	0.012044492
cg09455096	1.64965E+14	99456.82039	2.74E+23	0.002507985
cg09469394	5559.053215	1.793623677	17229407.17	0.035517706

cg09498106	3944704.61	647.4046916	24035498446	0.000636135
cg09507928	9942.839352	14.71754574	6717156.251	0.005625265
cg09535168	4.56612E+15	156.4285454	1.33E+29	0.022645501
cg09546332	16765694.9	27.06982094	1.03838E+13	0.014496853
cg09564133	586214.9902	61.8660693	5554709046	0.004470174
cg09597496	386.8084745	1.013314178	147654.8923	0.04949245
cg09649610	0.210148067	0.063513606	0.695318889	0.010613027
cg09650667	2529248371	1157.663207	5.52587E+15	0.003647546
cg09656405	984159979.9	14.71720351	6.58122E+16	0.024292864
cg09659887	8.73167E+15	6254.703418	1.22E+28	0.010093705
cg09660171	0.152109185	0.033861726	0.68328485	0.014017132
cg09664442	3.15E+23	2516569.235	3.95E+40	0.007066575
cg09712606	2.28539E+18	10.64682491	4.91E+35	0.037882169
cg09745307	4.505316494	1.337609434	15.17474099	0.015122076
cg09755102	67463.37946	18.71667655	243168575.1	0.00779057
cg09765256	9.31818E+18	14021.39782	6.19E+33	0.012131758
cg09822001	1747701622	30.83112018	9.90707E+16	0.019472573
cg09830278	0.004121649	0.000103817	0.163633369	0.003459251
cg09874600	5.06024E+11	72.61607295	3.53E+21	0.019778025
cg09892131	5.45851E+13	253.0326059	1.18E+25	0.017523111
cg09903430	0.000295882	1.03E-07	0.85227301	0.045576474
cg09911342	0.018153325	0.000497624	0.662233026	0.028922013
cg09926892	3.85562E+11	2983.641885	4.98243E+19	0.005116989
cg09976774	1.29621E+17	16437689.04	1.02E+27	0.000701518
cg10042178	8181037733	199.6412011	3.35248E+17	0.010704601
cg10045881	0.173638318	0.034357893	0.877535335	0.034174807
cg10075436	4.14992E+12	6.434580389	2.68E+24	0.036246634
cg10091705	2.41205E+17	1962.476838	2.96E+31	0.01560534
cg10185638	8.63E+20	588214.8116	1.27E+36	0.006819086
cg10201668	0.057689289	0.003489974	0.953604216	0.046244302
cg10235741	0.000514897	1.68E-06	0.157783139	0.009538456
cg10239941	117813.6015	38.03154089	364961407.7	0.004411999
cg10313675	631992248	1674.304571	2.38555E+14	0.001981685
cg10337772	32.70083206	2.190943378	488.0748759	0.011449421
cg10387901	13613.38283	4.786748912	38716087.99	0.018983249
cg10391629	2.99663E+11	781.8759267	1.15E+20	0.008777879
cg10423227	369417416.6	40.43436991	3.37508E+15	0.015848684
cg10432859	0.040909373	0.002827016	0.591994042	0.019052704
cg10441365	27.94953987	1.569378191	497.7619691	0.02340853
cg10458581	2.74E+24	560.5536969	1.34E+46	0.027220566
cg10497569	1.5805E+15	17002.26172	1.47E+26	0.006609011
cg10539418	15588560.53	541.1029189	4.49089E+11	0.00157098
cg10601939	3811131.776	72.50885754	2.00317E+11	0.006287923
cg10613440	1.02753E+17	1771.739874	5.96E+30	0.015412026
cg10634217	30.74871867	1.44410698	654.7186001	0.028129717
cg10665018	95.36807246	1.642030255	5538.916972	0.027858799
cg10698549	1.61252E+13	65.18518672	3.99E+24	0.023083707
cg10762132	4.27E-64	1.29E-112	1.41E-15	0.010470611

cg10780112	1518536301	5761.558998	4.00231E+14	0.00090141
cg10805447	1.70405E+18	255803.1656	1.14E+31	0.005327866
cg10806140	0.295319628	0.087621275	0.99534825	0.049127301
cg10857774	0.035693092	0.002177554	0.585058643	0.019510915
cg10869376	803844357.6	3.446334046	1.87494E+17	0.036994267
cg10872447	5.64E+60	2.50781E+19	1.27E+102	0.003983943
cg10883621	0.146111678	0.028158015	0.758172152	0.022049899
cg10887021	0.221762616	0.06233113	0.78899032	0.02002021
cg10891157	1.34915E+11	25.57404737	7.12E+20	0.024847203
cg10905613	3.48589E+11	17113.05524	7.10066E+18	0.001967033
cg10906135	5.57E-17	1.95E-27	1.59E-06	0.002310013
cg10971346	9.24572E+11	421.481314	2.03E+21	0.012049363
cg10971750	4.29232E+13	579.557916	3.18E+24	0.013963731
cg10996143	427817.8497	5.355116312	34178176873	0.024365395
cg11011602	54564585.24	241.0494616	1.23514E+13	0.004627785
cg11021744	0.216398871	0.057715875	0.811362057	0.023208878
cg11044823	1569257750	1680.673719	1.46523E+15	0.002537279
cg11050527	2373558.206	157.5617625	35756001131	0.002782162
cg11081833	0.196708149	0.042186992	0.917204425	0.038453729
cg11086568	7.26134E+13	1.54579065	3.41E+27	0.046913516
cg11108432	5.14378E+18	37.36593934	7.08E+35	0.032371775
cg11141013	4.30E+52	7.3783E+14	2.50E+90	0.006302878
cg11141561	65395925.18	36.52737296	1.1708E+14	0.014295054
cg11151811	2.9579E+15	264.8096102	3.30E+28	0.020130002
cg11206763	3.96263E+14	139.7175879	1.12E+27	0.021583999
cg11226328	490898.5222	554.1147712	434894306.5	0.000154074
cg11251877	0.028511454	0.00264519	0.307313645	0.003361223
cg11286618	4.65855E+13	380686.0897	5.70E+21	0.000925141
cg11304524	2.36E-07	3.34E-12	0.01670131	0.007400393
cg11368509	4.91141E+12	2411.196817	1.00E+22	0.007538303
cg11392765	0.090830226	0.011977361	0.688810346	0.020308056
cg11451801	4.17622E+11	22862.00818	7.62872E+18	0.0017097
cg11453347	999106.0659	55.12956703	18106670969	0.005753946
cg11473104	6891919.6	3.057056712	1.55373E+13	0.034885575
cg11485602	2.30559E+11	12.72239932	4.18E+21	0.029930707
cg11494699	7.977731349	1.414172598	45.00454721	0.018645235
cg11538128	0.081742027	0.016654221	0.401205126	0.002034766
cg11553177	16801.01114	4.205119939	67126260.27	0.021480897
cg11646704	1.01E+28	8702824.188	1.17E+49	0.009169469
cg11675413	0.021825631	0.000592229	0.80434813	0.037684347
cg11691938	4.89E+21	166647828	1.44E+35	0.001596748
cg11783451	4.3485E+13	4603.99064	4.11E+23	0.007368602
cg11787828	8319084.082	744.0473671	93014454476	0.000807606
cg11820497	4.78677E+15	55019.18031	4.16E+26	0.004965075
cg11828669	191104.2134	17.95280766	2034267903	0.010159977
cg11847459	474.962049	6.419644403	35140.41181	0.005005037
cg11879514	0.191836211	0.051010372	0.721444102	0.014562897
cg11944393	6.1205E+19	17.84566883	2.10E+38	0.036411313

cg12045676	38833676214	6114.432659	2.46638E+17	0.002281962
cg12082568	38085.65059	3.920972742	369937991.5	0.024344856
cg12090388	13723854205	100.4624138	1.87477E+18	0.01459489
cg12100077	1349.05634	4.772771959	381319.9173	0.01232529
cg12219753	2.38E+26	10543.98128	5.39E+48	0.020739548
cg12259537	0.143544827	0.030375749	0.678341046	0.014294701
cg12263485	131393644.2	28.90340601	5.9731E+14	0.016845694
cg12288365	1.48E+50	4.58313E+13	4.75E+86	0.007073177
cg12359315	0.093011657	0.009100809	0.950593372	0.045210643
cg12388309	0.280986748	0.086843368	0.909148897	0.034094844
cg12431699	23289.30207	2.300516784	235769456	0.03259643
cg12437239	234159240.7	113.2653852	4.84089E+14	0.009392016
cg12441964	1.67E-07	3.95E-12	0.007097802	0.004103002
cg12460105	12521555657	1715.654287	9.13875E+16	0.00393114
cg12468056	7.25553E+19	60.7664882	8.66E+37	0.031290845
cg12477012	1959461733	9.946716065	3.86006E+17	0.028112438
cg12477119	742695.0804	54.30514046	10157343812	0.005401257
cg12483860	6.46055E+18	48263.67057	8.65E+32	0.009060038
cg12489819	1.18E-22	1.22E-39	1.14E-05	0.011399562
cg12506373	506143.7978	41.38559466	6190113882	0.006233092
cg12515638	0.211892078	0.059110205	0.759568551	0.017211679
cg12530270	0.000682167	5.65E-07	0.823405229	0.044048038
cg12578480	8.09E-10	3.51E-17	0.018605666	0.015493232
cg12588476	1394210121	7655.943	2.53897E+14	0.000656532
cg12645220	0.161689979	0.042329642	0.617620379	0.007705916
cg12661229	9.37E+25	42414.20954	2.07E+47	0.017084264
cg12675800	2.07296E+16	12.54624081	3.43E+31	0.035602047
cg12687990	0.097222491	0.015517719	0.609123859	0.012794034
cg12739647	7.04929E+18	8270.18733	6.01E+33	0.013352687
cg12768605	0.283619524	0.081513	0.986836875	0.047614541
cg12800028	0.144233967	0.026240927	0.792785904	0.025945421
cg12814525	150658.9983	29.17173766	778086448.7	0.006271081
cg12820608	204130246.2	294.7056304	1.41392E+14	0.005292946
cg12830829	139202.2199	12.686959	1527336695	0.012588325
cg12903171	0.007826314	0.000394605	0.155221709	0.001461683
cg12909005	9878.90575	5.269546414	18520147.87	0.016748147
cg12939527	5.3458E+18	11260.18159	2.54E+33	0.012383399
cg12946690	275093.018	9.755447972	7757323784	0.016591078
cg12977318	3.2916E+13	16.19012123	6.69E+25	0.031355929
cg13041032	3.89E-05	1.59E-09	0.954085813	0.048943992
cg13052755	0.000257911	5.24E-07	0.126908378	0.008983523
cg13114389	2.9413E+11	77.76451383	1.11E+21	0.01893095
cg13118748	2.25E+21	14496.53619	3.49E+38	0.014916647
cg13135180	1.24089E+14	185.9902074	8.28E+25	0.019483407
cg13169373	0.015171855	0.000333165	0.69090489	0.031575131
cg13219107	7.17894E+11	231891.6961	2.22247E+18	0.000343498
cg13258606	2.23E+22	18924.34344	2.63E+40	0.015357897
cg13298382	3.6028E+11	2.427459193	5.35E+22	0.042607591

cg13301933	0.162196263	0.037368173	0.704011617	0.015159584
cg13315147	0.122853358	0.032053518	0.47086711	0.002223219
cg13322449	0.047875935	0.004182459	0.548028087	0.014544638
cg13342120	4453643582	85.68585974	2.31484E+17	0.014247567
cg13376158	8276983.296	1285.176021	53306668808	0.000371203
cg13393195	1131758569	214.4963297	5.97156E+15	0.00829763
cg13449778	0.157209256	0.039694375	0.622626001	0.008421819
cg13462160	0.000641351	4.12E-07	0.997477259	0.049921312
cg13463367	1098979.107	23.63084949	51109253507	0.011189946
cg13516796	2.82573E+11	17.55847311	4.55E+21	0.027882146
cg13560548	0.078439407	0.006474736	0.950268878	0.045495425
cg13575604	4.09886E+17	64434.87661	2.61E+30	0.007014746
cg13581941	4.91E+27	1228885.205	1.97E+49	0.011988919
cg13603099	90802066331	101.9722258	8.08555E+19	0.016403082
cg13614181	0.162590937	0.028234935	0.936280275	0.041984339
cg13634678	3.40E+25	1058367104	1.09E+42	0.002433071
cg13643796	0.30919772	0.107630492	0.88825414	0.029253832
cg13739345	69592355.56	2738.420598	1.76857E+12	0.000484058
cg13755535	355118.9098	7.87736676	16009085768	0.019415157
cg13756879	0.342971302	0.126051219	0.933186644	0.036138486
cg13782957	446164.6455	13.82427178	14399520935	0.014057431
cg13846555	181476232.8	3.628443395	9.07652E+15	0.035513674
cg13853761	0.10576363	0.021069198	0.530914619	0.006350275
cg13859541	1.77662E+12	1263.577149	2.50E+21	0.008678028
cg13887370	17162636.8	48.9172156	6.02152E+12	0.010554384
cg13896604	1.08635E+18	367565.9746	3.21E+30	0.00458763
cg13918581	6.97E+24	45325.01374	1.07E+45	0.01586277
cg13936125	0.208968726	0.063751258	0.684973593	0.009748341
cg13966710	0.058866173	0.003825608	0.905797588	0.042264747
cg13975369	0.120250253	0.019335601	0.747849702	0.023113343
cg13991233	0.081858601	0.015520253	0.431747515	0.003178217
cg14026602	22832726.64	70.31431001	7.41433E+12	0.008875936
cg14037413	24.56108242	1.550901269	388.9652949	0.023126823
cg14047244	6.18655E+15	3.377556667	1.13E+31	0.042576172
cg14049461	0.105060117	0.019172379	0.575704691	0.009427125
cg14086033	47934887.82	183.8458411	1.24983E+13	0.005445879
cg14086647	7.71536E+15	90.45359768	6.58E+29	0.025403136
cg14126210	2.02746E+12	262.8969796	1.56E+22	0.014701675
cg14135551	0.234889793	0.074862379	0.736995213	0.013026303
cg14174099	0.32577341	0.106328278	0.998119376	0.049616077
cg14196211	2.81E+27	195784.3031	4.04E+49	0.015179986
cg14203179	0.100750613	0.01801271	0.563529081	0.008977221
cg14206730	6.5725E+13	5278.120431	8.18E+23	0.007303645
cg14211646	173555.4066	4.396730899	6850880765	0.025469371
cg14217534	2103702.401	18.02864135	2.45474E+11	0.0144539
cg14329157	0.180459021	0.03701228	0.879855506	0.03414827
cg14334099	3.17534E+14	17150.80203	5.88E+24	0.005635882
cg14364739	9.81E+20	1225287.898	7.86E+35	0.005768973

cg14424111	1.93181E+13	9.511178234	3.92E+25	0.034366546
cg14473924	0.251995469	0.077857297	0.815616754	0.021444461
cg14489649	5.86794E+12	21341.32752	1.61E+21	0.003022922
cg14534967	1.65557E+14	86418.00362	3.17E+23	0.002679246
cg14538332	0.183842282	0.040884446	0.826670982	0.027235158
cg14550007	7920.352963	33.69008481	1862031.26	0.00127064
cg14550570	9.13474E+12	62.4450379	1.34E+24	0.02289695
cg14596431	4.90E+22	4097803285	5.87E+35	0.000672475
cg14607813	222075.6678	6.802401079	7250028576	0.020259006
cg14617642	0.267600719	0.073909932	0.96888392	0.044630913
cg14634336	4805258892	154.90123	1.49066E+17	0.011311522
cg14654926	0.155686706	0.029485546	0.822041781	0.028466968
cg14662756	0.001322313	9.44E-06	0.185185241	0.008569132
cg14663792	3.07161E+17	12954.28492	7.28E+30	0.010389269
cg14685339	1.50201E+12	6039.430431	3.74E+20	0.004474237
cg14712964	10290939129	4239.190859	2.4982E+16	0.002116498
cg14766198	87347137.44	5.845618055	1.30517E+15	0.030048328
cg14795305	0.076014672	0.005868254	0.984659159	0.048633151
cg14797438	3.37053E+11	14180.74594	8.01122E+18	0.002190122
cg14800883	0.005608673	7.39E-05	0.425545311	0.018936281
cg14817542	3952.411144	9.292308565	1681127.326	0.007322978
cg14838256	7.39255E+14	1625.298732	3.36E+26	0.012426403
cg14916213	1.11361E+13	132780.0865	9.34E+20	0.001250035
cg14932684	315619.1815	10.42136319	9558775173	0.016164738
cg14939691	7.94952E+14	4.003309541	1.58E+29	0.041097618
cg14962548	3.99E+21	127043.9615	1.25E+38	0.010277065
cg15042806	4380.61734	12.55788251	1528108.601	0.004999628
cg15054260	4.99658E+11	2724.4147	9.16E+19	0.005524191
cg15065896	3.73751E+11	5.268491422	2.65E+22	0.036589068
cg15077070	0.18270963	0.040827266	0.817659669	0.026198416
cg15100639	3.04E+22	199230.1948	4.65E+39	0.010335397
cg15104484	1.41E+22	709305.7118	2.81E+38	0.007732786
cg15105703	0.109765207	0.012982838	0.928025173	0.042504591
cg15109571	2.89945E+16	155.8580658	5.39E+30	0.023750532
cg15118204	2.55158E+12	332856.2877	1.95597E+19	0.00041228
cg15119375	3.40429E+15	6916.925993	1.68E+27	0.009223594
cg15120942	0.098635599	0.013259794	0.733720402	0.023673895
cg15188491	3833761397	1499.617423	9.80098E+15	0.003374057
cg15198335	5.91829E+13	2234405.177	1.57E+21	0.000276491
cg15205507	0.345161554	0.119404189	0.997758111	0.049517559
cg15219393	1.72E-05	5.44E-10	0.542352245	0.037920631
cg15239703	1.58E-08	7.44E-15	0.033732211	0.015698119
cg15286372	170844113.4	5.910083783	4.93863E+15	0.030567552
cg15301525	1.79E+37	8301539.958	3.86E+67	0.016082523
cg15309223	2.09138E+12	628.34725	6.96E+21	0.011215292
cg15334028	1.18E+36	2666781.889	5.18E+65	0.017087138
cg15361590	0.121437272	0.025104557	0.587423659	0.008755889
cg15368822	5.62947E+11	465.1333288	6.81E+20	0.01122578

cg15384392	3.94277E+17	1618.166555	9.61E+31	0.016523561
cg15425811	0.167281388	0.039303646	0.711971165	0.015534157
cg15432938	20679498431	2372.954172	1.80215E+17	0.003577869
cg15442702	14094533.21	51.13077296	3.88525E+12	0.010008393
cg15448245	0.040962567	0.002100566	0.798799801	0.035014624
cg15501381	0.092951197	0.011719425	0.737231149	0.024544499
cg15555727	5.16769E+15	43.19432096	6.18E+29	0.028694882
cg15615135	15198.9526	2.089653427	110548551.9	0.033803109
cg15663121	4.68162E+11	82.80809736	2.65E+21	0.019004288
cg15677132	100746702.6	22.56830424	4.49741E+14	0.018329257
cg15687659	2.00302E+11	55.98557264	7.17E+20	0.020417315
cg15729423	1.05417E+12	2943.288175	3.78E+20	0.005873435
cg15765532	19.31301724	1.233546977	302.3740821	0.034900578
cg15765896	10964008.94	6.386807967	1.88215E+13	0.026889603
cg15781794	11962458909	1407.115021	1.01698E+17	0.004365746
cg15790852	3.4678E+17	56564762.36	2.13E+27	0.00044404
cg15810744	1.87633E+14	58.10929991	6.06E+26	0.025326092
cg15817236	0.241913217	0.077593768	0.754210111	0.014437794
cg15824705	6.78E-08	1.50E-14	0.306274141	0.034745075
cg15842276	0.021425563	0.001600626	0.286796953	0.003689053
cg15843217	0.017084524	0.000486517	0.599939526	0.02500266
cg15863254	1.42483E+11	2757.442397	7.36239E+18	0.004593941
cg15873301	0.3256579	0.129263731	0.820439482	0.017322998
cg15876417	53.72998899	1.028524156	2806.848727	0.048393256
cg15881088	3.07325E+17	878122.9148	1.08E+29	0.002987032
cg15883761	1.34252E+14	229.7682929	7.84E+25	0.018608451
cg15947959	61188517.88	5.678275137	6.59361E+14	0.02999426
cg16004226	0.142212957	0.02811092	0.719454409	0.018371897
cg16011258	1.96E+41	58587605.88	6.53E+74	0.015773723
cg16022344	2.38062E+13	2426.521954	2.34E+23	0.008691413
cg16025584	4106103129	632.1604791	2.66706E+16	0.005679152
cg16072462	0.163917554	0.030857123	0.870754037	0.033805008
cg16085042	7.07795E+13	24029.18066	2.08E+23	0.004147684
cg16090392	5.06178E+11	138515.9978	1.84972E+18	0.000473246
cg16104446	50251398.6	225.3230754	1.1207E+13	0.004769874
cg16114640	0.277125566	0.079841435	0.961888758	0.043262935
cg16121444	17869555633	255.1004453	1.25175E+18	0.010430636
cg16160720	1.84062E+17	19.81260422	1.71E+33	0.034077406
cg16161425	1.54735E+18	4446748.227	5.38E+29	0.00200884
cg16189954	14210595.85	57.77261859	3.49545E+12	0.009309545
cg16208491	43771945818	339.9637842	5.63585E+18	0.010118315
cg16222698	4.93E+56	9.68E+21	2.51E+91	0.00136695
cg16257091	0.262007348	0.072548912	0.946228534	0.040921411
cg16286776	3.88E+42	5807.660744	2.59E+81	0.03155683
cg16306381	378943567.3	76.93943904	1.86638E+15	0.0119931
cg16328820	36919627753	3.667666146	3.72E+20	0.038400809
cg16348491	15192707.06	54.34195509	4.24752E+12	0.009755836
cg16353836	9875054096	4722.080966	2.06512E+16	0.001939678

cg16420530	8.83588E+16	32188.38754	2.43E+29	0.00757948
cg16438432	5.74804E+14	7.242634607	4.56E+28	0.03741408
cg16482226	1.56E+23	1480834531	1.65E+37	0.001188125
cg16491909	2.55E-48	8.40E-79	7.72E-18	0.002211387
cg16522484	0.098993631	0.010304456	0.951019511	0.045126897
cg16530429	0.165342295	0.028582786	0.956452411	0.044464844
cg16538604	314925.3492	39.68333099	2499235148	0.005719652
cg16551261	0.075539143	0.007573127	0.753475046	0.027723945
cg16614332	2.69E+20	1453.566153	4.99E+37	0.020399992
cg16639637	23.27537537	1.219141583	444.3643842	0.036470258
cg16652259	0.117559315	0.01955027	0.706905459	0.019339568
cg16685860	3.81E+27	2011301.945	7.21E+48	0.011065911
cg16722536	0.110629348	0.016337469	0.749127824	0.024074174
cg16731240	0.317873768	0.103763606	0.973787792	0.044806601
cg16823737	3.11709E+13	366.8697428	2.65E+24	0.015526333
cg16854524	10916.32871	11.10749508	10728452.43	0.008173718
cg16917279	1.5611E+18	16262.0199	1.50E+32	0.010764086
cg16954341	0.111255595	0.025256289	0.490088116	0.003700077
cg16978263	73.11211286	3.320511154	1609.806683	0.006513821
cg17021265	2893.404103	4.472331265	1871906.799	0.015797197
cg17044611	6.05E+20	78683.51332	4.65E+36	0.010347233
cg17055959	1.59E-16	3.31E-29	0.00076396	0.014618443
cg17067528	7603179.477	218.8531711	2.64142E+11	0.002977569
cg17127132	237860288.7	38.05174413	1.48686E+15	0.015702969
cg17138359	119.5650607	1.147210347	12461.36228	0.04360242
cg17158059	4.39868E+14	28682.64073	6.75E+24	0.004836708
cg17163751	0.265254502	0.082974663	0.847969105	0.025215502
cg17176395	6.82917E+12	783.7544921	5.95E+22	0.011385915
cg17178888	0.148027964	0.027350419	0.801167907	0.026605079
cg17194182	0.224772425	0.058258667	0.867212483	0.030251833
cg17229388	0.136917006	0.018889963	0.992392993	0.049123297
cg17232861	0.000127281	8.03E-08	0.201753678	0.017044542
cg17291001	0.028645442	0.002128949	0.385430244	0.007387784
cg17301902	0.125378227	0.017471213	0.899748625	0.038920725
cg17306637	2.36E-06	6.91E-11	0.080802914	0.015004642
cg17319849	2.21165E+17	436229.967	1.12E+29	0.003680566
cg17324707	4.36432E+12	2628.093464	7.25E+21	0.00721227
cg17384214	0.009611573	0.000148343	0.622759727	0.029072872
cg17391474	3.25E-05	1.38E-09	0.762411324	0.044136641
cg17398595	0.16626279	0.042061672	0.65720914	0.01051131
cg17414107	0.226209169	0.052590389	0.973002643	0.045854349
cg17484237	17.85218184	3.47303015	91.76436215	0.000559479
cg17498523	1711.770771	5.796328915	505519.8241	0.010303909
cg17592292	451742677.2	6262.758969	3.25849E+13	0.000479898
cg17597195	1.73568E+19	93314383.01	3.23E+30	0.000819641
cg17608500	503456272.5	809.9378262	3.12948E+14	0.003241016
cg17675882	22705.79116	33.98335465	15170749.25	0.00250784
cg17676129	0.024985875	0.001588979	0.392889938	0.008676643

cg17704839	0.033974116	0.004231653	0.272763523	0.001460731
cg17729667	0.120546163	0.016824445	0.863706181	0.035221781
cg17801256	4170887.933	21.99390225	7.9096E+11	0.013954618
cg17810944	0.019265539	0.000657012	0.564923048	0.021947914
cg17839278	6.73684E+11	2957.539722	1.53E+20	0.005538039
cg17889103	8889448.498	410.3128633	1.9259E+11	0.001682497
cg17891123	2187671226	439.1642563	1.08978E+16	0.006269899
cg17902858	2.21795E+12	364.0781124	1.35E+22	0.013398736
cg17947053	1.03555E+15	19.73318994	5.43E+28	0.031953716
cg17976829	12336955.99	211.91515	7.18214E+11	0.003536838
cg17977409	0.179332521	0.047715895	0.673992456	0.010958476
cg17997329	1.39E+24	11069979121	1.76E+38	0.000790438
cg18022322	3.79686E+18	17581.73136	8.20E+32	0.011072603
cg18023724	0.14727692	0.029576504	0.733369013	0.019357445
cg18075299	0.000284173	1.20E-07	0.675685722	0.03951318
cg18123596	1.41479E+15	328312.0009	6.10E+24	0.00205502
cg18130076	5.83E+20	375435493.3	9.07E+32	0.000842452
cg18211447	498038584.7	19.15799585	1.29472E+16	0.021509248
cg18226566	752.3390262	2.072277092	273136.2579	0.027648138
cg18264687	0.0016152	7.49E-06	0.348347855	0.019047956
cg18273566	85104.866	12.37774943	585149849.5	0.011800763
cg18277754	0.239999066	0.07100109	0.811248836	0.021642361
cg18284523	975776247.6	2064.095178	4.61287E+14	0.001903804
cg18333824	2.10465E+14	6430.370152	6.89E+24	0.007589388
cg18338021	0.070188293	0.005799022	0.849521907	0.036784193
cg18342900	380504.7134	7.362535182	19664943298	0.020313658
cg18349835	0.10531297	0.021768981	0.509478213	0.005135803
cg18362489	310797578.1	2.491638221	3.87677E+16	0.039787405
cg18453621	0.257280488	0.077201196	0.857412235	0.027074472
cg18491230	834234243.9	118.2600806	5.88488E+15	0.010674082
cg18502522	1572608.938	4.988241943	4.95786E+11	0.027192554
cg18591973	36111.32105	47.36959813	27528785.54	0.001939356
cg18652121	39551490.11	78.29117398	1.99808E+13	0.009034931
cg18695917	0.217479445	0.054426209	0.869017147	0.030881109
cg18697049	1.21533E+12	107.7675722	1.37E+22	0.018460217
cg18757066	1.63E+23	4208062.537	6.35E+39	0.006095901
cg18788872	7.75068E+13	77779.09957	7.72E+22	0.00248431
cg18909638	0.15327479	0.030269788	0.776125723	0.023439338
cg18943599	0.095329428	0.012918819	0.703446631	0.021171172
cg18979762	0.001300396	8.62E-06	0.196155792	0.009420831
cg18986713	2.40E+21	4491.227547	1.28E+39	0.01808939
cg19001226	0.33431077	0.115234945	0.969876724	0.043774043
cg19016517	3.19E+21	602798.8325	1.69E+37	0.007352236
cg19028804	10460.70886	11.23474908	9739997.667	0.007966499
cg19032144	2.54607E+18	108509711.1	5.97E+28	0.000503974
cg19100810	3809739.158	1.473824247	9.84793E+12	0.044278012
cg19175383	4.92E+23	770727018.7	3.14E+38	0.001709893
cg19185384	656424117.5	9.000843396	4.78725E+16	0.027960826

cg19187486	1.90486E+12	6484.824844	5.60E+20	0.004479607
cg19215261	2.49E-08	1.40E-12	0.00044554	0.000457098
cg19219437	0.15577174	0.03585787	0.676694831	0.013098394
cg19234089	0.017827486	0.000540312	0.588214796	0.023980593
cg19238398	5333.645172	7.034205401	4044205.308	0.011194483
cg19273182	1.32778E+11	76.30797506	2.31E+20	0.018311142
cg19275050	0.187192123	0.036386708	0.963013498	0.044956462
cg19283196	0.181549914	0.039898579	0.826103893	0.02730877
cg19307060	1.20E-13	1.40E-22	0.000101931	0.004568216
cg19308222	0.196380445	0.0488052	0.790187914	0.021935712
cg19313758	9507990.026	3.9210034	2.30558E+13	0.032183484
cg19317638	32335415.57	1672.663809	6.25098E+11	0.000594924
cg19339841	545.8801714	1.890107514	157655.1383	0.029242987
cg19350340	7731.912165	21.82888729	2738685.894	0.002794691
cg19401923	6.26E+23	1626346036	2.41E+38	0.001385081
cg19432434	3.31E+23	13727179.11	7.97E+39	0.004894107
cg19434303	776.2441496	2.067522136	291438.2242	0.027798996
cg19459675	1.28187E+14	2780567.432	5.91E+21	0.000308536
cg19490266	21382793670	96.43546641	4.74124E+18	0.015268406
cg19528976	0.177456279	0.043154543	0.729719945	0.01654165
cg19531713	3560922.669	128.9093951	98364981418	0.003837178
cg19552482	2.35E-07	4.87E-13	0.113902888	0.02229791
cg19564877	0.082452043	0.012300111	0.552705514	0.010147322
cg19570574	0.230915009	0.060684403	0.878672921	0.031581881
cg19572947	29783880361	42.28657891	2.09778E+19	0.02033
cg19584823	2779048.881	18.99581276	4.06569E+11	0.01447902
cg19678067	1.09807E+15	3.307894096	3.65E+29	0.042347413
cg19709625	0.148220091	0.02428325	0.90470574	0.038595648
cg19729279	33551988.73	5.271423369	2.13554E+14	0.030164063
cg19784449	4.88E-08	2.68E-14	0.088956854	0.022082744
cg19786920	0.113942602	0.017758229	0.731092961	0.02200874
cg19819891	5143001822	528.0319891	5.00925E+16	0.006458578
cg19846131	1.41252E+14	268840.9499	7.42E+22	0.001471414
cg19850348	0.207378659	0.0586259	0.733564999	0.014661202
cg19864851	1.90532E+13	736892.7777	4.93E+20	0.000445802
cg19885761	0.218611298	0.067480858	0.708214173	0.011237147
cg19918758	0.238969793	0.06334324	0.901541543	0.034603853
cg19921776	6.82E+23	561.202007	8.28E+44	0.026724697
cg19948393	0.153706075	0.026619478	0.887528968	0.036319323
cg19987840	4.86576E+16	512.677499	4.62E+30	0.019286262
cg20009671	1.92399E+12	12.28762398	3.01E+23	0.031499331
cg20011794	638697.7101	288.2265931	1415326603	0.00067146
cg20083871	1.67366E+15	1203.192843	2.33E+27	0.014004898
cg20103201	1.42632E+19	184.9482755	1.10E+36	0.026210194
cg20109151	6676887.731	873.3627381	51045032989	0.000572324
cg20114394	0.047849908	0.003197132	0.716146097	0.027679131
cg20116574	16750869.97	407.0177815	6.89384E+11	0.002152154
cg20123891	0.190537262	0.051374739	0.706659524	0.013169193

cg20126158	102900.8345	4.177914255	2534418155	0.025279407
cg20162159	5.89906E+14	203.5727154	1.71E+27	0.020175577
cg20188282	1768.103965	3.159204096	989550.3854	0.020542534
cg20193288	1304893390	237.0439227	7.18325E+15	0.008037799
cg20199629	0.103702389	0.011229914	0.957637423	0.045702657
cg20203792	2127402439	43.46108281	1.04135E+17	0.017431237
cg20239949	6.14582E+19	70292.56008	5.37E+34	0.009438356
cg20273774	2.93458E+11	32334.71667	2.66331E+18	0.001236636
cg20278498	1.54485E+13	103.1640352	2.31E+24	0.020717035
cg20300655	0.067224811	0.005082735	0.889122771	0.040445959
cg20301340	5.04E+22	400330.8586	6.36E+39	0.00926586
cg20337385	2.06E+23	107420.6646	3.96E+41	0.012444231
cg20349695	19158551320	719.6053525	5.10071E+17	0.006645232
cg20377673	164549.8375	34.05423897	795103630.3	0.005518767
cg20496643	0.028215392	0.001973545	0.403390082	0.008566518
cg20506766	1.71E+24	3481129.197	8.42E+41	0.007259967
cg20524216	1658424863	54.38137667	5.05756E+16	0.015759362
cg20645649	2.80626E+11	1177.940155	6.68547E+19	0.007394979
cg20684399	97676023649	42.23403754	2.26E+20	0.021435516
cg20695562	33147.56359	5.734199145	191615419	0.018516583
cg20727114	0.141143934	0.026110551	0.762971647	0.022954568
cg20732367	75524838.17	4.673870182	1.2204E+15	0.032189561
cg20770803	2.43936E+12	30115.12037	1.98E+20	0.002140999
cg20811273	890297345.2	5.753469465	1.37765E+17	0.032206927
cg20821095	4.98182E+17	63608.25629	3.90E+30	0.007142345
cg20862496	0.013430169	0.001139072	0.158347743	0.000617124
cg20899053	1533.680587	1.940618745	1212075.349	0.031184035
cg20906802	0.061299058	0.005659285	0.663966354	0.02162656
cg20908993	882290.5878	7.913161851	98372394754	0.020953944
cg20910436	5.38812E+14	104276.0826	2.78E+24	0.002953413
cg20923575	1.19603E+15	477.7001593	2.99E+27	0.017149634
cg20950277	0.021238511	0.001052044	0.428760086	0.011994752
cg20951821	170860.187	16.01668432	1822674588	0.010893994
cg20988728	2487881611	1.609940043	3.84459E+18	0.045061997
cg21011830	2.10114E+18	399157.8726	1.11E+31	0.004758716
cg21024145	1.47912E+14	12351.53025	1.77E+24	0.005856717
cg21039822	9.40E-59	5.13E-101	1.72E-16	0.007123462
cg21046940	280347187.7	39.06086108	2.0121E+15	0.015734892
cg21085625	52.30973502	1.380244409	1982.481045	0.032865041
cg21092462	0.119324957	0.015395212	0.924861941	0.04187859
cg21116410	1.64E+33	31168338332	8.62E+55	0.004167728
cg21123573	258.4440714	1.926525835	34670.35678	0.026262896
cg21219744	140056900.8	5.738837168	3.4181E+15	0.030673201
cg21255605	0.009269789	0.00015818	0.543236696	0.024211121
cg21256656	0.009545276	0.000231667	0.393289181	0.014212595
cg21282997	8.241306903	1.59009476	42.71389427	0.011990075
cg21289924	4.08E+23	587245.6632	2.84E+41	0.009495566
cg21300561	3.1173E+12	36.67234523	2.65E+23	0.025058801

cg21306212	2.03E+21	49726757.05	8.32E+34	0.002153462
cg21329628	37730697.22	12.01784324	1.18458E+14	0.022270399
cg21339926	1.00E-05	3.08E-10	0.326668287	0.029932026
cg21369679	3.63896E+11	3803.529574	3.48152E+19	0.004522612
cg21434440	19457.15134	121.5114033	3115598.437	0.000137082
cg21515243	109942.618	50.31118764	240252314.2	0.003089635
cg21548788	1.32E+21	6284628.717	2.79E+35	0.003849745
cg21552947	69005807.75	29.37659278	1.62095E+14	0.015883317
cg21566550	5.92E+53	1.01E+29	3.46E+78	2.09E-05
cg21584983	12429444745	25.73246706	6.00374E+18	0.022708214
cg21607066	8.34588E+11	3914.595898	1.78E+20	0.005025264
cg21625881	0.070925938	0.005079582	0.990335252	0.049162011
cg21643860	137179005.1	202.689674	9.28418E+13	0.006229928
cg21644628	0.030923713	0.001675644	0.570691689	0.019436098
cg21666675	1016.873397	20.73761853	49862.59655	0.000489192
cg21686523	229721987.6	1065.518084	4.95273E+13	0.002122683
cg21686900	1.79412E+11	565.0101141	5.697E+19	0.009475339
cg21692936	2904.931221	3.460381565	2438640.144	0.020268578
cg21693780	2.52E+20	1067552695	5.94E+31	0.00043823
cg21703572	177217115.5	15.33475675	2.04802E+15	0.02207969
cg21718857	0.005212932	3.69E-05	0.736184905	0.037413264
cg21743830	0.037191666	0.002472817	0.559370168	0.017312185
cg21751787	5.95764E+11	5.68700999	6.24E+22	0.036240236
cg21762107	4.85533E+17	5.673993301	4.15E+34	0.040635635
cg21796234	5029162720	510.8420653	4.95113E+16	0.006547828
cg21872391	1.31046E+12	2241.873991	7.66E+20	0.006747665
cg21885650	2.72759E+18	13073606.14	5.69E+29	0.001412054
cg21943652	9.93588E+14	579.042982	1.70E+27	0.016281219
cg21950493	311.7255108	2.356612521	41234.09903	0.021227818
cg21985356	1.61818E+16	5479404.405	4.78E+25	0.000794779
cg21989500	1.91794E+11	4103.918229	8.96339E+18	0.003935182
cg22036988	0.3264793	0.110020525	0.968807719	0.043688656
cg22062239	13056026977	1.654349184	1.03E+20	0.045149467
cg22068038	2.1282E+18	359.19708	1.26E+34	0.022756512
cg22068473	29197686838	38.53131366	2.2125E+19	0.020888272
cg22080282	9.28372E+14	100.1949216	8.60E+27	0.02367301
cg22082462	0.112585635	0.014697994	0.86239832	0.035511845
cg22088594	0.163476999	0.029494796	0.90608287	0.038186901
cg22091798	1.66513E+12	48092.13334	5.76528E+19	0.001487385
cg22111003	2.22553E+19	45012880.84	1.10E+31	0.00118409
cg22156632	0.137826134	0.02394722	0.793246267	0.026462617
cg22190090	4.27904E+14	233898.1136	7.83E+23	0.001960954
cg22194305	2690188513	875.5998303	8.26532E+15	0.004387362
cg22201387	4.52467E+15	7.465914318	2.74E+30	0.037919558
cg22234344	7.47435E+15	3746642.245	1.49E+25	0.000821754
cg22238923	1448905.139	20.81482117	1.00857E+11	0.012647399
cg22262549	9102570.905	73.57400575	1.12617E+12	0.007396959
cg22334665	0.183537213	0.045068036	0.747445671	0.017969018

cg22374901	50814.77366	97.47706148	26489731.87	0.000687155
cg22386774	5.919322405	1.047876499	33.43750697	0.044124983
cg22464182	238.9221557	3.894397105	14657.92906	0.009127073
cg22470827	1.28677E+16	1241.425139	1.33E+29	0.015271947
cg22478328	4.83915E+11	117010.7242	2.0013E+18	0.000537608
cg22496859	2030861560	8.435795308	4.88916E+17	0.029515529
cg22517351	4.73076E+17	1566.343806	1.43E+32	0.01673805
cg22571530	0.258447246	0.069943549	0.954984127	0.042454647
cg22572159	0.236235279	0.074719391	0.746889211	0.014015003
cg22580173	0.203646772	0.04346592	0.954127005	0.043429298
cg22621736	6.52087E+14	4072.521023	1.04E+26	0.009557854
cg22631938	0.232541784	0.056523437	0.956694857	0.043247651
cg22660578	0.182278479	0.045351307	0.732623738	0.016470652
cg22670349	2.55493E+13	287.3273423	2.27E+24	0.016393538
cg22688260	1.16604E+14	53364.64579	2.55E+23	0.003157046
cg22721186	24.05407567	1.378108834	419.8496826	0.029273771
cg22792938	190.5783514	1.423136894	25521.16257	0.03562451
cg22816171	353851.5299	45.82231145	2732531407	0.005151923
cg22836229	0.15329025	0.037679042	0.623633174	0.008805859
cg22836370	1.24084E+13	73.00407737	2.11E+24	0.022303335
cg22886089	0.207722424	0.050941799	0.847017704	0.028416052
cg22968727	1.36601E+16	6.746616603	2.77E+31	0.038816436
cg23088430	162405033.9	31.79434275	8.29563E+14	0.016444008
cg23104823	838504.8832	44.08221365	15949526597	0.006666425
cg23128146	4.17E-27	1.40E-46	1.24E-07	0.007929958
cg23142935	8.94197E+13	7211.113444	1.11E+24	0.006746211
cg23173032	80905.50295	4.868615599	1344468520	0.022656147
cg23182539	3.70431E+12	234843.2109	5.843E+19	0.000620703
cg23213688	94311964.82	54.03297824	1.64617E+14	0.012279101
cg23269225	1.75536E+16	37.66102979	8.18E+30	0.029966667
cg23303408	0.06684663	0.008558884	0.522085844	0.009888597
cg23318804	1.65463E+18	14030.21932	1.95E+32	0.011161971
cg23337289	32.37525422	4.031735725	259.9766347	0.001069082
cg23357981	0.15193321	0.032786427	0.704062707	0.016020213
cg23376526	8378047.512	2640.530452	26582416447	0.000106502
cg23377693	1731899272	2935.704799	1.02172E+15	0.00170269
cg23391785	0.360500053	0.133396961	0.974237254	0.044281089
cg23414431	0.000114386	1.37E-07	0.095548157	0.008192621
cg23418591	0.233151749	0.054590162	0.995779026	0.049336243
cg23422659	0.179666467	0.03562075	0.906214487	0.037594929
cg23442323	0.160615386	0.027547022	0.936482439	0.042061088
cg23478284	0.299127659	0.092331478	0.969088315	0.044186375
cg23508052	1.67178E+14	110.7123655	2.52E+26	0.02208304
cg23513644	8.01E+25	27709048.57	2.31E+44	0.005957067
cg23526055	2099668.844	30.82646582	1.43014E+11	0.010354798
cg23576473	1.56826E+19	108732.3554	2.26E+33	0.007881126
cg23599056	0.000113698	1.67E-07	0.077536829	0.006371291
cg23628240	209.7799921	2.918455073	15079.08944	0.014245564

cg23685580	8.36E-06	3.48E-10	0.200995315	0.023103639
cg23699324	0.208200044	0.050812715	0.853078968	0.029198853
cg23740844	890.8245223	4.668856554	169970.5957	0.01124175
cg23749163	42867805.39	392.3379917	4.68384E+12	0.002988705
cg23772500	3.21945E+15	2220.007639	4.67E+27	0.012444936
cg23828212	9625984585	25.44776961	3.64117E+18	0.022539883
cg23850272	0.012484341	0.000210164	0.741604452	0.035429351
cg23850377	1.52E+26	1.46008E+14	1.58E+38	1.95E-05
cg23859078	5.63446E+14	12591.95723	2.52E+25	0.006638241
cg23873703	0.158651632	0.030829483	0.816437321	0.027623174
cg23964386	0.107945031	0.014574467	0.799489247	0.029330998
cg23968678	1.16E+25	4.88977E+12	2.74E+37	7.19E-05
cg24014661	0.059208265	0.003838374	0.913308288	0.042875107
cg24058132	0.027395399	0.001729688	0.4338979	0.010699488
cg24098951	0.204948129	0.061457448	0.683460456	0.009900074
cg24194132	0.223182896	0.051504394	0.967113697	0.04499935
cg24229963	54734090933	1029.435534	2.91016E+18	0.006444839
cg24283842	2.92E+29	24614.88916	3.47E+54	0.021267464
cg24341944	1211.766775	4.050858553	362485.8033	0.014650147
cg24353217	0.037451225	0.002688555	0.521690825	0.014520207
cg24394865	5.13061E+16	95.54031634	2.76E+31	0.026185699
cg24399106	0.157113621	0.02596669	0.950629036	0.043895202
cg24527001	2304122.586	131.6056854	40340057310	0.003294168
cg24532476	0.113598011	0.013993092	0.922205633	0.04177412
cg24576270	3.53057E+19	90149.66435	1.38E+34	0.008653115
cg24595957	310567478.8	763.5094082	1.26327E+14	0.003004763
cg24608308	9.92528E+15	60.70619286	1.62E+30	0.027393671
cg24642516	4.44595E+13	451.7878965	4.38E+24	0.014961225
cg24680602	0.10993497	0.015932068	0.758576844	0.025068918
cg24692716	355.1589441	2.012157899	62687.86146	0.026090377
cg24705286	253080659.1	4902.683141	1.30642E+13	0.000474529
cg24743310	0.004098458	3.23E-05	0.519627521	0.026086236
cg24792749	10360424.6	25.93051701	4.13946E+12	0.014102165
cg24794531	0.312885116	0.104120812	0.940226009	0.038475203
cg24823993	1.58E+26	1.48749E+11	1.68E+41	0.000632722
cg24892074	1.16E+25	3626671.259	3.69E+43	0.007936569
cg24905739	7.25E+26	2.20709E+11	2.38E+42	0.000691751
cg24906202	189484.6092	59.99683852	598438484.4	0.003118033
cg24959428	0.054527637	0.004556484	0.652534521	0.021616119
cg25047001	0.11022813	0.023747331	0.511646573	0.004869197
cg25047102	6718744094	3.445521307	1.31015E+19	0.038143318
cg25094927	5.92164E+12	29.33418355	1.20E+24	0.026803805
cg25106358	9.12E-10	1.03E-17	0.080901377	0.025796091
cg25107978	1.8337E+17	259492.9781	1.30E+29	0.004296794
cg25162921	0.114095281	0.025973882	0.501185507	0.004042858
cg25201980	1.73637E+12	44.81957177	6.73E+22	0.023471892
cg25219047	2.04925E+12	80.41446937	5.22E+22	0.020404605
cg25255854	4.27108E+18	3271.424669	5.58E+33	0.015705158

cg25264554	96672823.83	140.9024841	6.6327E+13	0.007326887
cg25270252	378959801.9	3.217251137	4.46377E+16	0.037232985
cg25324046	8.0427E+11	1.220331242	5.30E+23	0.048347093
cg25346576	306.5228789	1.88308617	49894.83582	0.027555287
cg25363317	1.50E+20	860686529.5	2.63E+31	0.000435468
cg25396537	5.28901E+14	1889.387235	1.48E+26	0.01170433
cg25432696	0.147188154	0.02435142	0.889654611	0.036857516
cg25437385	0.132613929	0.033265389	0.528671232	0.00419241
cg25461905	0.000223772	1.68E-07	0.297569954	0.022006741
cg25484319	0.006809537	0.000123753	0.374695338	0.014686249
cg25492727	4784442.607	45.26634216	5.05693E+11	0.0091631
cg25495394	4531.360134	38.09364019	539019.7566	0.000554584
cg25503559	347069075.4	13.96909827	8.6231E+15	0.023606843
cg25511429	0.109117519	0.022464969	0.530008876	0.006009439
cg25519930	0.195631173	0.054104751	0.707360352	0.012849759
cg25605045	3892492522	9.065275327	1.67138E+18	0.029456431
cg25619607	0.003883462	2.37E-05	0.637106177	0.032907535
cg25682936	444900060.7	8.346658875	2.37144E+16	0.028255942
cg25683012	78575.35679	24.09361469	256254064.6	0.006316799
cg25722142	201788.3389	5.676135235	7173636998	0.022329219
cg25752527	5.78243E+12	658.2400607	5.08E+22	0.011886931
cg25755261	4.88371E+13	2767.283445	8.62E+23	0.008835563
cg25784394	7.14998E+13	153.7692886	3.32E+25	0.019947861
cg25824330	7.70921E+17	36.20157531	1.64E+34	0.031788051
cg25848060	12580883955	4711.003951	3.35976E+16	0.002068763
cg25889160	0.002976665	2.41E-05	0.368003129	0.017948072
cg25898500	3542979176	9136.120499	1.37396E+15	0.000810947
cg25905459	9.941E+17	1104.647951	8.95E+32	0.018333033
cg25924032	0.126426758	0.018826898	0.848983468	0.033299104
cg25932713	7.999191081	1.328122549	48.1785796	0.023225189
cg25955816	0.016388545	0.001056824	0.254142876	0.003288747
cg25959506	0.055516173	0.005963392	0.516827568	0.011091133
cg26007077	48186634683	63.19333198	3.67436E+19	0.018408308
cg26023204	23554.66285	29.24316355	18972712.76	0.003191007
cg26055770	0.19017619	0.04577157	0.790162612	0.022368092
cg26069745	0.129106111	0.026199939	0.636199496	0.011878584
cg26129270	2.54E+32	36275.03075	1.79E+60	0.022554651
cg26217633	968838039.9	128.3249733	7.31461E+15	0.010444457
cg26232187	0.173127168	0.037941827	0.789972937	0.023551589
cg26258845	0.244194828	0.068722991	0.867702537	0.029307108
cg26265187	7.89E-05	3.80E-08	0.164012811	0.015359768
cg26267341	4.0651E+13	689.0173429	2.40E+24	0.013270172
cg26404725	0.000981323	4.22E-06	0.228018599	0.01271056
cg26406994	1.24555E+14	3164.866472	4.90E+24	0.009120799
cg26490839	10302433.26	74.69015362	1.42107E+12	0.007488227
cg26525091	0.138529963	0.026960628	0.711799101	0.017929707
cg26637901	0.005242743	0.000249924	0.109978797	0.000720745
cg26661257	2.09E+36	9.28255E+14	4.69E+57	0.00085633

cg26666286	0.019253605	0.000531542	0.697407696	0.031026352
cg26683023	0.077984576	0.011116353	0.544773397	0.010100149
cg26705561	0.177039447	0.042035154	0.745636997	0.018272083
cg26706070	2283553.955	29.57595276	1.76313E+11	0.010778083
cg26760212	0.180196874	0.035786386	0.907353797	0.0377236
cg26840318	9.69632E+11	27555.26656	3.412E+19	0.001850823
cg26898336	0.194555059	0.05169535	0.73220649	0.015481938
cg26911140	1498598438	192.1771026	1.16861E+16	0.009069844
cg26964415	92027422.07	4.032488728	2.1002E+15	0.033899586
cg26974738	178.447577	3.052860915	10430.72011	0.012501503
cg27014642	1.717E+12	133476.3187	2.21E+19	0.000743608
cg27072323	1701484.833	382.1926272	7574846897	0.000816495
cg27127056	6.5304E+11	21316.5301	2.00061E+19	0.001979687
cg27182555	6048751825	2638.726173	1.38656E+16	0.002575801
cg27243140	0.022838848	0.000872409	0.597899861	0.023285432
cg27258787	1042.010481	1.246608213	870992.0497	0.042952374
cg27308387	5.44047E+11	17189.86135	1.72E+19	0.002164303
cg27320127	0.113285013	0.024220341	0.529864319	0.005659562
cg27378424	7.28372E+18	25457928.43	2.08E+30	0.001251218
cg27413543	1.06963E+12	1004.021687	1.14E+21	0.009010006
cg27416067	0.234901459	0.061949512	0.890704278	0.033157998
cg27447599	0.059188236	0.007246397	0.483446804	0.008333741
cg27462969	7784763631	71.99686081	8.41739E+17	0.015818539
cg27508821	115487925.8	1.053135163	1.26645E+16	0.04936275
cg27514224	3.35E-19	5.71E-31	1.96E-07	0.002090105
cg27533013	1.26E-05	1.88E-09	0.083915079	0.012025781
cg27556566	904701972.5	1475.006116	5.54903E+14	0.002420942
cg27560864	0.047205603	0.00484366	0.460058885	0.008581035
cg27614038	4.01481E+13	60.70646445	2.66E+25	0.024092874
cg27634151	0.083479902	0.010981727	0.63458998	0.01642186
cg27635983	2.51E+35	114.2392634	5.50E+68	0.037440126
cg27662379	3.81E-14	1.16E-24	0.001248814	0.012379689
cg27665659	50009008.89	589.2384986	4.24429E+12	0.002201613

Supplementary Table 5 **GO analysis of annotated genes from the 1061 CpG sites.**

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
BP	GO:0006086	acetyl-CoA biosynthetic process from pyruvate	8/1116	16/20488	6.57E-07	0.00153	0.001381	DLAT/DLD/PDK2/PDK1/MPC2/PDHB/GSTZ1/MPC1	8
BP	GO:0051188	cofactor biosynthetic process	40/1116	326/20488	1.38E-06	0.001927	0.001741	GAPDH/DLAT/DLD/ENO3/NMNAT1/BDH2/PDK2/NUP160/MMAB/FASN/CHAC1/PDK1/NFE2L2/TMEM14C/TP53/MPC2/DUOX1/DUOXA1/SUCLA2/PRKAG1/UROS/PDHB/MBIP/APP/GSTZ1/CBR4/GGT5/DHFR/MPC1/FLAD1/PANK4/PARP16/DDIT4/ACSL3/ENTPD5/SCD/HAGH/PARP9/HIF1A/NUP188	40
BP	GO:0034976	response to endoplasmic reticulum stress	35/1116	285/20488	6.06E-06	0.004948	0.004469	FBXO27/TBL2/UBE2K/TMCO1/SERINC3/THBS1/CHAC1/TMBIM6/NFE2L2/TP53/RNF103/ZBTB17/DERL2/TMTC3/ATF6/ANKZF1/CND1/SDF2/TMX1/ATF4/POMT2/ATP6V0D1/MANF/HSP90B1/DNAJC18/EDEM3/EIF2S1/DNAJB11/PARP16/UBXN1/FICD/UBXN4/RNFT1/SEC31A/IGFBP1	35
BP	GO:0032204	regulation of telomere maintenance	16/1116	81/20488	6.36E-06	0.004948	0.004469	PPP1R10/CCT6A/TERF2/RTEL1/UPF1/TCP1/PINX1/HNRNPA1/SMG6/USP7/HNRNPD/NAF1/TINF2/XRN1/TERF1/MAP2K7	16
BP	GO:0006414	translational elongation	21/1116	133/20488	1.03E-05	0.005498	0.004965	MRPS18B/MRPS28/MRPL3/EEF2K/RPLP1/MRPS25/MRPL18/MRPS31/MRPL12/SRP9/CHCHD1/MRPL45/MRPL47/MRPL49/MRPL19/DPH3/EEF1D/GTPBP2/MRPL11/MRPL24/MRPS18A	21
BP	GO:0006415	translational termination	18/1116	104/20488	1.20E-05	0.005498	0.004965	MRPS18B/MRPS28/MRRF/MRPL3/UPF1/MRPS25/MRPL18/MRPS31/MRPL12/CHCHD1/MRPL45/MRPL47/JMJD4/MRPL49/MRPL19/MRPL11/MRPL24/MRPS18A	18
BP	GO:0006085	acetyl-CoA biosynthetic process	8/1116	22/20488	1.22E-05	0.005498	0.004965	DLAT/DLD/PDK2/PDK1/MPC2/PDHB/GSTZ1/MPC1	8

BP	GO:0050821	protein stabilization	25/1116	178/2048 8	1.29E-05	0.005498	0.004965	GAPDH/SUMO1/DVL3/PFN1/ANK2/CCT6A/SMO/ZBED3/FBXW7/TP53/ATP1B3/RPL5/CCNH/NAA15/TCP1/CRTAP/CAMLG/RPL11/TAF9/TNIP2/USP7/CHEK2/USP33/TESC/ATF7IP	25
BP	GO:0032543	mitochondrial translation	21/1116	135/2048 8	1.30E-05	0.005498	0.004965	MALSU1/MRPS18B/MRPS28/MRRF/MRPL3/WARS2/MRPS25/MRPL18/MRPS31/CDK5RAP1/MRPL12/CHCHD1/MRPL45/MRPL47/MRPL49/MRPL19/RPUSD4/COA3/MRPL11/MRPL24/MRPS18A	21
BP	GO:0031647	regulation of protein stability	34/1116	284/2048 8	1.41E-05	0.005498	0.004965	GAPDH/SUMO1/DVL3/PFN1/ANK2/CCT6A/HTT/SMO/ZBED3/FBXW7/TP53/ATP1B3/RPL5/RNF149/CCNH/NAA15/TCP1/CRTAP/PINX1/CAMLG/CASP3/RPL11/TAF9/TNIP2/USP7/TADA3/PRKDC/CHEK2/USP33/CTSA/TESC/CHFR/KDM8/ATF7IP	34
BP	GO:0044774	mitotic DNA integrity checkpoint	18/1116	106/2048 8	1.57E-05	0.005498	0.004965	PIDD1/CNOT7/TAOK3/PPP1R10/BLM/MUS81/TP53/MUC1/PLAGL1/CCND1/RAD17/MDC1/RGCC/CNOT6/PRKDC/CHEK2/CNOT2/NEK11	18
BP	GO:0044773	mitotic DNA damage checkpoint	17/1116	97/20488	1.76E-05	0.005591	0.005049	PIDD1/CNOT7/TAOK3/PPP1R10/BLM/MUS81/TP53/MUC1/PLAGL1/CCND1/MDC1/RGCC/CNOT6/PRKDC/CHEK2/CNOT2/NEK11	17
BP	GO:2000278	regulation of DNA biosynthetic process	18/1116	108/2048 8	2.05E-05	0.00624	0.005635	CCT6A/TERF2/TP53/WRAP53/PARP4/TCP1/PINX1/HNRNPA1/SMG6/RGCC/FGFR4/HNRNPD/NAF1/TINF2/BMPR2/XRN1/TERF1/MAP2K7	18
BP	GO:0070126	mitochondrial translational termination	16/1116	89/20488	2.22E-05	0.006471	0.005844	MRPS18B/MRPS28/MRRF/MRPL3/MRPS25/MRPL18/MRPS31/MRPL12/CHCHD1/MRPL45/MRPL47/MRPL49/MRPL19/MRPL11/MRPL24/MRPS18A	16
BP	GO:0006084	acetyl-CoA metabolic process	10/1116	38/20488	2.58E-05	0.006815	0.006154	DLAT/DLD/PDK2/MVK/FASN/PDK1/MPC2/PDHB/GSTZ1/MPC1	10
BP	GO:0035384	thioester biosynthetic process	12/1116	54/20488	2.63E-05	0.006815	0.006154	DLAT/DLD/PDK2/FASN/PDK1/MPC2/PDHB/GSTZ1/CBR4/MPC1	12

								/ACSL3/SCD	
BP	GO:0071616	acyl-CoA biosynthetic process	12/1116	54/20488	2.63E-05	0.006815	0.006154	DLAT/DLD/PDK2/FASN/PDK1/MPC2/PDHB/GSTZ1/CBR4/MPC1 /ACSL3/SCD	12
BP	GO:0035966	response to topologically incorrect protein	26/1116	199/2048 8	3.18E-05	0.007687	0.006942	TBL2/HSPH1/THBS1/CHAC1/TMBIM6/NFE2L2/ZBTB17/DERL2/ATF6/ANKZF1/CCND1/SDF2/ATF4/POMT2/ATP6V0D1/MANF/HS P90B1/DNAJC18/EDEM3/EIF2S1/DNAJB11/PARP16/FICD/UBXN4/ SEC31A/IGFBP1	26
BP	GO:0000077	DNA damage checkpoint	21/1116	145/2048 8	3.93E-05	0.00917	0.008282	PIDD1/CNOT7/TAOK3/PPP1R10/BLM/BRCA1/MUS81/ETAA1/TP 53/MUC1/PLAGL1/RHNO1/CCND1/RAD17/MDC1/RGCC/CNOT6 /PRKDC/CHEK2/CNOT2/NEK11	21
BP	GO:0051052	regulation of DNA metabolic process	44/1116	429/2048 8	4.31E-05	0.009314	0.008411	RAC1/PPP1R10/NMNAT1/BLM/CCT6A/TERF2/BRCA1/FBXW7/R TEL1/TRIP12/CACYBP/GATA3/TP53/WRAP53/UPF1/PARP4/FOX M1/TCP1/PINX1/SUPT6H/SMC3/HNRNPA1/RAD17/SMG6/RGCC /USP7/FGF10/PPhLN1/FGFR4/PRKDC/MSH3/CHEK2/HNRNPD/ NAF1/TINF2/EREG/DHX9/BMP2/MBD2/XRN1/TERF1/PARP9/A TF7IP/MAP2K7	44
BP	GO:0140014	mitotic nuclear division	31/1116	264/2048 8	4.83E-05	0.009314	0.008411	SPAG5/CLASP2/PIBF1/CEP97/TUBG1/MIS12/KIF23/IK/MAU2/CE NPK/PINX1/KIF25/BCCIP/SMC3/NCAPD3/CDC23/RGCC/IGF2/C DC14A/SIRT7/CHEK2/SMC4/ANLN/EREG/CENPE/PHIP/CHMP2 B/MAD2L1BP/BIRC5/NCAPG/DRG1	31
BP	GO:0006614	SRP-dependent cotranslational protein targeting to membrane	17/1116	105/2048 8	5.05E-05	0.009314	0.008411	SEC63/RPL27A/RPL7/RPL5/RPS23/RPLP1/RPL7A/RPL11/SRP9/SR P54/RPL31/RPL32/RPL35/RPL18A/RPS15A/RPS11/RPL8	17
BP	GO:0006637	acyl-CoA metabolic process	17/1116	105/2048	5.05E-05	0.009314	0.008411	DLAT/DLD/PDK2/MVK/FASN/PDK1/ACOT13/MPC2/SUCLA2/P	17

				8				DHB/GSTZ1/CBR4/MPC1/DBI/ACSL3/SCD/MCEE	
BP	GO:0035383	thioester metabolic process	17/1116	105/2048 8	5.05E-05	0.009314	0.008411	DLAT/DLD/PDK2/MVK/FASN/PDK1/ACOT13/MPC2/SUCLA2/P DHB/GSTZ1/CBR4/MPC1/DBI/ACSL3/SCD/MCEE	17
CC	GO:0015934	large ribosomal subunit	24/1116	121/2048 8	3.08E-08	0.000216	0.000195	MALSU1/RPL27A/RSL24D1/MRPL3/RPL7/RPL5/RPLP1/MRPL18/ RPL7A/RPL11/MRPL12/MRPL45/MRPL47/RPL31/RPL32/MRPL49/ MRPL19/RPL35/RPL18A/NDUFAB1/MRPL11/MRPL24/MRPS18A/ RPL8	24
CC	GO:0044391	ribosomal subunit	30/1116	190/2048 8	1.43E-07	0.000499	0.000451	MALSU1/MRPS18B/RPL27A/MRPS28/RSL24D1/MRPL3/RPL7/RPL 5/RPS23/RPLP1/MRPL18/MRPS31/RPL7A/RPL11/MRPL12/MRPL4 5/MRPL47/RPL31/RPL32/MRPL49/MRPL19/RPL35/RPL18A/RPS15 A/NDUFAB1/MRPL11/MRPL24/MRPS18A/RPS11/RPL8	30
CC	GO:0098798	mitochondrial protein complex	35/1116	262/2048 8	8.74E-07	0.00153	0.001381	DLAT/MALSU1/MRPS18B/TIMM10/MRPS28/PDK2/TIMM10B/CO X5A/MRPL3/PDK1/MTX1/COX6A1/NDUFC1/NDUFA2/ANKZF1/ UQCRQ/MRPL18/MRPS31/SPG7/MRPL12/CHCHD1/MRPL45/UQC RB/MRPL47/NDUFB5/MRPL49/MRPL19/MFN1/COA3/NDUFAB1/ MRPL11/NDUFB1/MRPL24/MRPS18A/BCKDK	35
CC	GO:0005743	mitochondrial inner membrane	51/1116	473/2048 8	2.66E-06	0.003104	0.002803	COX8C/MRPS18B/TIMM10/MRPS28/TIMM10B/COX5A/MRPL3/U QCR11/LETM1/TIMM44/TMEM14C/COX6A1/COX18/MPC2/SLC25 A29/NDUFC1/NDUFA2/MPV17/MRPS25/UQCRQ/MRPL18/MRPS3 1/NDUFAF4/CYP2E1/SPG7/MRPL12/SLC25A10/CHCHD1/COX5B/ MRS2/MRPL45/MPC1/TMEM126B/MTCH2/UQCRB/MRPL47/NDU FB5/SLC25A2/MRPL49/MRPL19/ACAD9/COA3/SIRT4/GUF1/ECSI T/NDUFAB1/TMEM70/MRPL11/NDUFB1/MRPL24/MRPS18A	51

CC	GO:0016607	nuclear speck	44/1116	397/2048 8	6.33E-06	0.004948	0.004469	CNOT7/SUMO1/GLIS2/SRSF11/RBM4/MORF4L1/DDX17/PRPF40A/PPP1R8/TRIP12/PIAS1/SAP130/RBM19/SNRNP40/IK/S100PBP/RBM39/SRRM1/KAT6A/CDK12/HAUS6/TKT/GLYR1/SRP54/PRPF4B/BDNF/SMC4/DGKQ/RBM14/SF3A3/SART1/PNN/TUT1/DAZAP2/SMNDC1/HIPK1/SPRTN/FBXL4/RSRC1/NDUFB1/NSRP1/SAP18/BAZ2A/HIF1A	44
CC	GO:0098687	chromosomal region	40/1116	349/2048 8	7.44E-06	0.00521	0.004705	SPAG5/FBXO28/PPP1R10/BLM/CLASP2/FEN1/DCTN5/NUP160/UVRAG/TERF2/RTEL1/WRAP53/MIS12/HELLS/XPO1/UPF1/CENPK/PINX1/SMC3/CBX5/RAD17/SMG6/NCAPD3/SCMH1/SIRT7/MCM4/PRKDC/CHEK2/CKAP5/TINF2/CENPE/KAT8/PHF2/DCTN4/RANGAP1/MBD6/TERF1/MCM7/BIRC5/NCAPG	40
CC	GO:0005840	ribosome	33/1116	272/2048 8	1.43E-05	0.005498	0.004965	MALSU1/MRPS18B/RPL27A/MRPS28/RSL24D1/MRPL3/RPL7/RPL5/RPS23/RPLP1/MRPS25/MRPL18/MRPS31/RPL7A/RPL11/MRPL12/CHCHD1/MRPL45/MRPL47/RPL31/RPL32/MRPL49/MRPL19/DHX9/RPL35/RPL18A/RPS15A/NDUFAB1/MRPL11/MRPL24/MRPS18A/RPS11/RPL8	33
CC	GO:0000313	organellar ribosome	16/1116	87/20488	1.65E-05	0.005498	0.004965	MALSU1/MRPS18B/MRPS28/MRPL3/MRPL18/MRPS31/MRPL12/CHCHD1/MRPL45/MRPL47/MRPL49/MRPL19/NDUFAB1/MRPL11/MRPL24/MRPS18A	16
CC	GO:0005761	mitochondrial ribosome	16/1116	87/20488	1.65E-05	0.005498	0.004965	MALSU1/MRPS18B/MRPS28/MRPL3/MRPL18/MRPS31/MRPL12/CHCHD1/MRPL45/MRPL47/MRPL49/MRPL19/NDUFAB1/MRPL11/MRPL24/MRPS18A	16
CC	GO:0005844	polysome	14/1116	72/20488	2.87E-05	0.007183	0.006486	PSMA1/NAA38/RPS23/RPL7A/RPL11/LIN28A/RPL31/RPL32/DHX9/EIF2S1/RPL18A/IMPACT/RPL8/DRG1	14

CC	GO:0005759	mitochondrial matrix	47/1116	469/2048 8	4.28E-05	0.009314	0.008411	DLAT/DLD/MALSU1/MRPS18B/MRPS28/PDK2/MMAB/MRRF/MRPL3/WARS2/TIMM44/ACSS3/PDK1/AK3/TP53/PPM1K/ACADL/AGXT2/SUCLA2/MRPL18/MRPS31/PDHB/PRIMPOL/ATG4D/FDX1/MRPL12/GSTZ1/CBR4/CHCHD1/REXO2/MRPL45/FLAD1/MRPL47/MRPL49/MRPL19/RPUSD4/SIRT4/GUF1/NDUFAB1/HIBCH/MCEE/MRPL11/MRPL24/MRPS18A/FAHD1/HAGH/BCKDK	47
CC	GO:0000315	organellar large ribosomal subunit	12/1116	57/20488	4.66E-05	0.009314	0.008411	MALSU1/MRPL3/MRPL18/MRPL12/MRPL45/MRPL47/MRPL49/MRPL19/NDUFAB1/MRPL11/MRPL24/MRPS18A	12
CC	GO:0005762	mitochondrial large ribosomal subunit	12/1116	57/20488	4.66E-05	0.009314	0.008411	MALSU1/MRPL3/MRPL18/MRPL12/MRPL45/MRPL47/MRPL49/MRPL19/NDUFAB1/MRPL11/MRPL24/MRPS18A	12
MF	GO:0003735	structural constituent of ribosome	27/1116	202/2048 8	1.49E-05	0.005498	0.004965	MRPS18B/RPL27A/RSL24D1/MRPL3/RPL7/RPL5/RPS23/RPLP1/MRPS25/MRPL18/MRPS31/RPL7A/RPL11/MRPL12/MRPL47/RPL31/RPL32/MRPL49/MRPL19/RPL35/RPL18A/RPS15A/MRPL11/MRPL24/MRPS18A/RPS11/RPL8	27
MF	GO:0003735	structural constituent of ribosome	27/1116	202/2048 8	1.49E-05	0.005498	0.004965	MRPS18B/RPL27A/RSL24D1/MRPL3/RPL7/RPL5/RPS23/RPLP1/MRPS25/MRPL18/MRPS31/RPL7A/RPL11/MRPL12/MRPL47/RPL31/RPL32/MRPL49/MRPL19/RPL35/RPL18A/RPS15A/MRPL11/MRPL24/MRPS18A/RPS11/RPL8	27
MF	GO:0003735	structural constituent of ribosome	27/1116	202/2048 8	1.49E-05	0.005498	0.004965	MRPS18B/RPL27A/RSL24D1/MRPL3/RPL7/RPL5/RPS23/RPLP1/MRPS25/MRPL18/MRPS31/RPL7A/RPL11/MRPL12/MRPL47/RPL31/RPL32/MRPL49/MRPL19/RPL35/RPL18A/RPS15A/MRPL11/MRPL24/MRPS18A/RPS11/RPL8	27

Table S6. Differential analysis of methylation sites among the clusters.

Cluster 1 diff					
CpG sites	conMean	treatMean	logFC	P Value	fdr
cg00622677	0.136847	0.550918	2.00927	1.43E-09	1.26E-08
cg00658626	0.127131	0.53062	2.061361	6.17E-13	7.52E-11
cg00755043	0.195078	0.53625	1.458857	7.63E-11	1.24E-09
cg01015879	0.080353	0.417104	2.375989	1.23E-08	8.09E-08
cg02197293	0.146605	0.587376	2.002354	3.39E-10	4.19E-09
cg02244695	0.176323	0.52942	1.586194	2.52E-09	2.07E-08
cg02548238	0.180052	0.561087	1.639813	7.54E-13	7.87E-11
cg02755525	0.125625	0.451519	1.845666	4.91E-07	2.61E-06
cg02784848	0.066551	0.241384	1.858798	3.23E-06	1.63E-05
cg02899772	0.23933	0.579743	1.276415	4.54E-10	5.02E-09
cg02930996	0.133091	0.409489	1.621413	0.000284	0.001227
cg02959669	0.148698	0.45589	1.616299	2.76E-10	3.49E-09
cg03048535	0.135272	0.428579	1.663704	6.55E-11	1.20E-09
cg03079681	0.072241	0.295257	2.031077	4.57E-07	2.44E-06
cg03439703	0.308182	0.630506	1.032729	1.75E-09	1.51E-08
cg04051458	0.137501	0.491645	1.838171	7.02E-10	7.23E-09
cg04367351	0.034509	0.290831	3.075145	1.57E-07	8.96E-07
cg04402875	0.225894	0.603667	1.41811	2.32E-13	6.15E-11
cg04532952	0.123139	0.601067	2.287239	5.27E-14	5.59E-11
cg04603184	0.164985	0.618363	1.906123	2.16E-11	5.37E-10
cg04726446	0.169284	0.409581	1.274704	8.49E-05	0.000382
cg04988423	0.289904	0.61036	1.074087	7.18E-11	1.24E-09
cg05203877	0.264116	0.653183	1.306316	2.23E-11	5.37E-10
cg05647859	0.395547	0.800471	1.017	6.75E-11	1.21E-09
cg05886626	0.175319	0.558558	1.671728	6.05E-08	3.58E-07
cg06230736	0.273769	0.655697	1.26007	3.66E-11	7.92E-10
cg06377278	0.192663	0.541573	1.491078	4.26E-09	3.28E-08
cg06533629	0.236979	0.629179	1.408714	3.51E-09	2.80E-08
cg07027513	0.14392	0.405878	1.495779	0.000185	0.000815
cg08555772	0.244044	0.583536	1.257681	8.94E-12	3.50E-10
cg08717396	0.11566	0.05707	-1.01908	0.000345	0.001464
cg08909157	0.228797	0.46075	1.009917	9.33E-05	0.000418
cg09022993	0.099827	0.251522	1.333183	0.00247	0.008855
cg09068528	0.141787	0.567002	1.99963	9.23E-12	3.50E-10
cg09416313	0.277612	0.600763	1.113729	4.54E-10	5.02E-09
cg09649610	0.309087	0.710098	1.200006	5.97E-13	7.52E-11
cg09660171	0.185403	0.5925	1.676154	1.63E-11	4.67E-10

cg10806140	0.244801	0.615566	1.330304	2.23E-11	5.37E-10
cg11021744	0.271278	0.554707	1.031951	5.61E-09	4.19E-08
cg11392765	0.081083	0.475194	2.551051	9.84E-12	3.60E-10
cg11538128	0.247269	0.505774	1.032414	1.78E-08	1.14E-07
cg11879514	0.247718	0.629913	1.346451	3.51E-09	2.80E-08
cg12359315	0.068192	0.369282	2.43704	1.07E-06	5.60E-06
cg12388309	0.20171	0.652916	1.694614	3.20E-12	1.79E-10
cg12687990	0.155177	0.514452	1.729119	2.47E-12	1.64E-10
cg13301933	0.222207	0.543795	1.291157	5.80E-11	1.10E-09
cg13449778	0.212414	0.563133	1.406594	4.41E-13	7.52E-11
cg13643796	0.242663	0.681392	1.489532	1.44E-11	4.36E-10
cg13756879	0.338714	0.721649	1.091229	3.93E-10	4.63E-09
cg13936125	0.191666	0.629324	1.715209	5.20E-12	2.51E-10
cg13966710	0.067821	0.298264	2.136776	4.67E-05	0.000214
cg14049461	0.138206	0.456824	1.724821	5.13E-11	1.01E-09
cg14135551	0.238398	0.644173	1.434077	7.86E-11	1.24E-09
cg14174099	0.243005	0.609348	1.326278	4.68E-11	9.55E-10
cg14538332	0.232816	0.549651	1.239328	5.72E-12	2.64E-10
cg14617642	0.22231	0.527734	1.247241	9.39E-09	6.43E-08
cg14654926	0.267619	0.559313	1.063474	7.44E-10	7.59E-09
cg14795305	0.0818	0.410892	2.328586	2.81E-12	1.66E-10
cg15105703	0.140426	0.502613	1.839641	2.63E-12	1.64E-10
cg15205507	0.275551	0.667444	1.276327	1.62E-10	2.17E-09
cg16004226	0.208944	0.54272	1.377091	9.43E-11	1.41E-09
cg16114640	0.15361	0.627372	2.030047	1.56E-12	1.27E-10
cg16530429	0.257567	0.535357	1.05555	2.13E-09	1.78E-08
cg16551261	0.106885	0.346847	1.698236	3.23E-06	1.63E-05
cg16652259	0.21482	0.484177	1.172404	3.34E-08	2.06E-07
cg17163751	0.230244	0.573879	1.317585	8.66E-09	5.97E-08
cg17178888	0.103318	0.418576	2.018403	2.16E-07	1.20E-06
cg17194182	0.190693	0.57159	1.583728	7.86E-11	1.24E-09
cg17301902	0.186351	0.497955	1.417995	3.92E-09	3.06E-08
cg17729667	0.169087	0.515155	1.607238	1.15E-11	3.94E-10
cg17977409	0.247687	0.630315	1.347554	8.90E-13	7.87E-11
cg18453621	0.199675	0.640778	1.68217	8.39E-12	3.42E-10
cg18695917	0.180146	0.613613	1.768163	8.61E-13	7.87E-11
cg18909638	0.151499	0.529578	1.80554	1.32E-09	1.18E-08
cg18943599	0.095444	0.416147	2.124367	4.01E-08	2.42E-07
cg19219437	0.148999	0.51573	1.791316	9.36E-10	9.02E-09
cg19275050	0.126668	0.550043	2.118496	1.96E-09	1.65E-08
cg19528976	0.248451	0.524918	1.079129	4.11E-08	2.47E-07

cg19564877	0.107723	0.455335	2.079603	9.91E-09	6.70E-08
cg19570574	0.188481	0.58795	1.641274	5.46E-09	4.11E-08
cg19709625	0.073108	0.438826	2.585547	1.62E-10	2.17E-09
cg19786920	0.159826	0.397347	1.313902	0.000919	0.003692
cg19850348	0.211011	0.586588	1.475031	4.16E-10	4.85E-09
cg19918758	0.1851	0.539241	1.542623	8.35E-11	1.28E-09
cg20123891	0.150715	0.668924	2.150015	1.27E-11	4.07E-10
cg20199629	0.063521	0.393298	2.630316	2.06E-07	1.15E-06
cg20496643	0.132585	0.324078	1.289418	0.001209	0.004733
cg20727114	0.17216	0.400467	1.217935	7.23E-06	3.55E-05
cg21092462	0.235213	0.475634	1.015888	1.12E-11	3.94E-10
cg21718857	0.047754	0.185269	1.955933	2.10E-05	0.0001
cg22088594	0.138541	0.50143	1.85573	1.74E-08	1.12E-07
cg22156632	0.299026	0.614616	1.039417	1.16E-10	1.69E-09
cg22571530	0.293779	0.601932	1.034872	3.33E-11	7.53E-10
cg22580173	0.116484	0.514681	2.143544	7.17E-09	5.10E-08
cg22886089	0.213015	0.54791	1.362986	7.40E-11	1.24E-09
cg23391785	0.30551	0.64908	1.087176	1.05E-09	9.94E-09
cg23422659	0.142972	0.507746	1.82837	1.19E-11	3.94E-10
cg23442323	0.139997	0.441433	1.656793	4.96E-10	5.37E-09
cg23478284	0.194639	0.611289	1.651054	6.08E-10	6.51E-09
cg23699324	0.210211	0.567921	1.433851	8.84E-10	8.60E-09
cg23850272	0.083235	0.227749	1.452191	2.19E-05	0.000104
cg23964386	0.241062	0.494243	1.035819	8.62E-08	5.03E-07
cg24014661	0.083599	0.324583	1.957033	3.09E-08	1.93E-07
cg24098951	0.244476	0.66122	1.435436	4.83E-11	9.66E-10
cg24194132	0.195958	0.543513	1.471772	7.86E-11	1.24E-09
cg24399106	0.221474	0.499031	1.171988	2.45E-10	3.17E-09
cg24680602	0.162159	0.480906	1.568345	9.65E-09	6.56E-08
cg24794531	0.296964	0.645152	1.119349	4.82E-10	5.27E-09
cg25047001	0.213005	0.525928	1.303977	3.81E-10	4.60E-09
cg25519930	0.296421	0.622157	1.069635	4.42E-12	2.23E-10
cg25924032	0.118692	0.393076	1.727582	2.37E-11	5.59E-10
cg25959506	0.113711	0.440942	1.955217	2.68E-10	3.43E-09
cg26055770	0.265307	0.546692	1.043065	1.26E-08	8.26E-08
cg26232187	0.225805	0.553656	1.293912	1.03E-10	1.52E-09
cg26258845	0.215896	0.606368	1.489859	2.16E-11	5.37E-10
cg26898336	0.296412	0.685272	1.20907	1.59E-13	6.15E-11
cg27416067	0.210602	0.625702	1.570957	4.41E-13	7.52E-11
cg27447599	0.247815	0.551147	1.153171	1.31E-10	1.88E-09

Cluster 3 diff

CpG sites	conMean	treatMean	logFC	pValue	fdr
cg00622677	0.32036	0.054861	-2.54584	5.51E-12	4.79E-11
cg00658626	0.300579	0.053373	-2.49355	1.38E-19	5.05E-18
cg00755043	0.349084	0.124329	-1.48942	1.15E-11	9.79E-11
cg01015879	0.206261	0.040304	-2.35549	8.84E-07	4.94E-06
cg01656955	0.503498	0.213745	-1.23609	1.13E-17	2.40E-16
cg02064106	0.545829	0.264565	-1.04482	3.77E-14	3.74E-13
cg02197293	0.299714	0.107525	-1.47892	1.02E-05	5.48E-05
cg02548238	0.349714	0.103704	-1.7537	2.60E-14	2.76E-13
cg02755525	0.263194	0.06893	-1.93293	0.000112	0.000546
cg02784848	0.139722	0.036856	-1.92261	1.44E-06	7.91E-06
cg02899772	0.407003	0.152753	-1.41384	1.54E-14	1.67E-13
cg02930996	0.231905	0.105387	-1.13784	0.013454	0.040667
cg02959669	0.295512	0.075701	-1.96484	5.61E-15	6.40E-14
cg03048535	0.261488	0.081504	-1.6818	1.20E-15	1.63E-14
cg03079681	0.160766	0.039852	-2.01224	4.02E-08	2.51E-07
cg04051458	0.279964	0.083915	-1.73824	4.45E-10	3.15E-09
cg04367351	0.111345	0.025705	-2.11493	0.00071	0.003074
cg04402875	0.416897	0.124192	-1.74712	6.75E-17	1.14E-15
cg04532952	0.301572	0.066597	-2.17897	4.79E-11	3.79E-10
cg04603184	0.378657	0.060681	-2.64158	4.70E-15	5.42E-14
cg04988423	0.477607	0.174332	-1.45399	1.83E-20	1.39E-18
cg05203877	0.486889	0.129638	-1.9091	5.70E-20	2.88E-18
cg05647859	0.644833	0.235697	-1.45199	1.55E-19	5.50E-18
cg05886626	0.317154	0.1314	-1.27121	1.68E-05	8.85E-05
cg06230736	0.451972	0.187952	-1.26587	4.93E-10	3.46E-09
cg06243556	0.478961	0.212852	-1.17006	5.59E-14	5.50E-13
cg06377278	0.378249	0.08826	-2.0995	3.25E-14	3.32E-13
cg06533629	0.39791	0.174029	-1.19312	5.76E-09	3.77E-08
cg06638433	0.586325	0.258103	-1.18376	6.80E-20	3.14E-18
cg07017374	0.638276	0.271785	-1.23171	2.39E-17	4.45E-16
cg07027513	0.238745	0.116325	-1.03731	0.005553	0.019575
cg07295678	0.519846	0.239901	-1.11565	4.46E-22	1.18E-19
cg07312445	0.144703	0.04782	-1.59741	0.000165	0.000778
cg08555772	0.432735	0.133201	-1.69987	8.86E-21	9.40E-19
cg08623787	0.577448	0.269795	-1.09783	4.07E-19	1.35E-17
cg08897388	0.4974	0.233607	-1.09033	5.95E-18	1.40E-16
cg09068528	0.302012	0.089801	-1.7498	1.02E-07	6.18E-07
cg09416313	0.457432	0.171864	-1.41229	8.32E-18	1.92E-16
cg09649610	0.507803	0.205735	-1.30348	1.83E-16	2.90E-15

cg09660171	0.375439	0.093827	-2.0005	1.26E-16	2.05E-15
cg10806140	0.441193	0.134794	-1.71065	1.67E-17	3.22E-16
cg10887021	0.433232	0.177113	-1.29047	2.76E-13	2.57E-12
cg11021744	0.451843	0.152458	-1.56741	6.41E-20	3.09E-18
cg11392765	0.224355	0.038871	-2.52901	1.18E-09	8.00E-09
cg11879514	0.407257	0.183278	-1.15191	1.86E-08	1.18E-07
cg12359315	0.165892	0.049358	-1.7489	0.000165	0.000778
cg12388309	0.420714	0.090654	-2.21439	7.09E-16	1.02E-14
cg12515638	0.569506	0.261362	-1.12366	5.21E-20	2.88E-18
cg12645220	0.465706	0.172876	-1.42968	2.53E-21	3.84E-19
cg12687990	0.323116	0.074101	-2.12449	6.10E-19	1.90E-17
cg13301933	0.391954	0.127472	-1.6205	8.13E-20	3.45E-18
cg13449778	0.394288	0.112805	-1.80542	8.56E-18	1.93E-16
cg13643796	0.498841	0.08535	-2.54712	4.68E-21	6.20E-19
cg13756879	0.590656	0.169068	-1.80472	1.91E-22	6.75E-20
cg13936125	0.410116	0.077073	-2.41172	1.41E-17	2.83E-16
cg14049461	0.292649	0.060018	-2.28569	5.15E-17	8.81E-16
cg14135551	0.464671	0.105069	-2.14488	9.15E-20	3.73E-18
cg14174099	0.460946	0.10705	-2.10631	5.70E-20	2.88E-18
cg14538332	0.403014	0.136103	-1.56614	4.91E-20	2.88E-18
cg14617642	0.392474	0.122124	-1.68425	9.21E-16	1.27E-14
cg14654926	0.411974	0.192659	-1.0965	1.44E-15	1.93E-14
cg14795305	0.193939	0.055106	-1.81533	4.94E-09	3.25E-08
cg15105703	0.257924	0.1178	-1.13061	1.39E-06	7.70E-06
cg15205507	0.501173	0.138693	-1.85341	1.26E-17	2.58E-16
cg15817236	0.589225	0.246042	-1.25992	9.43E-22	1.67E-19
cg15873301	0.602084	0.272164	-1.14549	1.71E-13	1.62E-12
cg16004226	0.359657	0.139677	-1.36453	8.27E-14	8.05E-13
cg16114640	0.34501	0.080991	-2.0908	3.17E-14	3.27E-13
cg16257091	0.639847	0.305488	-1.06661	6.10E-22	1.29E-19
cg16530429	0.393069	0.18843	-1.06075	3.34E-14	3.34E-13
cg16551261	0.188041	0.088119	-1.09353	0.011223	0.035438
cg16652259	0.340269	0.154558	-1.13852	1.26E-11	1.05E-10
cg17163751	0.426551	0.111986	-1.92939	2.67E-15	3.37E-14
cg17178888	0.238551	0.046015	-2.37412	1.90E-09	1.27E-08
cg17194182	0.379241	0.092755	-2.03162	1.63E-15	2.17E-14
cg17398595	0.552247	0.270029	-1.0322	1.33E-18	4.02E-17
cg17977409	0.433036	0.153931	-1.49221	3.12E-15	3.67E-14
cg18277754	0.539001	0.256148	-1.07331	1.98E-18	5.52E-17
cg18453621	0.413631	0.09127	-2.18014	4.30E-16	6.42E-15
cg18695917	0.376648	0.089307	-2.07637	4.78E-16	7.04E-15

cg18909638	0.294516	0.104644	-1.49285	2.31E-07	1.39E-06
cg18943599	0.228116	0.04274	-2.41609	1.03E-14	1.15E-13
cg19001226	0.539003	0.26483	-1.02523	1.54E-14	1.67E-13
cg19219437	0.322496	0.063874	-2.33599	3.04E-11	2.44E-10
cg19275050	0.290316	0.07021	-2.04787	7.14E-07	4.03E-06
cg19283196	0.473986	0.215992	-1.13387	1.98E-18	5.52E-17
cg19528976	0.398796	0.161971	-1.29991	2.89E-15	3.52E-14
cg19564877	0.233825	0.070794	-1.72373	1.35E-05	7.22E-05
cg19570574	0.356172	0.120055	-1.56887	1.28E-07	7.73E-07
cg19709625	0.216671	0.021828	-3.31126	3.95E-13	3.64E-12
cg19786920	0.263097	0.115074	-1.19303	0.000251	0.001172
cg19850348	0.421833	0.086019	-2.29395	3.99E-20	2.82E-18
cg19918758	0.359477	0.095098	-1.91842	6.55E-16	9.52E-15
cg20123891	0.366865	0.063532	-2.5297	2.81E-15	3.47E-14
cg20199629	0.173804	0.039155	-2.15018	0.00011	0.000541
cg21718857	0.101154	0.029135	-1.79572	7.38E-07	4.14E-06
cg22036988	0.608575	0.230318	-1.40181	2.73E-23	2.89E-20
cg22088594	0.272479	0.097373	-1.48455	2.43E-07	1.45E-06
cg22571530	0.479714	0.176438	-1.44301	1.39E-22	6.75E-20
cg22572159	0.590829	0.255761	-1.20795	1.48E-20	1.21E-18
cg22580173	0.269747	0.064129	-2.07255	1.35E-08	8.75E-08
cg22886089	0.379678	0.125893	-1.59258	2.35E-15	3.08E-14
cg23357981	0.474119	0.235715	-1.0082	1.26E-19	4.79E-18
cg23391785	0.517614	0.169208	-1.61308	3.71E-17	6.74E-16
cg23422659	0.308882	0.065903	-2.22863	3.29E-18	8.32E-17
cg23442323	0.254627	0.101952	-1.3205	4.73E-08	2.94E-07
cg23478284	0.411002	0.075963	-2.43577	8.80E-18	1.95E-16
cg23699324	0.389906	0.11524	-1.75849	3.12E-15	3.67E-14
cg24014661	0.179105	0.048773	-1.87665	1.20E-10	8.90E-10
cg24098951	0.436559	0.153534	-1.50762	7.81E-13	7.03E-12
cg24194132	0.346391	0.131249	-1.40009	5.11E-11	4.01E-10
cg24399106	0.342845	0.168389	-1.02576	7.38E-12	6.37E-11
cg24680602	0.274729	0.13179	-1.05976	8.18E-06	4.43E-05
cg24794531	0.49017	0.183647	-1.41635	3.21E-16	4.86E-15
cg25047001	0.383669	0.114557	-1.7438	8.13E-20	3.45E-18
cg25437385	0.499549	0.240311	-1.05572	3.04E-15	3.66E-14
cg25519930	0.484154	0.182439	-1.40805	9.99E-20	3.93E-18
cg25924032	0.259813	0.042095	-2.62574	3.69E-18	9.10E-17
cg25959506	0.24441	0.065267	-1.90488	8.01E-11	6.07E-10
cg26055770	0.406219	0.191103	-1.08791	7.51E-11	5.74E-10
cg26232187	0.403106	0.124378	-1.69643	1.03E-20	9.95E-19

cg26258845	0.417814	0.105648	-1.9836	1.40E-18	4.14E-17
cg26898336	0.475382	0.211852	-1.16603	2.67E-15	3.37E-14
cg27320127	0.475396	0.206697	-1.20161	1.24E-20	1.09E-18
cg27416067	0.400532	0.12161	-1.71966	7.24E-15	8.17E-14

Supplementary Table 7 The 41 specific hyper/hypomethylation CpG sites for each cluster.

CpG sites	Cluster	CpG sites	Cluster
cg02244695	Cluster 1	cg07017374	Cluster 3
cg03439703	Cluster 1	cg07295678	Cluster 3
cg04726446	Cluster 1	cg07312445	Cluster 3
cg08717396	Cluster 1	cg08623787	Cluster 3
cg08909157	Cluster 1	cg08897388	Cluster 3
cg09022993	Cluster 1	cg10887021	Cluster 3
cg11538128	Cluster 1	cg12515638	Cluster 3
cg13966710	Cluster 1	cg12645220	Cluster 3
cg17301902	Cluster 1	cg15817236	Cluster 3
cg17729667	Cluster 1	cg15873301	Cluster 3
cg20496643	Cluster 1	cg16257091	Cluster 3
cg20727114	Cluster 1	cg17398595	Cluster 3
cg21092462	Cluster 1	cg18277754	Cluster 3
cg22156632	Cluster 1	cg19001226	Cluster 3
cg23850272	Cluster 1	cg19283196	Cluster 3
cg23964386	Cluster 1	cg22036988	Cluster 3
cg27447599	Cluster 1	cg22572159	Cluster 3
cg01656955	Cluster 3	cg23357981	Cluster 3
cg02064106	Cluster 3	cg25437385	Cluster 3
cg06243556	Cluster 3	cg27320127	Cluster 3
cg06638433	Cluster 3		

Supplementary Table 8 **KEGG pathway analysis of genes corresponding to the 41 specific CpG sites.**

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa04151	PI3K-Akt signaling pathway	4/19	354/8031	0.00849890299942237	0.21164338620804	0.179556054284905	FLT3/LAMA4/BDNF/NGF	4
hsa05223	Non-small cell lung cancer	2/19	68/8031	0.0110082697374581	0.21164338620804	0.179556054284905	RXRG/ALK	2
hsa04920	Adipocytokine signaling pathway	2/19	69/8031	0.0113209640769447	0.21164338620804	0.179556054284905	RXRG/CPT1C	2
hsa03320	PPAR signaling pathway	2/19	77/8031	0.0139621477674749	0.21164338620804	0.179556054284905	RXRG/CPT1C	2
hsa04014	Ras signaling pathway	3/19	232/8031	0.0163802461074068	0.21164338620804	0.179556054284905	FLT3/BDNF/NGF	3
hsa05222	Small cell lung cancer	2/19	92/8031	0.0195587706951738	0.21164338620804	0.179556054284905	RXRG/LAMA4	2
hsa05146	Amoebiasis	2/19	102/8031	0.0237328908155486	0.21164338620804	0.179556054284905	LAMA4/GNA14	2
hsa04922	Glucagon signaling pathway	2/19	106/8031	0.0254972054523731	0.21164338620804	0.179556054284905	PDE3B/CPT1C	2
hsa04010	MAPK signaling pathway	3/19	294/8031	0.0304722032933232	0.21164338620804	0.179556054284905	FLT3/BDNF/NGF	3
hsa04722	Neurotrophin signaling pathway	2/19	119/8031	0.0315885651056777	0.21164338620804	0.179556054284905	BDNF/NGF	2
hsa00230	Purine metabolism	2/19	130/8031	0.0371501140064946	0.226277967130467	0.191971880990499	NT5C1A/PDE3B	2
hsa04550	Signaling pathways regulating pluripotency of stem cells	2/19	143/8031	0.0441746949073979	0.245186249562337	0.208013471741809	HOXD1/WNT6	2
hsa05226	Gastric cancer	2/19	149/8031	0.0475734514076175	0.245186249562337	0.208013471741809	RXRG/WNT6	2