

## Appendix

### Selinexor in Advanced, Metastatic Dedifferentiated Liposarcoma: A Multinational, Randomized, Double-Blind, Placebo-Controlled Trial

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#### Table of Contents

1. SUPPLEMENTAL METHODS.....	2
2. FIGURE A1 .....	3
3. FIGURE A2 .....	4
4. FIGURE A3 .....	5
5. TABLE A1. INCLUSION/EXCLUSION CRITERIA .....	6
6. TABLE A2. SET 1: SENSITIVE AND RESISTANT TUMORS BY CHANGE IN TARGET SIZE .....	8
7. TABLE A3. SET 2: PATIENTS WITH FAVORABLE OR POOR RESPONSE BY PFS.....	9
8. TABLE A4. SUBSEQUENT THERAPIES OF ALL ENROLLED PATIENTS .....	11
9. TABLE A5. SERIOUS TREATMENT-EMERGENT ADVERSE EVENTS .....	12
10. TABLE A6. SET 1: DIFFERENTIALLY EXPRESSED GENES BETWEEN SENSITIVE AND RESISTANT TUMORS 13	
11. TABLE A7: SET 2: SIGNIFICANTLY DIFFERENTIALLY EXPRESSED GENES BETWEEN PATIENTS WITH FAVOURABLE AND POOR RESPONSE .....	16
12. TABLE A8. BASELINE CHARACTERISTICS OF PATIENTS BY <i>CALB1</i> EXPRESSION STATUS .....	27
13. TABLE A9. BASELINE CHARACTERISTICS OF PATIENTS WITH SEQUENCED TUMORS VS. PATIENTS WITHOUT SEQUENCED TUMORS .....	29
14. REFERENCES .....	31
15. REMARK CHECKLIST .....	32

## 1. Supplemental Methods

### Procedures

The study was designed to address the medical need for patients who have progressed through standard therapies including anthracyclines and the newer agents trabectedin and/or eribulin. Therefore, in order to avoid toxicities typically associated with cytotoxic agents with no known clinical benefit, placebo was chosen as the control. The randomization of 2:1 reduced the number of patients who received placebo, and those allocated to placebo were permitted to cross over to selinexor following confirmed objective progression. Of course, patients could receive additional agents when their disease progressed.

### Outcomes

Although the primary endpoint was PFS, as the study permitted crossover, it was designed with sufficient power to detect a clinically meaningful decrement in OS for patients treated with selinexor, using a non-inferiority analysis. The number of OS events required was a maximum of 195 for the Phase 3 portion of the study to have 80% power with a log-rank test at a 1-sided significance level of 0.1 to rule out a non-inferiority HR of 1.15 (median OS 15 months for placebo and 13 months for selinexor), under the alternative HR of 0.83 (median OS 15 months for placebo and 18 months for selinexor). The OS for non-inferiority was a prespecified key secondary endpoint, defined as the time from randomization until death due to any cause, for all randomized patients.

### Exploratory Molecular Correlative Studies

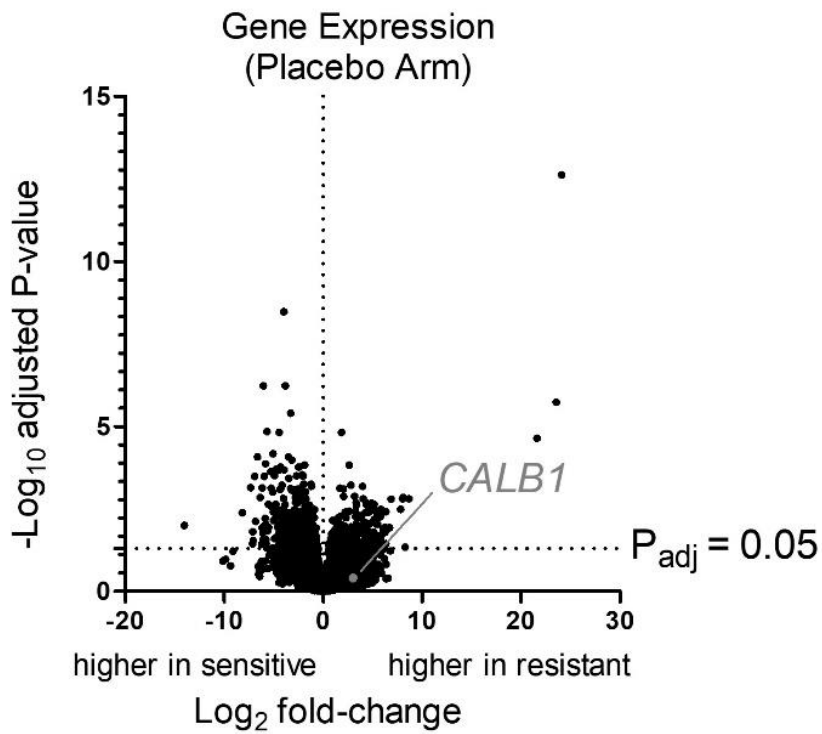
Pre-treatment biopsies from 86 patients were sequenced, including 55 treated with selinexor and 31 who received placebo. Differential expression analysis comparing selinexor-treated patients was performed in two sets: Set 1 (17 patients) compared biopsies of target lesions that clearly decreased (n=8) or increased (n=9) during treatment, and Set 2 (38 patients) compared the remaining samples stratified by short patient PFS (<3 months, n=22) vs. long PFS (>6 months) or PR (n=16), using any available biopsy from each patient (**Appendix Table A2-3**). Placebo treated patients were stratified by short patient PFS (<3 months, n=25) vs. long PFS (>5.5 months, n=6) (**Appendix Table A3**).

In a separate analysis, paired post-treatment selinexor-sensitive and resistant tumors were resected from the same patient, then RNA sequenced (see **Figure 3E**).

The object of the molecular correlative studies was to identify predictive biomarkers of response to selinexor through assessment of RNA-levels of all expressed genes in tumor biopsies from treated patients. Studies were exploratory with no prespecified hypothesis. RNA was extracted from formalin-fixed paraffin-embedded resected tumors or tumor biopsies of patients who were treated on study for at least one complete cycle. FFPE blocks and slides were stored at room temperature. Ribodepleted RNA sequencing was performed by HudsonAlpha Discovery Sequencing and Bioinformatics Division (Huntsville, AL) as follows: RNA was extracted using the HudsonAlpha Discovery proprietary dual DNA/RNA extraction protocol from FFPE. The concentration of extracted RNA was quantified using Ribogreen assays (Invitrogen). 20-500 ng RNA was used as input for library prep with the TruSeq™ Stranded Total RNA With Ribo-Zero™ Plus rRNA Depletion protocol (Illumina). Fragment size estimation was performed using the Caliper DNA-HS chip, and Kapa qPCR quantification was performed to estimate the nanomolar concentration of the final libraries. RNA libraries were pooled and sequenced at 100 base pair read length with a target depth of 100M paired-end reads on NovaSeq 6000 instruments (Illumina). Samples with fewer than 30M pass-filter reads were removed.

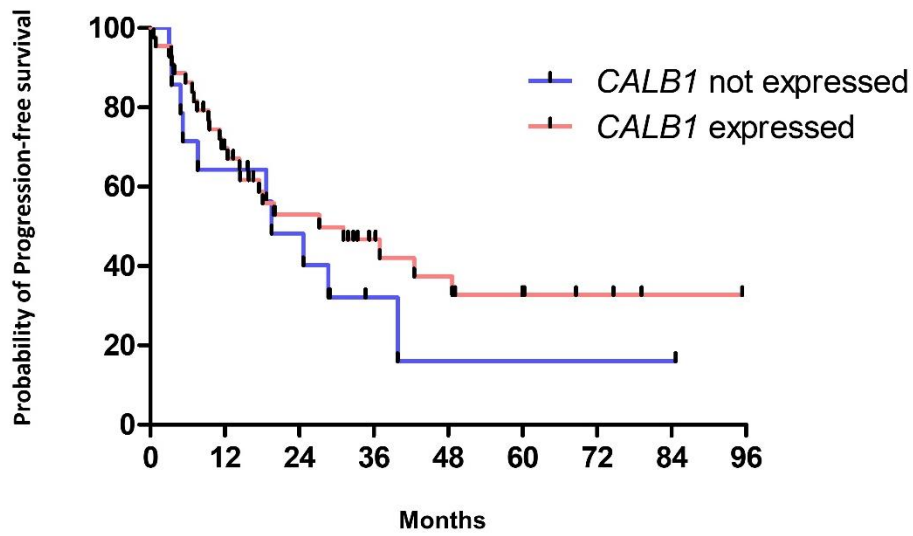
Reads were aligned with HiSAT2,<sup>1</sup> then gene-level expressions were determined with featurecounts.<sup>2</sup> Differential expression analysis was performed for 58,395 genes in the human GRCh38.92.gtf reference, using a negative binomial distribution with DeSeq2.<sup>3</sup> P-values were calculated with Wald's method<sup>4</sup> and adjusted with Benjamini and Hochberg method.<sup>5</sup> Visual examination of MA plots validated symmetry and examination of dispersion plots showed values generally scatter around the fitted curve, which decreases with increasing mean expression levels (**Appendix Figure A3**). Analysis of publicly available data from The Cancer Genome Atlas was performed by filtering TCGA-PanCancer study for patients with "Dedifferentiated Liposarcoma" as "Cancer Type Detail", downloading *CALB1* RNA expressions as batch normalized RSEM (RNA-Seq by Expectation Maximization), then comparing progression-free survival of patients with *CALB1*=0 vs. patients with *CALB1* > 0 using log-rank tests.

2. Figure A1

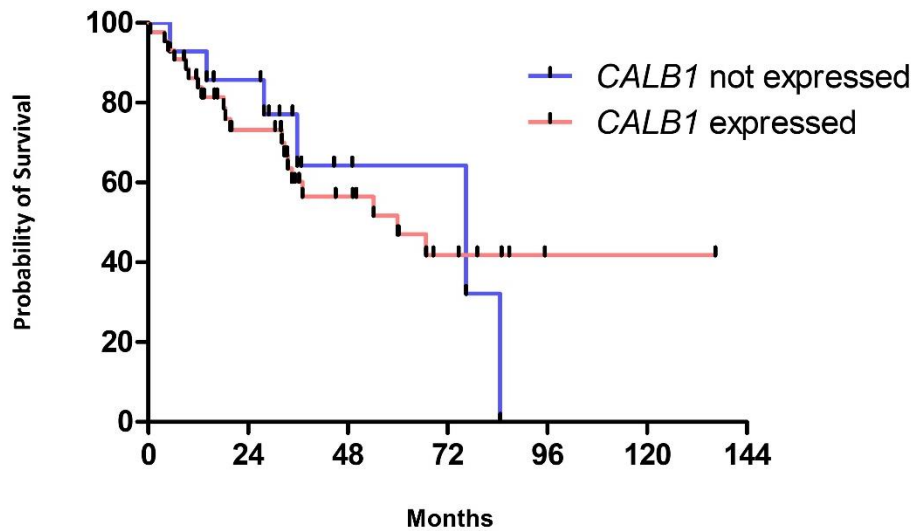


**Figure A1. Differential Expression Analysis of Samples from Patients Treated with Placebo.** Volcano plot showing the significance (y-axis) and fold-change (x-axis) of all genes compared between tumors in the Placebo Treated Set of patients, stratified by PFS short (< 3mo) and PFS long (> 5.5mo). *CALB1* was not significantly different between the two groups ( $P_{adj} = 0.40$ ).

3. Figure A2



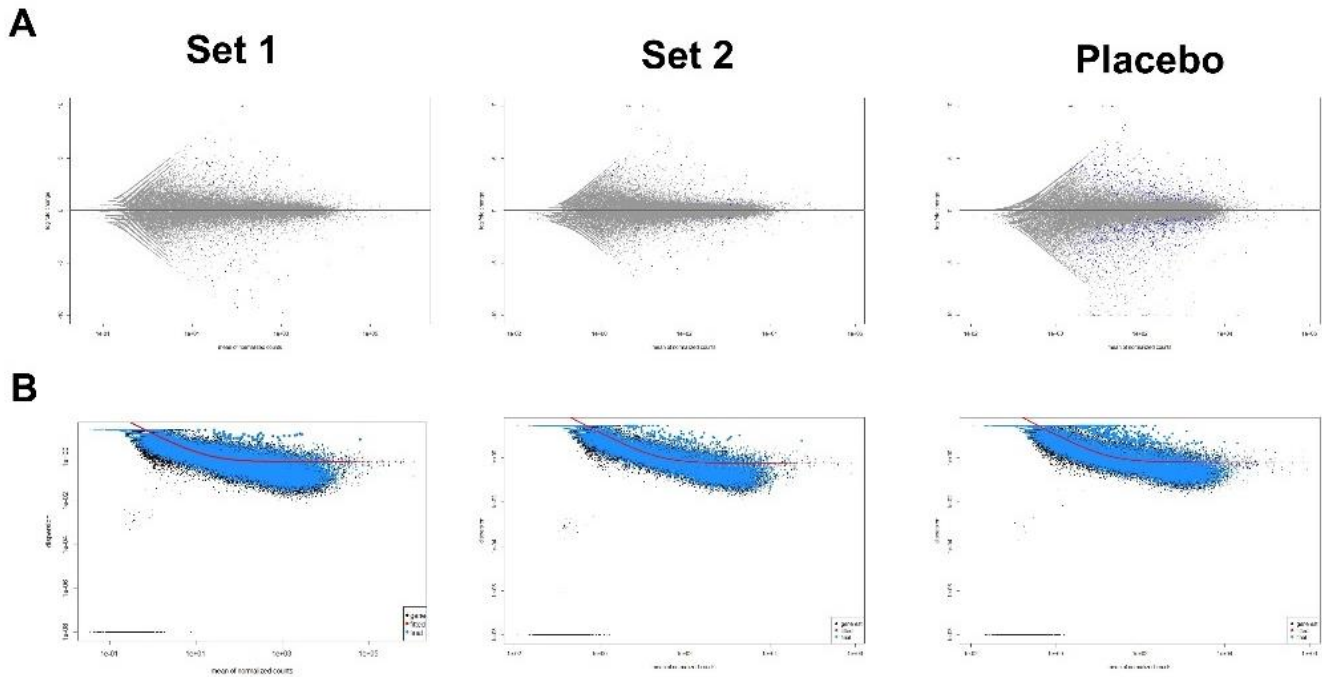
Not expressed	14	9	6	2	1	1	1	1	0
expressed	44	28	17	11	8	5	3	1	0



Not expressed	14	11	3	2	0	0	0
expressed	44	26	14	6	2	1	0

**Figure A2. CALB1 Is Not a General Marker of Good Prognosis in The Cancer Genome Atlas (TCGA) for DDLS.** Kaplan-Meier curves for progression-free and overall survival of patients with DDLS from publicly available TCGA for sarcoma data, stratified by *CALB1* expression. P-values from log-rank tests are not significant ( $>0.05$ ). Data accessed from cbioportal.org on 25 March 2021.

#### 4. Figure A3



**Figure A3. Quality Control Metric Plots for RNA Sequencing Differential Expression Analysis.** **A.** MA plots show the  $\log_{10}$  fold change (y-axis) and average normalized counts (x-axis) for all assessed genes from patients treated with selinexor in Set 1 and Set 2, and those treated with placebo. **B.** Dispersion plots show the dispersion estimates over the average normalized counts for all assessed genes from patients treated with selinexor in Set 1 and Set 2, and those treated with placebo. Black dots are the expression estimates, blue dots are the final model and the red dots are plots on the fitted estimate curve.

## 5. Table A1. Inclusion/Exclusion Criteria

Inclusion Criteria	Exclusion Criteria
<ol style="list-style-type: none"> <li>1. Written informed consent in accordance with national, local, and institutional guidelines obtained prior to any screening procedures</li> <li>2. Must be willing and able to comply with the protocol</li> <li>3. Patients <math>\geq 12</math> years of age (patients <math>&lt;18</math> years of age are permitted only in countries in which adolescents have been approved by the national/local regulatory/ethical authority).</li> <li>4. Patients with a body surface area (BSA) <math>\geq 1.2 \text{ m}^2</math> as calculated per Dubois 1916<sup>6</sup> or Mosteller 1987<sup>7</sup></li> <li>5. Documented histologic evidence of DDLS at any time from initial diagnosis to randomization AND current evidence of DDLS requiring treatment (documented evidence of disease progression from the most recent treatment): <ul style="list-style-type: none"> <li>• Documentation of histologic evidence of DDLS requires the following: <ul style="list-style-type: none"> <li>○ This information will be provided based on prior diagnostic testing and is required for randomization.</li> <li>○ Tissue (fresh or archival) will be provided for confirmatory histology at a central laboratory but confirmatory results are not required prior to randomization.</li> <li>○ If archival tissue <math>&gt; 12</math> months old, the quality of the sample for confirmatory histology must be confirmed by the site histopathologist prior to randomization.</li> </ul> </li> </ul> </li> <li>6. Must have measurable disease according to: <ul style="list-style-type: none"> <li>• The bidimensional WHO Response Criteria<sup>8</sup> (Phase 2 patients only)</li> <li>• RECIST v. 1.1<sup>9</sup> (Phase 3 patients only)</li> </ul> </li> <li>7. Radiologic evidence of progressive disease (PD) within 6 months prior to randomization. If the patient received other intervening therapy after PD is documented, further PD must be documented after the completion of the intervening therapy, with the exception of patients who discontinued most recent treatment after no more than 1 dose.</li> <li>8. Must have received at least 2 but no more than 5 prior systemic therapies for the treatment of liposarcoma.</li> <li>9. Patients should have recovered from all major surgery, radiation or other interventions <math>\geq 21</math> days prior to randomization. Patients must have recovered from any clinically significant therapy-related toxicity to <math>\leq</math> Grade 1 per CTCAE v. 4.03. Minor procedures, such as biopsies, dental work, or placement of a port or intravenous line for infusion, are permitted.</li> <li>10. If patients received any previous systemic therapy, the last dose must have been <math>\geq 21</math> days prior to randomization (or <math>\geq 5</math> half-lives of that drug [whichever is shorter]), with all clinically significant therapy-related toxicities having resolved to <math>\leq</math> Grade 1 CTCAE v. 4.03.</li> <li>11. ECOG performance status <math>\leq 1</math><sup>10</sup></li> <li>12. Adequate laboratory functional values: <ul style="list-style-type: none"> <li>• Adequate hematopoietic function: <ul style="list-style-type: none"> <li>○ Absolute neutrophil count (ANC) <math>\geq 1500/\text{mm}^3</math></li> <li>○ Platelets <math>\geq 100,000/\text{mm}^3</math></li> <li>○ Hemoglobin (Hb) <math>\geq 9 \text{ g/dL}</math></li> <li>○ Transfusions, hematopoietic growth factors, and hematinics are NOT permitted during screening</li> </ul> </li> <li>• Adequate hepatic function: <ul style="list-style-type: none"> <li>○ Bilirubin <math>\leq 1.5 \times</math> upper limit of normal (ULN) (except patients with Gilbert's syndrome [hereditary indirect hyperbilirubinemia] who must have a total bilirubin of <math>\leq 3 \times</math> ULN)</li> <li>○ Alkaline phosphatase (ALP), aspartate aminotransferase (AST), and alanine aminotransferase (ALT) <math>&lt; 3.0 \times</math> ULN (except patients with liver involvement of their liposarcoma who must have an AST and ALT <math>\leq 5 \times</math> ULN).</li> </ul> </li> <li>• Adequate renal function: Serum creatinine of <math>\leq 1.5 \text{ mg/dL}</math> or estimated creatinine clearance of <math>\geq 30 \text{ mL/min}</math>, calculated using the Cockcroft and Gault formula <math>(140 - \text{Age}) \cdot \text{Mass (kg)} / (72 \cdot \text{creatinine mg/dL})</math>; multiply by 0.85 if female<sup>11</sup></li> </ul> </li> <li>13. Female patients of childbearing potential must have a negative serum pregnancy test at Screening. Female patients of childbearing potential and fertile male patients who are sexually active with a female of childbearing potential must</li> </ol>	<ol style="list-style-type: none"> <li>1. Patients with liposarcoma of pure WDLS, myxoid/round cell or pleomorphic tumor histologic subtypes.</li> <li>2. Significant cardiovascular impairment, defined as: <ol style="list-style-type: none"> <li>a. Cardiac failure, New York Heart Association (NYHA) Class <math>\geq 3</math> according to the NYHA Functional Classification</li> <li>b. Unstable angina or myocardial infarction within 3 months of enrollment</li> <li>c. Serious and potentially life-threatening arrhythmia.</li> </ol> </li> <li>3. Patients with known central nervous system metastases.</li> <li>4. Female patients who are pregnant or nursing.</li> <li>5. Prior malignancy that required treatment, or has shown evidence of recurrence (except for non melanoma skin cancer or adequately treated cervical carcinoma in situ) during the 5 years prior to randomization. Cancer treated with curative intent <math>&gt; 5</math> years prior to randomization and without evidence of recurrence is allowed.</li> <li>6. Known active hepatitis B infection, as defined by seropositivity for hepatitis B surface antigen (HBs Ag); or known hepatitis C infection, as defined by seropositivity for hepatitis C antibody, with elevated liver aminotransferases (i.e., above the levels specified in inclusion criterion #12) or any other evidence of active hepatitis.</li> <li>7. Known human immunodeficiency virus (HIV) infection.</li> <li>8. Any medical condition, such as an uncontrolled infection or uncontrolled diabetes mellitus (Type 2), which in the opinion of the Investigator would make study involvement unreasonably hazardous</li> <li>9. Psychiatric illness that would prevent the patient from giving informed consent or being compliant with the study procedures</li> <li>10. Patients unable to swallow tablets, patients with malabsorption syndrome, or any other GI disease or GI dysfunction that could interfere with absorption of study treatment</li> <li>11. Inability or unwillingness to take supportive medications such as anti-nausea and anti-anorexia agents as recommended by the NCCN CPGO for antiemesis and anorexia/cachexia (palliative care).</li> <li>12. Patients who had involuntary weight loss of <math>\geq 10\%</math> in the 3 months prior to randomization.</li> <li>13. Participation in an investigational anticancer study <math>\leq 21</math> days prior to randomization.</li> <li>14. A circulating lymphocyte count of <math>&gt; 50,000/\mu\text{L}</math> (for sites in France only)</li> </ol>

agree to use highly effective contraception throughout the study and for 3 months following the last dose of study treatment.

ALP= alkaline phosphatase, ALT= alanine aminotransferase, ANC= absolute neutrophil count, AST= aspartate aminotransferase, BSA= body surface area, CNS=central nervous system, CTCAE= Common Terminology Criteria for Adverse Events, DDLS= dedifferentiated liposarcoma, ECOG= Eastern Cooperative Oncology Group, G-CSF=granulocyte colony stimulating factor, GM-CSF=granulocyte-macrophage colony stimulating factor, EPO=erythropoietin, GVHD=graft versus host disease, HIV= human immunodeficiency virus, Hb= hemoglobin, HBsAg=hepatitis B virus surface antigen, HCV=hepatitis C virus, HIV=human immunodeficiency virus, PD=progressive disease, NCCN CPGO= National Comprehensive Cancer Network Clinical Practice Guidelines in Oncology, NYHA = New York Heart Association, MM=multiple myeloma, RECIST= Response Evaluation Criteria in Solid Tumors, RNA=ribonucleic acid, ULN= upper limit of normal, WDLS= well-differentiated liposarcoma ,WHO= World Health Organization.

## 6. Table A2. Set 1: Sensitive and Resistant Tumors by Change in Target Size

Tumor response	Change in target lesions from baseline by RECIST (%)	Selinexor treatment duration (days)
sensitive*	-72.9	247
sensitive	-62.6	353
sensitive	-33.3	52
sensitive	-24.9	387
sensitive*	-21	71
sensitive	-12.7	204
sensitive	-12.5	136
sensitive	-6.2	253
resistant	92.9	52
resistant	53.5	38
resistant	44.9	41
resistant	31.2	45
resistant	27.8	66
resistant*	25.1	38
resistant	22.3	50
resistant	12.5	52
resistant	10	143

\*Open label cross-over patient



**7. Table A3. Set 2: Patients with Favorable or Poor Response by PFS**

<b>Response Group</b>	<b>Treatment Randomization Arm</b>	<b>Best Overall Response</b>	<b>PFS (Months)</b>
favorable	selinexor	PR	2.76
favorable	selinexor	PR	2.89
favorable	selinexor	PR	11.5
favorable	selinexor	SD	16.76
favorable	selinexor	SD	16.76*
favorable	selinexor	SD	16.62
favorable	selinexor	SD	13.83*
favorable	selinexor	SD	10.84*
favorable	selinexor	SD	8.54
favorable	selinexor	SD	8.41
favorable	selinexor	SD	8.31
favorable	selinexor	SD	8.31
favorable	selinexor	SD	8.28
favorable	selinexor	SD	7.13*
favorable	selinexor	SD	6.74
favorable	selinexor	SD	6.54*
poor	selinexor	SD	1.45
poor	selinexor	SD	1.61
poor	selinexor	SD	2.73
poor	selinexor	SD	2.73
poor	selinexor	SD	2.76
poor	selinexor	SD	2.76
poor	selinexor	SD	2.76
poor	selinexor	SD	1.97
poor	selinexor	PD	1.41
poor	selinexor	PD	1.41
poor	selinexor	PD	1.54
poor	selinexor	PD	1.61
poor	selinexor	PD	1.15
poor	selinexor	PD	1.22
poor	selinexor	PD	1.35
poor	selinexor	PD	1.38
poor	selinexor	PD	1.45
poor	selinexor	PD	1.48
poor	selinexor	PD	1.51
poor	selinexor	PD	1.58
poor	selinexor	PD	1.68
poor	selinexor	PD	2.43

favorable	placebo	SD	5.55
favorable	placebo	PD	5.55
favorable	placebo	PD	5.59
favorable	placebo	PD	5.52
favorable	placebo	SD	6.93
favorable	placebo	SD	5.68
poor	placebo	SD	2.79
poor	placebo	SD	1.45
poor	placebo	PD	1.41
poor	placebo	SD	1.45
poor	placebo	PD	2.79
poor	placebo	PD	2.79
poor	placebo	PD	1.64
poor	placebo	SD	1.41
poor	placebo	PD	1.25
poor	placebo	PD	1.41
poor	placebo	PD	1.45
poor	placebo	PD	1.87
poor	placebo	SD	2.53
poor	placebo	PD	1.45
poor	placebo	PD	1.38
poor	placebo	PD	1.41
poor	placebo	PD	1.45
poor	placebo	PD	2.73
poor	placebo	PD	1.64
poor	placebo	PD	1.38
poor	placebo	SD	1.41
poor	placebo	PD	1.58
poor	placebo	PD	1.45
poor	placebo	PD	1.51
poor	placebo	SD	1.41

PFS, progression free survival; SD, stable disease; PD, progressive disease; PR, partial response  
 \*Censored for PFS

**8. Table A4. Subsequent therapies of all enrolled patients**

<b>Therapy post treatment (n, %)</b>	<b>Selinexor (n=188)</b>	<b>Placebo (n=97)</b>	<b>Placebo-Open Selinexor (n=57)</b>
Patient with any post-treatment antineoplastic therapy	71 (37.8)	13 (32.5)	17 (29.8)
Chemotherapy	59 (31.4)	12 (30.0)	16 (28.1)
Immunotherapy	4 (2.1)	1 (2.5)	3 (5.3)
Radiation	12 (6.4)	2 (5.0)	1 (1.8)
Surgery	1 (0.5)	0	2 (3.5)
Other	4 (2.1)	0	2 (3.5)
Biologic therapy	1 (0.5)	0	0
Cryoablation	0	0	1 (1.8)
Eribulin	1 (0.5)	0	0
Olaratumab	1 (0.5)	0	0
Palbociclib	1 (0.5)	0	0
Palbociclib (Ibrance)CDK4/6 inhibitor	1 (0.5)	0	0
Biological therapy	1 (0.5)	0	0

**9. Table A5. Serious Treatment-Emergent Adverse Events**

<b>Event</b>	<b>Selinexor (N = 187) n (%)</b>	<b>Placebo (N = 97) n (%)</b>	<b>Total (N = 284) n (%)</b>
Abdominal pain	6 (3.2)	1 (1.0)	7 (2.5)
Nausea	4 (2.1)	0	4 (1.4)
Small intestinal obstruction	2 (1.1)	2 (2.1)	4 (1.4)
Acute kidney injury	2 (1.1)	1 (1.0)	3 (1.1)
Anemia	3 (1.6)	0	3 (1.1)
Decreased appetite	2 (1.1)	1 (1.0)	3 (1.1)
Pleural effusion	3 (1.6)	0	3 (1.1)
Pneumonia	3 (1.6)	0	3 (1.1)
Pulmonary embolism	2 (1.1)	1 (1.0)	3 (1.1)
Vomiting	2 (1.1)	1 (1.0)	3 (1.1)
Back pain	0	2 (2.1)	2 (0.7)
Bronchitis viral	2 (1.1)	0	2 (0.7)
Cardiac failure	2 (1.1)	0	2 (0.7)
Cataract	2 (1.1)	0	2 (0.7)
Cellulitis	1 (0.5)	1 (1.0)	2 (0.7)
Chronic obstructive pulmonary disease	1 (0.5)	1 (1.0)	2 (0.7)
Dehydration	2 (1.1)	0	2 (0.7)
Dyspnea	1 (0.5)	1 (1.0)	2 (0.7)
General physical health deterioration	2 (1.1)	0	2 (0.7)
Hyperglycaemia	2 (1.1)	0	2 (0.7)
Influenza	2 (1.1)	0	2 (0.7)
Myelodysplastic syndrome	2 (1.1)	0	2 (0.7)
Pneumothorax	2 (1.1)	0	2 (0.7)
Sepsis	0	2 (2.1)	2 (0.7)
Syncope	2 (1.1)	0	2 (0.7)
Thrombocytopenia	2 (1.1)	0	2 (0.7)
Tumor pain	2 (1.1)	0	2 (0.7)
Upper gastrointestinal hemorrhage	2 (1.1)	0	2 (0.7)
Urinary tract infection	1 (0.5)	1 (1.0)	2 (0.7)

Note: For patients who cross over, AEs that occur after the crossover are not included.

**10. Table A6. Set 1: Differentially Expressed Genes between Sensitive and Resistant Tumors**

Gene Name	Log <sub>2</sub> Fold Change*	SE of the Log <sub>2</sub> Fold Change	Wald Statistic	Wald Test P-value	Benjamini-Hochberg Adjusted P-value
<i>CALB1</i>	24.72	2.42	10.18	2.42E-24	7.53E-20
<i>MYBPC1</i>	-9.71	1.35	-7.22	5.31E-13	8.25E-09
<i>NEB</i>	-5.11	0.83	-6.16	7.30E-10	7.57E-06
<i>C4BPA</i>	7.52	1.29	5.83	5.67E-09	4.41E-05
<i>SLN</i>	-5.62	1.07	-5.23	1.68E-07	0.00104401
<i>NLGN1</i>	3.84	0.75	5.14	2.69E-07	0.00139174
<i>HJV</i>	-7.18	1.43	-5.03	5.01E-07	0.00222483
<i>GRM1</i>	-6.15	1.24	-4.95	7.29E-07	0.00283411
<i>CLLU1</i>	-5.82	1.19	-4.91	9.24E-07	0.00319218
<i>KCNB2</i>	5.15	1.06	4.87	1.09E-06	0.00338826
<i>AC009501.2</i>	5.09	1.05	4.84	1.29E-06	0.00365149
<i>UNC45B</i>	-4.50	0.94	-4.79	1.64E-06	0.00423665
<i>CACNA1S</i>	-4.82	1.01	-4.77	1.86E-06	0.00444133
<i>WNT11</i>	3.37	0.71	4.71	2.47E-06	0.00451712
<i>GATM</i>	-1.86	0.39	-4.71	2.52E-06	0.00451712
<i>MYL6F</i>	-5.04	1.06	-4.75	2.07E-06	0.00451712
<i>DNAH17</i>	3.20	0.68	4.71	2.51E-06	0.00451712
<i>AC024028.1</i>	6.18	1.32	4.70	2.62E-06	0.00451712
<i>FRRS1L</i>	4.58	0.98	4.65	3.35E-06	0.00547504
<i>NPY6R</i>	-6.38	1.39	-4.59	4.45E-06	0.00692376
<i>ASB5</i>	-8.36	1.83	-4.56	5.17E-06	0.00765169
<i>LINC02397</i>	-5.97	1.32	-4.54	5.61E-06	0.00792847
<i>SMPX</i>	-9.22	2.04	-4.51	6.43E-06	0.00799396
<i>ADAMTS19</i>	5.67	1.25	4.53	5.93E-06	0.00799396
<i>PCDH9</i>	2.12	0.47	4.52	6.31E-06	0.00799396
<i>ESR1</i>	-2.57	0.58	-4.45	8.39E-06	0.00966109
<i>MEX3A</i>	2.31	0.52	4.46	8.09E-06	0.00966109
<i>LMOD3</i>	-5.27	1.19	-4.43	9.41E-06	0.01022451
<i>COL4A3</i>	-4.20	0.95	-4.43	9.54E-06	0.01022451
<i>NPNT</i>	-2.17	0.49	-4.40	1.11E-05	0.01042765
<i>LINC01285</i>	2.15	0.49	4.40	1.06E-05	0.01042765
<i>AC073316.1</i>	5.16	1.17	4.40	1.08E-05	0.01042765
<i>AL023495.1</i>	-5.78	1.31	-4.41	1.04E-05	0.01042765
<i>MYOM2</i>	-3.09	0.70	-4.38	1.18E-05	0.01082719
<i>AC023403.1</i>	-4.85	1.12	-4.34	1.45E-05	0.01291156
<i>MROCK1</i>	-3.69	0.85	-4.32	1.55E-05	0.01335768
<i>BEX1</i>	4.81	1.13	4.27	1.97E-05	0.01430472
<i>CHRNA3</i>	-8.83	2.05	-4.30	1.73E-05	0.01430472
<i>SLC10A5P1</i>	3.00	0.70	4.27	1.98E-05	0.01430472

<i>LINC01087</i>	-4.45	1.04	-4.27	1.92E-05	0.01430472
<i>ALI36114.1</i>	-6.14	1.44	-4.27	1.92E-05	0.01430472
<i>AC022893.2</i>	4.98	1.16	4.29	1.79E-05	0.01430472
<i>AC007529.2</i>	6.32	1.48	4.28	1.87E-05	0.01430472
<i>DUSP26</i>	-5.25	1.23	-4.26	2.05E-05	0.0144329
<i>FOXG1</i>	4.64	1.09	4.26	2.09E-05	0.0144329
<i>CASQ2</i>	-4.02	0.95	-4.25	2.14E-05	0.0144787
<i>MS4A14</i>	-1.82	0.43	-4.24	2.24E-05	0.01480022
<i>AC183088.2</i>	-6.65	1.57	-4.23	2.37E-05	0.01536777
<i>PTGES</i>	2.16	0.51	4.22	2.45E-05	0.01556701
<i>TMEM132A</i>	1.51	0.36	4.18	2.92E-05	0.01629943
<i>FRK</i>	-2.76	0.66	-4.18	2.94E-05	0.01629943
<i>MATN4</i>	4.52	1.08	4.19	2.82E-05	0.01629943
<i>LINC02599</i>	2.71	0.65	4.20	2.72E-05	0.01629943
<i>AC092967.1</i>	4.63	1.11	4.19	2.76E-05	0.01629943
<i>MARCOL</i>	6.59	1.57	4.19	2.77E-05	0.01629943
<i>SPIB</i>	-3.47	0.83	-4.18	2.94E-05	0.01629943
<i>DUSP13</i>	-5.56	1.33	-4.16	3.15E-05	0.01651678
<i>TNNI1</i>	-4.90	1.18	-4.17	3.08E-05	0.01651678
<i>GAP43</i>	3.86	0.93	4.15	3.29E-05	0.01651678
<i>RPL10P6</i>	3.85	0.93	4.16	3.18E-05	0.01651678
<i>MIR133A1HG</i>	-5.56	1.34	-4.16	3.25E-05	0.01651678
<i>SFTPD-AS1</i>	-3.14	0.76	-4.16	3.25E-05	0.01651678
<i>SNTG1</i>	5.23	1.26	4.15	3.36E-05	0.01659268
<i>LINC00689</i>	-3.96	0.96	-4.12	3.73E-05	0.01810697
<i>KLHL41</i>	-3.95	0.96	-4.12	3.81E-05	0.01819736
<i>GABRB3</i>	4.74	1.15	4.11	3.89E-05	0.01830284
<i>C6</i>	-4.01	0.98	-4.08	4.50E-05	0.02087711
<i>CHRNA8</i>	-6.47	1.59	-4.07	4.71E-05	0.0214154
<i>TRIM55</i>	-4.71	1.16	-4.07	4.75E-05	0.0214154
<i>MYPN</i>	-5.05	1.25	-4.05	5.09E-05	0.02258368
<i>HTR2B</i>	-2.72	0.67	-4.04	5.27E-05	0.02308366
<i>MTX1</i>	0.78	0.19	4.03	5.67E-05	0.02447209
<i>ZIC3</i>	8.28	2.07	4.00	6.22E-05	0.02648722
<i>SPATA8</i>	-6.00	1.50	-3.99	6.53E-05	0.02741253
<i>REEP6</i>	1.90	0.48	3.97	7.25E-05	0.02966874
<i>LINC02301</i>	-4.63	1.17	-3.97	7.18E-05	0.02966874
<i>LDB3</i>	-2.52	0.64	-3.95	7.87E-05	0.03178629
<i>HTR7P1</i>	0.72	0.18	3.94	8.22E-05	0.03277257
<i>NPW</i>	2.73	0.69	3.93	8.40E-05	0.03277257
<i>GREB1</i>	2.22	0.56	3.93	8.43E-05	0.03277257
<i>TMPRSS11A</i>	6.18	1.58	3.92	8.85E-05	0.03396639
<i>AMIGO2</i>	1.89	0.48	3.91	9.06E-05	0.03436166
<i>DLX6</i>	3.39	0.87	3.90	9.56E-05	0.03454878
<i>PLCD4</i>	-2.04	0.52	-3.90	9.45E-05	0.03454878

<i>MYH8</i>	-6.37	1.63	-3.90	9.53E-05	0.03454878
<i>TTN</i>	-3.50	0.90	-3.90	9.47E-05	0.03454878
<i>GORAB</i>	-2.02	0.52	-3.89	0.00010184	0.03556925
<i>CHRNA1</i>	-3.60	0.93	-3.89	0.00010083	0.03556925
<i>ALI57895.2</i>	-4.78	1.23	-3.89	0.00010166	0.03556925
<i>LMOD2</i>	-6.70	1.73	-3.88	0.00010558	0.0360645
<i>CCDC144NL</i>	-3.29	0.85	-3.88	0.00010543	0.0360645
<i>ZBTB8B</i>	2.49	0.64	3.87	0.00011051	0.03733872
<i>CDH15</i>	-4.22	1.10	-3.85	0.00011884	0.03929996
<i>LBP</i>	-4.63	1.20	-3.85	0.00011853	0.03929996
<i>FAM163A</i>	4.00	1.04	3.84	0.00012169	0.0398196
<i>CLEC19A</i>	-2.82	0.74	-3.84	0.00012416	0.04020473
<i>SMYD5</i>	0.74	0.19	3.83	0.0001275	0.04044354
<i>LINC01937</i>	3.77	0.98	3.83	0.000127	0.04044354
<i>IBSP</i>	-6.60	1.73	-3.82	0.00013359	0.04152787
<i>AKAP6</i>	-2.96	0.77	-3.82	0.00013271	0.04152787
<i>CFAP61</i>	-2.77	0.73	-3.82	0.00013552	0.04170968
<i>MYH7</i>	-7.57	1.98	-3.81	0.00013691	0.04172272
<i>PRKAG3</i>	-4.67	1.23	-3.80	0.00014193	0.04283449
<i>SGCA</i>	-3.20	0.84	-3.80	0.0001471	0.0429106
<i>SCN3B</i>	-3.09	0.81	-3.79	0.00014839	0.0429106
<i>STAC3</i>	-1.90	0.50	-3.80	0.00014537	0.0429106
<i>CERS1</i>	4.26	1.12	3.80	0.00014583	0.0429106
<i>LINC01193</i>	-5.42	1.43	-3.79	0.00014909	0.0429106
<i>XIRP2</i>	-5.22	1.38	-3.77	0.00016067	0.04549239
<i>OGDHL</i>	3.91	1.04	3.77	0.00016098	0.04549239
<i>LINC02282</i>	6.91	1.83	3.77	0.00016429	0.0460096
<i>CACNA1A</i>	3.37	0.90	3.75	0.00017977	0.04979784
<i>CYP4B1</i>	6.58	1.76	3.74	0.00018263	0.04979784
<i>MTX1P1</i>	0.71	0.19	3.74	0.00018151	0.04979784

SE, standard error; est, estimate

\*Positive higher in resistant tumors

**11. Table A7: Set 2: Significantly Differentially Expressed Genes between Patients with Favourable and Poor Response**

Gene Name	Log <sub>2</sub> Fold Change*	SE of the Log <sub>2</sub> Fold Change	Wald Statistic	Wald Test P-value	Benjamini-Hochberg Adjusted P-value
<i>ATP2B1-AS1</i>	2.58	0.43	-5.97	2.35E-09	7.45E-05
<i>PSMD8</i>	0.88	0.15	-5.75	8.84E-09	0.0001404
<i>COX5B</i>	0.91	0.16	-5.58	2.47E-08	0.00026179
<i>EIF3I</i>	0.76	0.14	-5.35	8.97E-08	0.00071216
<i>FBL</i>	1.09	0.21	-5.25	1.53E-07	0.0009721
<i>TBCE</i>	-0.64	0.12	5.15	2.59E-07	0.00106088
<i>COLCA1</i>	-2.36	0.45	5.19	2.07E-07	0.00106088
<i>CIRBP-AS1</i>	2.57	0.50	-5.15	2.67E-07	0.00106088
<i>HMX1</i>	5.78	1.14	-5.05	4.47E-07	0.00132677
<i>AL596247.1</i>	-1.91	0.38	5.04	4.60E-07	0.00132677
<i>HOTAIR</i>	-3.60	0.71	5.05	4.46E-07	0.00132677
<i>RPL5P13</i>	-2.12	0.42	4.99	5.93E-07	0.00156863
<i>AL354861.3</i>	-6.10	1.23	4.98	6.43E-07	0.00157147
<i>EDAR</i>	-4.74	0.96	4.94	7.70E-07	0.00174554
<i>LINC00924</i>	-3.20	0.65	4.92	8.44E-07	0.0017868
<i>LINC00923</i>	-3.66	0.75	4.91	9.17E-07	0.00182074
<i>CHRNA7</i>	7.24	1.49	-4.85	1.22E-06	0.00227061
<i>AUP1</i>	0.57	0.12	-4.82	1.45E-06	0.00256245
<i>KIF5A</i>	3.98	0.83	-4.78	1.73E-06	0.00261634
<i>MYDGF</i>	0.80	0.17	-4.78	1.72E-06	0.00261634
<i>PRKCSH</i>	0.95	0.20	-4.78	1.72E-06	0.00261634
<i>AP003900.1</i>	5.06	1.06	-4.77	1.86E-06	0.00268925
<i>SLC5A9</i>	3.38	0.71	-4.75	2.01E-06	0.00278139
<i>RNA5SP344</i>	-1.66	0.35	4.74	2.13E-06	0.00281179
<i>AC064875.1</i>	-2.79	0.60	4.66	3.15E-06	0.00299133
<i>LTF</i>	-2.16	0.46	4.65	3.36E-06	0.00299133
<i>MIR570</i>	-1.11	0.24	4.69	2.80E-06	0.00299133
<i>LEF1</i>	-2.15	0.47	4.63	3.74E-06	0.00299133
<i>ADGRV1</i>	-3.09	0.66	4.64	3.45E-06	0.00299133
<i>MDH2</i>	0.92	0.20	-4.70	2.56E-06	0.00299133
<i>PAK3</i>	-2.34	0.50	4.65	3.25E-06	0.00299133
<i>H3P32</i>	-3.68	0.79	4.66	3.17E-06	0.00299133
<i>PTGS1</i>	1.95	0.42	-4.67	3.01E-06	0.00299133
<i>SYTI</i>	-2.52	0.54	4.66	3.17E-06	0.00299133
<i>NDUFA12</i>	1.51	0.32	-4.70	2.55E-06	0.00299133
<i>RBFOX1</i>	4.57	0.97	-4.71	2.49E-06	0.00299133
<i>BCAS1</i>	2.98	0.64	-4.63	3.60E-06	0.00299133
<i>RPS15</i>	0.88	0.19	-4.64	3.53E-06	0.00299133
<i>RAD23A</i>	0.94	0.20	-4.62	3.77E-06	0.00299133



<i>C19orf53</i>	0.78	0.17	-4.69	2.77E-06	0.00299133
<i>ATP1A4</i>	-2.91	0.63	4.61	4.03E-06	0.00312093
<i>VAMP4</i>	-1.56	0.34	4.60	4.26E-06	0.00318374
<i>BANK1</i>	-2.56	0.56	4.60	4.31E-06	0.00318374
<i>MYH7</i>	7.68	1.68	-4.57	4.79E-06	0.003459
<i>AC020978.7</i>	-0.81	0.18	4.57	4.93E-06	0.00347654
<i>CHORDC1P4</i>	-0.90	0.20	4.56	5.04E-06	0.00347654
<i>AC091057.4</i>	-1.14	0.25	4.56	5.15E-06	0.00348103
<i>FRG1FP</i>	2.51	0.55	-4.54	5.68E-06	0.00375621
<i>FGGY</i>	1.80	0.40	-4.49	7.12E-06	0.00443495
<i>AC006538.3</i>	-2.53	0.56	4.49	7.07E-06	0.00443495
<i>PSMC4</i>	0.90	0.20	-4.50	6.94E-06	0.00443495
<i>ERFE</i>	2.35	0.53	-4.48	7.35E-06	0.00448677
<i>TCL6</i>	-3.16	0.71	4.46	8.18E-06	0.00490173
<i>AC020612.1</i>	-0.98	0.22	4.45	8.74E-06	0.00514115
<i>CNTN5</i>	-5.07	1.14	4.44	9.01E-06	0.00520013
<i>IL9R</i>	-2.12	0.48	4.41	1.04E-05	0.0058843
<i>PTPRR</i>	3.81	0.86	-4.40	1.07E-05	0.0058843
<i>PSMB5</i>	0.71	0.16	-4.40	1.07E-05	0.0058843
<i>MED17</i>	-0.61	0.14	4.39	1.15E-05	0.00621241
<i>DDOST</i>	0.75	0.17	-4.38	1.18E-05	0.0062631
<i>GET3</i>	1.12	0.26	-4.37	1.25E-05	0.00648428
<i>NUDC</i>	0.70	0.16	-4.35	1.34E-05	0.00686848
<i>DES</i>	3.34	0.77	-4.34	1.43E-05	0.00711522
<i>RBM42</i>	0.78	0.18	-4.34	1.42E-05	0.00711522
<i>SNRPC</i>	0.83	0.19	-4.33	1.49E-05	0.00725695
<i>AC078799.1</i>	-1.09	0.25	4.32	1.58E-05	0.00735802
<i>RNU7-77P</i>	-1.22	0.28	4.32	1.56E-05	0.00735802
<i>ZNF641</i>	-0.66	0.15	4.32	1.54E-05	0.00735802
<i>LINC01632</i>	3.79	0.88	-4.31	1.63E-05	0.00738891
<i>MIF</i>	1.32	0.31	-4.31	1.62E-05	0.00738891
<i>PSMC3</i>	0.75	0.18	-4.30	1.73E-05	0.0076422
<i>LINC02408</i>	-2.63	0.61	4.30	1.71E-05	0.0076422
<i>PTBP1</i>	0.55	0.13	-4.29	1.78E-05	0.00775418
<i>PRRC2C</i>	-1.17	0.27	4.27	1.95E-05	0.00811867
<i>RPL26L1</i>	0.71	0.17	-4.27	1.96E-05	0.00811867
<i>H2BC4</i>	0.89	0.21	-4.26	2.04E-05	0.00811867
<i>ITIH2</i>	-6.12	1.44	4.26	2.05E-05	0.00811867
<i>PSMA3-ASI</i>	-0.58	0.14	4.26	2.01E-05	0.00811867
<i>C1QBP</i>	0.74	0.17	-4.27	1.97E-05	0.00811867
<i>TNNT1</i>	4.85	1.14	-4.26	2.02E-05	0.00811867
<i>AC004858.1</i>	-1.07	0.25	4.25	2.11E-05	0.00828112
<i>ALYREF</i>	0.93	0.22	-4.24	2.20E-05	0.00851923
<i>AMT</i>	-1.42	0.33	4.24	2.24E-05	0.00857885
<i>MIR4274</i>	-2.56	0.61	4.23	2.31E-05	0.00861493

<i>TUBB4B</i>	1.02	0.24	-4.23	2.30E-05	0.00861493
<i>RN7SL269P</i>	-1.12	0.26	4.23	2.37E-05	0.00865671
<i>MGAT4C</i>	2.96	0.70	-4.23	2.37E-05	0.00865671
<i>EIF6</i>	0.91	0.22	-4.21	2.50E-05	0.00902945
<b><i>CALB1</i></b>	<b>3.80</b>	<b>0.90</b>	<b>-4.21</b>	<b>2.54E-05</b>	<b>0.00905551</b>
<i>KHSRP</i>	0.58	0.14	-4.20	2.70E-05	0.00953275
<i>C5orf46</i>	3.54	0.85	-4.19	2.81E-05	0.00954252
<i>HCG27</i>	-0.95	0.23	4.19	2.78E-05	0.00954252
<i>MTCO3P15</i>	4.66	1.11	-4.19	2.81E-05	0.00954252
<i>SNORD3A</i>	1.10	0.26	-4.19	2.82E-05	0.00954252
<i>UPBI</i>	-1.18	0.28	4.18	2.87E-05	0.00960839
<i>RPL7AP30</i>	1.12	0.27	-4.18	2.97E-05	0.00962483
<i>ZNF663P</i>	3.45	0.82	-4.18	2.94E-05	0.00962483
<i>DPM1</i>	0.87	0.21	-4.18	2.94E-05	0.00962483
<i>ITPKB-IT1</i>	-1.42	0.34	4.16	3.20E-05	0.00987384
<i>SULT1C2</i>	-3.04	0.73	4.16	3.17E-05	0.00987384
<i>RN7SL517P</i>	-0.84	0.20	4.17	3.08E-05	0.00987384
<i>NHS</i>	-1.62	0.39	4.16	3.19E-05	0.00987384
<i>AC009120.2</i>	-0.58	0.14	4.16	3.20E-05	0.00987384
<i>MOCS3</i>	1.01	0.24	-4.15	3.25E-05	0.00993843
<i>LMOD3</i>	4.80	1.16	-4.15	3.37E-05	0.01000054
<i>RPL14P3</i>	0.93	0.22	-4.15	3.33E-05	0.01000054
<i>UBL5</i>	0.65	0.16	-4.15	3.36E-05	0.01000054
<i>BCL2</i>	-0.68	0.16	4.13	3.58E-05	0.01053889
<i>SUPT16H</i>	0.50	0.12	-4.12	3.72E-05	0.01084954
<i>AC012170.1</i>	-0.98	0.24	4.12	3.84E-05	0.01094071
<i>KLHL14</i>	-2.11	0.51	4.12	3.86E-05	0.01094071
<i>RPL18A</i>	0.73	0.18	-4.12	3.84E-05	0.01094071
<i>PPIAP22</i>	0.89	0.22	-4.11	3.94E-05	0.01106297
<i>TWIST2</i>	1.56	0.38	-4.10	4.06E-05	0.01118376
<i>MYOT</i>	5.65	1.38	-4.11	4.02E-05	0.01118376
<i>RPL13AP23</i>	5.34	1.30	-4.10	4.09E-05	0.01118376
<i>SATB1-AS1</i>	-2.09	0.51	4.09	4.30E-05	0.01165791
<i>OR1J4</i>	3.92	0.96	-4.09	4.33E-05	0.01165791
<i>AP002812.4</i>	-0.89	0.22	4.08	4.57E-05	0.01219348
<i>AC135731.2</i>	-3.71	0.91	4.07	4.64E-05	0.01227278
<i>AC125437.1</i>	-0.78	0.19	4.07	4.71E-05	0.01227278
<i>FAM83D</i>	1.83	0.45	-4.07	4.71E-05	0.01227278
<i>AC016405.1</i>	-0.95	0.23	4.06	4.86E-05	0.01234029
<i>AC023034.1</i>	2.55	0.63	-4.06	4.81E-05	0.01234029
<i>SLC7A4</i>	2.53	0.62	-4.06	4.83E-05	0.01234029
<i>UXT</i>	0.76	0.19	-4.06	5.01E-05	0.01236922
<i>HTATSF1</i>	0.84	0.21	-4.06	4.95E-05	0.01236922
<i>AC009558.2</i>	-4.28	1.06	4.05	5.02E-05	0.01236922
<i>AC007599.2</i>	-1.04	0.26	4.06	4.92E-05	0.01236922

<i>RN7SKP139</i>	-4.38	1.08	4.05	5.23E-05	0.01275761
<i>SNX22</i>	-1.91	0.47	4.04	5.26E-05	0.01275761
<i>ALI39246.2</i>	-1.80	0.44	4.04	5.31E-05	0.01276893
<i>PGAM4</i>	1.12	0.28	-4.03	5.57E-05	0.01330112
<i>CD151</i>	0.73	0.18	-4.02	5.72E-05	0.01350219
<i>RPN2</i>	0.77	0.19	-4.02	5.74E-05	0.01350219
<i>EXOSC10-AS1</i>	2.45	0.61	-4.01	6.16E-05	0.01400099
<i>OSTCP8</i>	-0.84	0.21	4.01	6.05E-05	0.01400099
<i>SLC35G1</i>	-1.03	0.26	4.00	6.22E-05	0.01400099
<i>FOXC2</i>	-2.34	0.58	4.01	6.20E-05	0.01400099
<i>EEF1A2</i>	3.45	0.86	-4.01	6.17E-05	0.01400099
<i>ZNF83</i>	-0.63	0.16	4.01	6.16E-05	0.01400099
<i>APEX1</i>	0.57	0.14	-4.00	6.28E-05	0.01404733
<i>NDUFS5</i>	0.70	0.17	-3.99	6.54E-05	0.01410842
<i>PRDX4</i>	0.84	0.21	-3.99	6.56E-05	0.01410842
<i>ANK1</i>	2.35	0.59	-3.99	6.54E-05	0.01410842
<i>RPL18AP3</i>	0.80	0.20	-3.99	6.58E-05	0.01410842
<i>RPL36AL</i>	0.77	0.19	-4.00	6.43E-05	0.01410842
<i>TRIM72</i>	2.76	0.69	-4.00	6.36E-05	0.01410842
<i>H3P31</i>	-0.89	0.22	3.98	6.75E-05	0.01429805
<i>UHRF1</i>	1.32	0.33	-3.98	6.75E-05	0.01429805
<i>CLCA1</i>	6.04	1.52	-3.98	7.01E-05	0.01466622
<i>PPP1R7</i>	0.55	0.14	-3.98	7.02E-05	0.01466622
<i>RN7SL398P</i>	-0.93	0.24	3.95	7.82E-05	0.01624085
<i>LINC02055</i>	4.76	1.21	-3.95	7.90E-05	0.0162804
<i>THSD7B</i>	-2.08	0.53	3.94	8.02E-05	0.01631878
<i>FCFIP4</i>	-3.29	0.84	3.94	8.06E-05	0.01631878
<i>TSTA3</i>	0.62	0.16	-3.94	8.07E-05	0.01631878
<i>AURKA</i>	1.68	0.43	-3.94	8.16E-05	0.01639215
<i>CD1C</i>	-1.82	0.46	3.94	8.30E-05	0.01640144
<i>HSPE1P13</i>	-1.00	0.26	3.94	8.26E-05	0.01640144
<i>AC092745.2</i>	2.89	0.73	-3.94	8.32E-05	0.01640144
<i>RPS2</i>	0.73	0.19	-3.93	8.49E-05	0.01665178
<i>ENSG00000279312</i>	-1.14	0.29	3.93	8.59E-05	0.01674287
<i>GBA3</i>	4.00	1.02	-3.92	8.75E-05	0.01695202
<i>AC019322.1</i>	-2.71	0.69	3.91	9.25E-05	0.01774836
<i>KPNA2</i>	1.24	0.32	-3.91	9.28E-05	0.01774836
<i>TAGLN2</i>	1.32	0.34	-3.90	9.43E-05	0.01780421
<i>RABGAP1L-IT1</i>	-0.95	0.24	3.90	9.59E-05	0.01780421
<i>RN7SKP106</i>	4.12	1.06	-3.90	9.56E-05	0.01780421
<i>LINC01388</i>	3.44	0.88	-3.90	9.47E-05	0.01780421
<i>EEF2</i>	0.82	0.21	-3.90	9.58E-05	0.01780421
<i>RABGAP1L</i>	-0.67	0.17	3.90	9.76E-05	0.0180174
<i>AC011369.2</i>	-4.08	1.05	3.88	0.00010296	0.01889856
<i>CLIC4P3</i>	1.37	0.35	-3.88	0.00010523	0.01909719

<i>MRPL28</i>	0.81	0.21	-3.88	0.00010524	0.01909719
<i>GTF2IP7</i>	-2.55	0.66	3.87	0.00010838	0.01944449
<i>TSPAN8</i>	3.51	0.91	-3.87	0.0001083	0.01944449
<i>ELOVL1</i>	0.55	0.14	-3.87	0.0001096	0.01955388
<i>EIF4EBP1</i>	0.69	0.18	-3.87	0.00011102	0.01958743
<i>MTND6P5</i>	-1.13	0.29	3.86	0.00011164	0.01958743
<i>TOP1</i>	0.46	0.12	-3.86	0.0001116	0.01958743
<i>ATRAID</i>	0.81	0.21	-3.86	0.00011481	0.01971304
<i>MLLT3</i>	-0.67	0.17	3.86	0.00011484	0.01971304
<i>AP003969.2</i>	-1.40	0.36	3.86	0.00011437	0.01971304
<i>MT-RNR2</i>	1.75	0.45	-3.86	0.00011423	0.01971304
<i>PQBP1</i>	0.85	0.22	-3.85	0.00011676	0.01993386
<i>FOXD3-AS1</i>	3.43	0.89	-3.84	0.00012098	0.02032798
<i>LDB3</i>	2.36	0.61	-3.84	0.00012074	0.02032798
<i>FFAR1</i>	-3.66	0.95	3.85	0.00012031	0.02032798
<i>AC023202.1</i>	4.16	1.08	-3.84	0.00012413	0.02061168
<i>AC079600.3</i>	-1.73	0.45	3.84	0.00012462	0.02061168
<i>FARSA</i>	1.10	0.29	-3.84	0.00012367	0.02061168
<i>AC074138.1</i>	-0.93	0.24	3.83	0.00012616	0.02075827
<i>RPLP0</i>	0.78	0.20	-3.83	0.00012844	0.0209163
<i>TECR</i>	0.71	0.19	-3.83	0.00012782	0.0209163
<i>HNRNPCP2</i>	0.50	0.13	-3.83	0.00012985	0.02103845
<i>TTC34</i>	-1.55	0.40	3.82	0.00013201	0.02110702
<i>H2AC16</i>	1.53	0.40	-3.82	0.00013324	0.02110702
<i>ZDHHC21</i>	-0.70	0.18	3.82	0.0001336	0.02110702
<i>FAM111A</i>	-0.59	0.15	3.82	0.00013245	0.02110702
<i>FXD2</i>	-1.56	0.41	3.82	0.00013249	0.02110702
<i>GOLGA8H</i>	-1.60	0.42	3.81	0.00013798	0.02160392
<i>TBCB</i>	0.51	0.13	-3.81	0.0001381	0.02160392
<i>TAGLN2P1</i>	1.60	0.42	-3.81	0.00013902	0.02164016
<i>FSD2</i>	3.18	0.83	-3.80	0.00014211	0.02201328
<i>USH2A</i>	2.43	0.64	-3.80	0.00014479	0.02221279
<i>DDX10</i>	-0.54	0.14	3.80	0.00014433	0.02221279
<i>AC011503.1</i>	-4.99	1.31	3.80	0.00014647	0.02236275
<i>AL359555.4</i>	-2.77	0.73	3.79	0.00015066	0.02289201
<i>AC127502.2</i>	-0.76	0.20	3.79	0.00015173	0.02294501
<i>MSRB3</i>	-1.77	0.47	3.79	0.0001533	0.02296332
<i>HPD</i>	2.98	0.79	-3.79	0.00015298	0.02296332
<i>AC096531.2</i>	2.16	0.57	-3.78	0.00015558	0.0231958
<i>SMARCA2</i>	-0.63	0.17	3.78	0.00015681	0.02326962
<i>H3P47</i>	1.18	0.31	-3.78	0.00015851	0.02330423
<i>AC026150.1</i>	-2.59	0.69	3.78	0.00015821	0.02330423
<i>MUC20-OT1</i>	-0.80	0.21	3.77	0.00016166	0.02333449
<i>C14orf180</i>	3.07	0.81	-3.77	0.00016049	0.02333449
<i>CTSA</i>	0.73	0.19	-3.77	0.00016128	0.02333449

<i>UBA52</i>	0.66	0.18	-3.77	0.00016047	0.02333449
<i>APEX2</i>	0.50	0.13	-3.77	0.00016429	0.02360665
<i>MANEAL</i>	1.33	0.35	-3.76	0.00016683	0.02386436
<i>ALI36164.3</i>	-1.17	0.31	3.76	0.00016781	0.02387425
<i>KATNAL2</i>	1.11	0.29	-3.76	0.0001684	0.02387425
<i>PSMD3</i>	0.41	0.11	-3.76	0.00016947	0.02388589
<i>AC092279.1</i>	-0.51	0.14	3.76	0.00016999	0.02388589
<i>DYRK1B</i>	0.90	0.24	-3.76	0.00017139	0.02397643
<i>ACTA1</i>	5.18	1.38	-3.75	0.00017357	0.02406897
<i>UBE2C</i>	1.39	0.37	-3.76	0.00017325	0.02406897
<i>WSBI</i>	-0.48	0.13	3.75	0.00017539	0.02421562
<i>PAICS</i>	0.69	0.18	-3.75	0.0001762	0.02422272
<i>PCNA</i>	0.89	0.24	-3.75	0.00017807	0.02437362
<i>NEB</i>	2.57	0.69	-3.74	0.0001808	0.02453593
<i>LINC00472</i>	-1.07	0.28	3.74	0.00018066	0.02453593
<i>FOXO3</i>	3.32	0.89	-3.73	0.00018784	0.02508078
<i>RPS15P4</i>	1.18	0.32	-3.73	0.00018837	0.02508078
<i>EXOC5P1</i>	-1.44	0.39	3.74	0.00018761	0.02508078
<i>AC109635.3</i>	4.38	1.17	-3.73	0.00018876	0.02508078
<i>NPHS1</i>	-2.96	0.79	3.73	0.0001885	0.02508078
<i>HSD17B10</i>	1.02	0.27	-3.73	0.00019348	0.02528416
<i>RBP4</i>	-2.38	0.64	3.73	0.00019345	0.02528416
<i>AC138649.1</i>	-2.45	0.66	3.73	0.00019303	0.02528416
<i>APCDD1</i>	1.72	0.46	-3.73	0.00019337	0.02528416
<i>NDUFB10</i>	0.72	0.19	-3.72	0.00019811	0.02573884
<i>NACCI</i>	0.85	0.23	-3.72	0.00019858	0.02573884
<i>TECRP1</i>	1.06	0.29	-3.72	0.0002005	0.02588203
<i>MRPL51</i>	0.59	0.16	-3.71	0.00020323	0.026128
<i>AP001059.1</i>	-1.80	0.49	3.71	0.00020437	0.02616864
<i>ALG3</i>	0.71	0.19	-3.71	0.00020739	0.02630045
<i>AP000866.6</i>	-0.74	0.20	3.71	0.00020954	0.02630045
<i>GAS6-AS1</i>	-1.17	0.32	3.71	0.00020711	0.02630045
<i>UBL7</i>	0.57	0.16	-3.71	0.00020939	0.02630045
<i>AF015720.1</i>	2.52	0.68	-3.71	0.00020872	0.02630045
<i>CLCNKB</i>	-2.74	0.74	3.70	0.00021751	0.02719382
<i>AC139426.3</i>	-3.49	0.95	3.70	0.00021874	0.02720737
<i>PSMA7</i>	0.64	0.17	-3.70	0.00021933	0.02720737
<i>RBIS</i>	-0.58	0.16	3.69	0.00022063	0.02726164
<i>AFP</i>	3.54	0.96	-3.69	0.00022528	0.02730491
<i>LINC01018</i>	3.69	1.00	-3.69	0.00022444	0.02730491
<i>CENPW</i>	1.73	0.47	-3.69	0.00022481	0.02730491
<i>KCNB2</i>	3.51	0.95	-3.69	0.00022527	0.02730491
<i>AC008147.2</i>	-1.09	0.29	3.69	0.0002235	0.02730491
<i>IDH2</i>	0.79	0.21	-3.69	0.00022802	0.02753182
<i>COG2</i>	-0.60	0.16	3.68	0.00023184	0.02778245

<i>AC068896.3</i>	-1.14	0.31	3.68	0.00023179	0.02778245
<i>AC012046.1</i>	-1.07	0.29	3.68	0.00023449	0.02799466
<i>FLNC</i>	1.54	0.42	-3.68	0.00023607	0.02807731
<i>SARNP</i>	-0.62	0.17	3.67	0.00024099	0.02855593
<i>ALI36984.1</i>	-0.87	0.24	3.67	0.00024287	0.02867104
<i>AC009229.4</i>	-2.31	0.63	3.67	0.00024541	0.02874913
<i>NPY2R</i>	3.17	0.86	-3.67	0.00024625	0.02874913
<i>PRMT1</i>	0.67	0.18	-3.67	0.00024469	0.02874913
<i>DOLPP1</i>	0.63	0.17	-3.66	0.00024862	0.02891995
<i>STX7</i>	-0.77	0.21	3.66	0.00025157	0.02894508
<i>AC024293.1</i>	0.76	0.21	-3.66	0.00025006	0.02894508
<i>SLC1A5</i>	0.69	0.19	-3.66	0.00025118	0.02894508
<i>PPIAP11</i>	1.04	0.28	-3.66	0.000254	0.02911935
<i>PRKCQ-AS1</i>	-1.93	0.53	3.66	0.00025634	0.02915314
<i>GPN3</i>	0.86	0.23	-3.66	0.00025609	0.02915314
<i>CD22</i>	-2.04	0.56	3.66	0.00025705	0.02915314
<i>XRCC5</i>	0.39	0.11	-3.65	0.00026003	0.02938634
<i>ICMT</i>	0.55	0.15	-3.65	0.00026346	0.02945969
<i>NDUFB11</i>	0.90	0.25	-3.65	0.00026266	0.02945969
<i>PHB</i>	0.54	0.15	-3.65	0.00026269	0.02945969
<i>C2orf83</i>	4.33	1.19	-3.65	0.00026702	0.02975267
<i>AC019197.1</i>	-2.16	0.59	3.64	0.00027566	0.02978345
<i>TFPI</i>	1.07	0.29	-3.64	0.00026917	0.02978345
<i>NMURI</i>	-2.19	0.60	3.64	0.00027668	0.02978345
<i>STRIT1</i>	4.69	1.29	-3.64	0.00027541	0.02978345
<i>H2AC12</i>	1.28	0.35	-3.64	0.00027314	0.02978345
<i>EPC1</i>	-0.38	0.10	3.64	0.00027625	0.02978345
<i>MYPN</i>	3.58	0.98	-3.64	0.00027388	0.02978345
<i>AC112777.1</i>	1.29	0.35	-3.64	0.0002701	0.02978345
<i>ADRM1</i>	0.68	0.19	-3.64	0.00027375	0.02978345
<i>CLPP</i>	0.60	0.16	-3.64	0.00027495	0.02978345
<i>MCM4</i>	0.91	0.25	-3.63	0.00028411	0.03048009
<i>DNTTIP1</i>	0.66	0.18	-3.63	0.00028553	0.03052929
<i>RPL21P123</i>	-1.26	0.35	3.63	0.00028734	0.03053475
<i>CARM1</i>	0.90	0.25	-3.63	0.0002875	0.03053475
<i>CDC26</i>	0.70	0.19	-3.62	0.00029532	0.03115698
<i>AC004784.1</i>	3.09	0.85	-3.62	0.00029497	0.03115698
<i>CDKN2AIPNL</i>	0.83	0.23	-3.62	0.00029866	0.03125215
<i>UBE2MP1</i>	1.19	0.33	-3.62	0.00029814	0.03125215
<i>LMNB2</i>	1.06	0.29	-3.61	0.00030114	0.03125215
<i>SGTA</i>	0.58	0.16	-3.61	0.00030047	0.03125215
<i>AC022432.1</i>	2.63	0.73	-3.62	0.00029979	0.03125215
<i>RNU6-148P</i>	3.13	0.87	-3.61	0.00030352	0.03139559
<i>MRPS2</i>	0.68	0.19	-3.61	0.0003047	0.03141592
<i>CSEIL</i>	0.75	0.21	-3.61	0.00030582	0.03142893

<i>MED30</i>	0.75	0.21	-3.61	0.00030723	0.03145959
<i>EMC7</i>	0.49	0.14	-3.61	0.0003081	0.03145959
<i>AC108727.1</i>	-1.02	0.28	3.61	0.00031131	0.03158296
<i>CLDN16</i>	-2.57	0.71	3.60	0.00031229	0.03158296
<i>RPL35</i>	0.62	0.17	-3.61	0.00031207	0.03158296
<i>MLIP</i>	2.99	0.83	-3.60	0.00031534	0.03168934
<i>TRAF7</i>	0.65	0.18	-3.60	0.00031501	0.03168934
<i>CPNE1</i>	0.63	0.18	-3.60	0.00031756	0.03181117
<i>CYP19A1</i>	2.58	0.72	-3.60	0.00031907	0.03186251
<i>PGD</i>	0.74	0.21	-3.60	0.00032101	0.03195647
<i>IL9RP3</i>	-1.46	0.41	3.60	0.00032269	0.03202327
<i>POLR2E</i>	0.54	0.15	-3.60	0.00032393	0.03204617
<i>RN7SL200P</i>	-1.16	0.32	3.59	0.00033321	0.03243407
<i>SIRLNT</i>	4.35	1.21	-3.59	0.00033305	0.03243407
<i>AC078962.2</i>	-1.45	0.40	3.59	0.00033175	0.03243407
<i>MYBPC1</i>	4.83	1.35	-3.59	0.00033195	0.03243407
<i>AC020978.6</i>	-0.72	0.20	3.59	0.00033398	0.03243407
<i>SNTA1</i>	0.98	0.27	-3.59	0.00032936	0.03243407
<i>LINC01226</i>	-2.23	0.62	3.58	0.00033848	0.03247398
<i>BX679664.2</i>	-1.15	0.32	3.58	0.00033761	0.03247398
<i>OR2M4</i>	3.36	0.94	-3.59	0.00033658	0.03247398
<i>MYBPC3</i>	-1.65	0.46	3.58	0.00033847	0.03247398
<i>AURKAIP1</i>	0.98	0.27	-3.58	0.00034588	0.03269804
<i>AL365209.1</i>	-2.21	0.62	3.58	0.00034597	0.03269804
<i>MIR6083</i>	-1.57	0.44	3.58	0.0003421	0.03269804
<i>CERS5</i>	-0.52	0.15	3.58	0.00034547	0.03269804
<i>KRT42P</i>	-2.78	0.78	3.58	0.00034289	0.03269804
<i>AL049780.2</i>	-1.59	0.45	3.57	0.00035815	0.0336492
<i>SIRT2</i>	1.00	0.28	-3.57	0.0003573	0.0336492
<i>PCSK7</i>	-0.59	0.16	3.57	0.00035956	0.03368169
<i>AC091979.1</i>	3.54	0.99	-3.57	0.00036246	0.0338537
<i>RNU6-522P</i>	-1.11	0.31	3.56	0.00036884	0.03434879
<i>PCOLCE</i>	1.07	0.30	-3.56	0.00037006	0.03436116
<i>ANKRD20A11P</i>	-1.86	0.52	3.56	0.00037513	0.03473109
<i>CHRND</i>	4.54	1.28	-3.56	0.00037636	0.03474352
<i>GPAT2</i>	1.75	0.49	-3.55	0.00038372	0.03501515
<i>LSM14B</i>	0.51	0.14	-3.55	0.00038244	0.03501515
<i>CCDC124</i>	0.68	0.19	-3.55	0.00038171	0.03501515
<i>Z95114.4</i>	2.30	0.65	-3.55	0.00038285	0.03501515
<i>PLTP</i>	1.37	0.39	-3.55	0.0003849	0.03502294
<i>MCM2</i>	1.05	0.30	-3.55	0.00039155	0.03552581
<i>RACK1</i>	0.57	0.16	-3.54	0.00039576	0.03580573
<i>MYOZ1</i>	3.46	0.98	-3.54	0.00040474	0.0362943
<i>PTGES3P4</i>	1.77	0.50	-3.54	0.0004053	0.0362943
<i>AC046158.2</i>	-0.71	0.20	3.54	0.00040688	0.0362943

<i>DMAC2</i>	0.59	0.17	-3.54	0.00040471	0.0362943
<i>RUVBL2</i>	0.67	0.19	-3.54	0.0004059	0.0362943
<i>CTU1</i>	0.79	0.22	-3.53	0.00041553	0.03696282
<i>AC104506.1</i>	2.63	0.75	-3.53	0.00042261	0.03710411
<i>AL357054.3</i>	-1.99	0.57	3.52	0.00042402	0.03710411
<i>MTCO1P11</i>	-1.03	0.29	3.52	0.00042361	0.03710411
<i>CHORDC1</i>	-0.74	0.21	3.52	0.00042413	0.03710411
<i>CUTC</i>	0.88	0.25	-3.53	0.00042079	0.03710411
<i>MRPS12</i>	1.03	0.29	-3.53	0.00042227	0.03710411
<i>H2AC20</i>	0.87	0.25	-3.52	0.00043548	0.03796842
<i>PSMB6</i>	0.79	0.23	-3.52	0.0004364	0.03796842
<i>RNA5SP300</i>	-2.07	0.59	3.52	0.00043775	0.03798125
<i>CELSR3</i>	1.86	0.53	-3.51	0.00044041	0.03810849
<i>CHIT1</i>	-1.83	0.52	3.51	0.00044364	0.03813138
<i>DNAJB14</i>	-0.75	0.21	3.51	0.00045011	0.03813138
<i>POLD2</i>	0.74	0.21	-3.51	0.00044341	0.03813138
<i>EIF4A1P10</i>	0.80	0.23	-3.51	0.00045029	0.03813138
<i>NSDHL</i>	0.87	0.25	-3.51	0.00044911	0.03813138
<i>MIR624</i>	-0.84	0.24	3.51	0.00045026	0.03813138
<i>AC011939.2</i>	-0.95	0.27	3.51	0.00044849	0.03813138
<i>EIF3D</i>	0.50	0.14	-3.51	0.0004489	0.03813138
<i>B3GALT6</i>	0.65	0.18	-3.51	0.00045429	0.03836802
<i>AC005746.1</i>	-0.75	0.22	3.50	0.0004569	0.03848621
<i>PRICKLE1</i>	-1.18	0.34	3.50	0.00045969	0.03861911
<i>P2RY14</i>	-1.74	0.50	3.50	0.00046725	0.03915077
<i>TRAF5</i>	-0.73	0.21	3.50	0.00047334	0.03951878
<i>TUBBP1</i>	0.76	0.22	-3.49	0.00047662	0.03951878
<i>LINC00092</i>	-2.11	0.60	3.49	0.00047436	0.03951878
<i>SLC7A6OS</i>	-0.41	0.12	3.49	0.0004765	0.03951878
<i>AC011352.1</i>	3.67	1.05	-3.49	0.00047892	0.0396054
<i>PADI4</i>	2.75	0.79	-3.49	0.00048179	0.0397394
<i>NOP14</i>	0.53	0.15	-3.49	0.00048952	0.03978528
<i>RN7SKP110</i>	-1.46	0.42	3.49	0.00048712	0.03978528
<i>AP003168.2</i>	-0.74	0.21	3.49	0.0004897	0.03978528
<i>GADD45GIP1</i>	0.85	0.24	-3.49	0.00048545	0.03978528
<i>ACTN4</i>	0.56	0.16	-3.49	0.0004897	0.03978528
<i>SLC17A7</i>	1.69	0.49	-3.49	0.00048986	0.03978528
<i>ACAP2-IT1</i>	-0.80	0.23	3.48	0.00049382	0.03990297
<i>CD83</i>	-1.08	0.31	3.48	0.00049339	0.03990297
<i>NUP37</i>	0.69	0.20	-3.48	0.00049523	0.03991539
<i>PLOD1</i>	0.85	0.25	-3.48	0.00049761	0.04000534
<i>AC119673.1</i>	-1.06	0.31	3.48	0.00050911	0.0405199
<i>OR7E66P</i>	1.99	0.57	-3.48	0.00050764	0.0405199
<i>SNORD101</i>	-0.86	0.25	3.48	0.00050821	0.0405199
<i>ENSG00000237721</i>	1.87	0.54	-3.48	0.00050911	0.0405199



<i>AC022919.1</i>	-0.73	0.21	3.47	0.00051574	0.04094456
<i>GOT1</i>	0.89	0.26	-3.47	0.0005215	0.04119575
<i>PMP22</i>	0.80	0.23	-3.47	0.00052054	0.04119575
<i>TOMM7</i>	0.55	0.16	-3.47	0.00052493	0.04135397
<i>COL13A1</i>	-1.85	0.53	3.47	0.00052611	0.04135397
<i>MKRN9P</i>	3.41	0.98	-3.47	0.00052754	0.04136451
<i>FAM50A</i>	0.79	0.23	-3.46	0.0005335	0.04142571
<i>CEND1</i>	2.87	0.83	-3.46	0.00053354	0.04142571
<i>MED28P6</i>	-2.78	0.80	3.46	0.00053328	0.04142571
<i>CFAP61</i>	2.44	0.70	-3.46	0.00053349	0.04142571
<i>MSTIP2</i>	1.50	0.43	-3.46	0.00053532	0.04146227
<i>PELP1</i>	0.50	0.15	-3.46	0.00053672	0.04146392
<i>TVP23C</i>	-0.51	0.15	3.46	0.00053795	0.04146392
<i>AC120045.1</i>	-2.73	0.79	3.46	0.00054221	0.0415923
<i>USP6</i>	1.70	0.49	-3.46	0.00054223	0.0415923
<i>PPDPF</i>	0.76	0.22	-3.45	0.00055247	0.042275
<i>TK1</i>	1.23	0.36	-3.45	0.00055691	0.04251255
<i>MYOCOS</i>	-1.89	0.55	3.45	0.00055963	0.04261783
<i>ADGRG5</i>	-1.78	0.51	3.45	0.00056159	0.04266485
<i>ANKRD44-IT1</i>	-1.33	0.38	3.45	0.00056494	0.04281652
<i>ALI36146.2</i>	-1.09	0.32	3.45	0.00056684	0.0428587
<i>KCNIP2</i>	-0.86	0.25	3.45	0.00056838	0.04287276
<i>CCNH</i>	-0.49	0.14	3.44	0.00057504	0.04327252
<i>MRPL24</i>	0.56	0.16	-3.44	0.00057969	0.04351905
<i>AC097460.2</i>	-0.98	0.28	3.44	0.00058732	0.04391929
<i>TMEM218</i>	-0.48	0.14	3.44	0.00059055	0.04391929
<i>AC092115.2</i>	0.74	0.22	-3.44	0.00058796	0.04391929
<i>SOD1</i>	0.72	0.21	-3.44	0.00058969	0.04391929
<i>AC130448.2</i>	-2.19	0.64	3.43	0.00059747	0.04432995
<i>AL512328.1</i>	-2.14	0.62	3.43	0.00060669	0.04448336
<i>PPM1K</i>	-0.68	0.20	3.43	0.00061382	0.04448336
<i>MYOZ2</i>	2.58	0.75	-3.43	0.00060708	0.04448336
<i>SLC39A7</i>	0.53	0.15	-3.42	0.00061495	0.04448336
<i>RNU6-1163P</i>	3.97	1.16	-3.43	0.00061319	0.04448336
<i>ST18</i>	-1.75	0.51	3.43	0.00060896	0.04448336
<i>KDM4C</i>	-0.60	0.18	3.43	0.00060655	0.04448336
<i>EIF3A</i>	0.35	0.10	-3.43	0.00060415	0.04448336
<i>GAPDH</i>	0.88	0.26	-3.43	0.00061029	0.04448336
<i>TPPP3</i>	1.34	0.39	-3.43	0.00061242	0.04448336
<i>MRPL58</i>	0.80	0.23	-3.43	0.00060133	0.04448336
<i>COPS6</i>	0.43	0.13	-3.42	0.00061752	0.04456791
<i>CDHR1</i>	2.12	0.62	-3.42	0.00062044	0.04467708
<i>RPS2P46</i>	0.63	0.19	-3.42	0.00062219	0.04470174
<i>AC090948.1</i>	-0.91	0.27	3.42	0.00063594	0.04538195
<i>HUWE1</i>	0.34	0.10	-3.42	0.00063554	0.04538195

<i>SGSM1</i>	-1.36	0.40	3.42	0.00063485	0.04538195
<i>DNAH3</i>	2.95	0.86	-3.41	0.00063812	0.0454356
<i>EIF4G1</i>	0.40	0.12	-3.41	0.00064565	0.04576632
<i>PHB2</i>	0.52	0.15	-3.41	0.00064458	0.04576632
<i>CYC1</i>	0.80	0.24	-3.41	0.00064793	0.04582542
<i>CYP26B1</i>	1.33	0.39	-3.41	0.00065191	0.04600463
<i>ACOXL</i>	-3.27	0.96	3.41	0.00066013	0.0463296
<i>PPP4C</i>	0.57	0.17	-3.41	0.00065999	0.0463296
<i>IMPA2</i>	0.93	0.27	-3.41	0.00066164	0.0463296
<i>ECH1</i>	0.74	0.22	-3.40	0.00066235	0.0463296
<i>P4HB</i>	0.58	0.17	-3.40	0.00066844	0.04665254
<i>ASB5</i>	4.32	1.27	-3.40	0.00067192	0.04679241
<i>CACNA1S</i>	3.44	1.01	-3.40	0.0006743	0.04685569
<i>AC009229.1</i>	-2.82	0.83	3.40	0.00067784	0.04699893
<i>RTN2</i>	1.17	0.35	-3.40	0.00068348	0.04728669
<i>WTAPP1</i>	-2.45	0.72	3.39	0.00068811	0.04750348
<i>ANXA2P2</i>	0.87	0.26	-3.39	0.00069669	0.04788735
<i>RPL6</i>	0.51	0.15	-3.39	0.00069557	0.04788735
<i>DCDC2C</i>	-3.81	1.12	3.39	0.0006999	0.04790092
<i>SUPT3H</i>	-0.85	0.25	3.39	0.00069893	0.04790092
<i>SPIB</i>	-2.08	0.61	3.39	0.00070469	0.04812522
<i>AC009032.1</i>	-0.66	0.19	3.39	0.00070656	0.04814948
<i>AC016734.2</i>	-0.65	0.19	3.38	0.00071269	0.04832676
<i>TRIM27</i>	-0.36	0.11	3.38	0.00071373	0.04832676
<i>RNU7-40P</i>	-1.17	0.35	3.38	0.00071249	0.04832676
<i>SCARNA22</i>	1.36	0.40	-3.38	0.00071707	0.04834679
<i>VGLL2</i>	3.10	0.92	-3.38	0.00071644	0.04834679
<i>TCLIA</i>	-2.57	0.76	3.38	0.0007274	0.04893914
<i>ADGRF2</i>	2.99	0.89	-3.37	0.00074144	0.04895078
<i>IDH3G</i>	0.51	0.15	-3.38	0.00073686	0.04895078
<i>AC104964.1</i>	-1.19	0.35	3.38	0.00072925	0.04895078
<i>AP003497.2</i>	-2.54	0.75	3.38	0.00073312	0.04895078
<i>ALI36982.3</i>	-0.69	0.21	3.38	0.00073608	0.04895078
<i>TSR3</i>	0.70	0.21	-3.37	0.00074086	0.04895078
<i>GPX4</i>	1.05	0.31	-3.37	0.00073984	0.04895078
<i>PAK4</i>	1.00	0.30	-3.37	0.00073825	0.04895078
<i>XRCC6</i>	0.49	0.14	-3.37	0.00074069	0.04895078
<i>SH3BGR</i>	1.63	0.48	-3.37	0.00074666	0.0491931
<i>CHST7</i>	1.06	0.31	-3.37	0.00074851	0.04921292
<i>AL031599.1</i>	2.64	0.78	-3.37	0.00075171	0.04921893
<i>AC073896.5</i>	-2.68	0.80	3.37	0.00075118	0.04921893
<i>HKDC1</i>	-2.42	0.72	3.37	0.00076142	0.04965028
<i>AAR2</i>	0.55	0.16	-3.37	0.00076077	0.04965028
<i>LAMTOR2</i>	0.68	0.20	-3.36	0.00076754	0.04994695

SE, standard error; \*Positive higher in resistant tumors

**12. Table A8. Baseline Characteristics of Patients by CALBI Expression Status**

Characteristic	CALBI Expressed			CALBI Not Expressed			Total
	Selinexor (N = 29)	Placebo (N = 17)	Total (N = 47)	Selinexor (N = 16)	Placebo (N = 14)	Total (N = 30)	Total (N = 76)
<b>Age</b>							
Median (range) — year	63 (44-79)	67 (46-80)	63 (44-80)	66 (51-75)	66.5 (40-77)	66.5 (40-77)	64.5 (40-80)
Distribution – no. (%)							
18 - 64	16 (55.2)	8 (47.1)	24 (52.2)	8 (50.0)	6 (42.9)	14 (46.7)	38 (50.0)
65-74	11 (37.9)	6 (35.3)	17 (37.0)	7 (43.8)	6 (42.9)	13 (43.3)	30 (39.5)
≥ 75	2 (6.9)	3 (17.6)	5 (10.9)	1 (6.3)	2 (14.3)	3 (10.0)	8 (10.5)
Male sex – no. (%)	18 (62.1)	13 (76.5)	31 (67.4)	9 (56.3)	11 (78.6)	20 (66.7)	51 (67.1)
<b>Race n (%)</b>							
Asian	1 (3.4)	0	1 (2.2)	1 (6.3)	0	1 (3.3)	2 (2.6)
Black or African American	0	0	0	0	1 (7.1)	1 (3.3)	1 (1.3)
White	23 (79.3)	16 (94.1)	39 (84.8)	12 (75.0)	12 (85.7)	24 (80.0)	63 (82.9)
Other/Missing	5 (17.2)	1 (5.9)	6 (13.0)	3 (18.8)	1 (7.1)	4 (13.3)	10 (13.2)
<b>Geographic Region n (%)</b>							
North America	15 (51.7)	15 (88.2)	30 (65.2)	5 (31.3)	7 (50.0)	12 (40.0)	42 (55.3)
Europe and Israel	14 (48.3)	2 (11.8)	16 (34.8)	11 (68.8)	7 (50.0)	18 (60.0)	34 (44.7)
<b>ECOG performance-status score — no. (%)<sup>†</sup></b>							
0	15 (51.7)	10 (58.8)	25 (54.3)	5 (31.3)	7 (50.0)	12 (40.0)	37 (48.7)
1	14 (48.3)	7 (41.2)	21 (45.7)	11 (68.8)	7 (50.0)	18 (60.0)	39 (51.3)
<b>Median duration from most recent progression (range) — months</b>							
Median time since initial diagnosis (range) — months	41.6 (11-328)	36.1 (11-140)	40.2 (11-328)	58.3 (11-195)	79.6 (23-173)	63.6 (11-195)	47.9 (11-328)
<b>Disease Stage Category at Study Entry, n (%)</b>							
Metastasis	24 (82.8)	15 (88.2)	39 (84.8)	14 (87.5)	11 (78.6)	25 (83.3)	64 (84.2)
Lung	4 (13.8)	1 (5.9)	5 (10.9)	3 (18.8)	2 (14.3)	5 (16.7)	10 (13.2)
Liver	2 (6.9)	3 (17.6)	5 (10.9)	1 (6.3)	0	1 (3.3)	6 (7.9)
Peritoneal Cavity	7 (24.1)	7 (41.2)	14 (30.4)	5 (31.3)	3 (21.4)	8 (26.7)	22 (28.9)
Other	11 (37.9)	4 (23.5)	15 (32.6)	5 (31.3)	6 (42.9)	11 (36.7)	26 (34.2)
<b>Site of Study Entry Liposarcoma Lesion, n (%)</b>							
Primary/Extension	27 (93.1)	16 (94.1)	43 (93.5)	15 (93.8)	14 (100.0)	29 (96.7)	72 (94.7)
Extremity (Lower + Upper)	0	0	0	1 (6.3)	0	1 (3.3)	1 (1.3)
Retroperitoneum	22 (75.9)	9 (52.9)	31 (67.4)	9 (56.3)	10 (71.4)	19 (63.3)	50 (65.8)
Other	5 (17.2)	7 (41.2)	12 (26.1)	5 (31.3)	4 (28.6)	9 (30.0)	21 (27.6)
<b>Median Prior Antineoplastic Regimen — no. (range)</b>							
	2 (1-5)	2 (2-5)	2 (1-5)	2 (1-5)	2 (1-5)	2 (1-5)	2 (1-5)

Characteristic	CALBI Expressed			CALBI Not Expressed			Total
	Selinexor (N = 29)	Placebo (N = 17)	Total (N = 47)	Selinexor (N = 16)	Placebo (N = 14)	Total (N = 30)	Total (N = 76)
Number of prior antineoplastic regimen — no. (%)							
≤2	16 (55.2)	9 (52.9)	25 (54.3)	10 (62.5)	8 (57.1)	18 (60.0)	43 (56.6)
≥3	13 (44.8)	8 (47.1)	21 (45.7)	6 (37.5)	6 (42.9)	12 (40.0)	33 (43.4)
Previous Systemic Therapy							
Eribulin	10 (34.5)	7 (41.2)	17 (37.0)	3 (18.8)	5 (35.7)	8 (26.7)	25 (32.9)
Anthracyclines	23 (79.3)	15 (88.2)	38 (82.6)	14 (87.5)	10 (71.4)	24 (80.0)	62 (81.6)
Anthracyclines + Alkylating Agents	23 (79.3)	15 (88.2)	38 (82.6)	14 (87.5)	11 (78.6)	25 (83.3)	63 (82.9)
Gemcitabine + Taxanes	10 (34.5)	8 (47.1)	18 (39.1)	5 (31.3)	4 (28.6)	9 (30.0)	27 (35.5)
Trabectedin	11 (37.9)	6 (35.3)	17 (37.0)	8 (50.0)	4 (28.6)	12 (40.0)	29 (38.2)
Dacarbazine	3 (10.3)	1 (5.9)	4 (8.7)	2 (12.5)	1 (7.1)	3 (10.0)	7 (9.2)
MDM2 inhibitor	1 (3.4)	0	1 (2.2)	1 (6.3)	0	1 (3.3)	2 (2.6)
CDK4 inhibitor	9 (31.0)	5 (29.4)	14 (30.4)	0	4 (28.6)	4 (13.3)	18 (23.7)
Immune checkpoint inhibitor	2 (6.9)	4 (23.5)	6 (13.0)	2 (12.5)	2 (14.3)	4 (13.3)	10 (13.2)
Tyrosine kinase inhibitor	8 (27.6)	8 (47.1)	16 (34.8)	1 (6.3)	4 (28.6)	5 (16.7)	21 (27.6)
Others	2 (6.9)	2 (11.8)	4 (8.7)	0	1 (7.1)	1 (3.3)	5 (6.6)
Prior radiotherapy, n (%)							
Yes	17 (58.6)	6 (35.3)	23 (50.0)	6 (37.5)	6 (42.9)	12 (40.0)	35 (46.1)
Prior surgery, n (%)							
Yes	27 (93.1)	14 (82.4)	41 (89.1)	14 (87.5)	13 (92.9)	27 (90.0)	68 (89.5)
Number of Prior Surgeries							
Median (range)	2.0 (1-5)	2.0 (1-7)	2.0 (1-7)	2.0 (1-7)	2.0 (1-5)	2.0 (1-7)	2.0 (1-7)

<sup>†</sup>Eastern Cooperative Oncology Group (ECOG) performance-status scores range from 0 to 5, with higher scores reflecting greater disability.

**13. Table A9. Baseline Characteristics of Patients with Sequenced Tumors vs. Patients without Sequenced Tumors**

Characteristic	Selinexor		Placebo	
	Patients with Sequenced Tumors (N=45)*	Patients without Sequenced Tumors (N=143)	Patients with Sequenced Tumors (N=31)	Patients without Sequenced Tumors (N=66)
Age				
Median (range) — year	63 (44-79)	65 (33-84)	67 (40-80)	65 (31-85)
Distribution — no. (%)				
18 - 64	24 (53.3)	68 (47.5)	14 (45.2)	32 (48.5)
65-74	18 (40.0)	55 (38.5)	12 (38.7)	29 (43.9)
≥ 75	3 (6.7)	20 (14.0)	5 (16.1)	5 (7.6)
Male sex — no. (%)	27 (60.0)	87 (60.8)	24 (77.4)	40 (60.6)
Race n (%)				
Asian	2 (4.4)	7 (4.9)	0	3 (4.5)
Black or African American	0	3 (2.1)	1 (3.2)	0
White	35 (77.8)	104 (72.7)	28 (90.3)	52 (78.8)
Other/Missing	0	1 (0.7)	0	0
Geographic Region n (%)				
North America	20 (44.4)	70 (49.0)	22 (71.0)	33 (50.0)
Europe and Israel	25 (55.6)	73 (51.0)	9 (29.0)	33 (50.0)
ECOG performance-status score — no. (%) <sup>†</sup>				
0	20 (44.4)	51 (35.7)	17 (54.8)	24 (36.4)
1	25 (55.6)	92 (64.3)	14 (45.2)	42 (63.6)
Median duration from most recent progression (range) — months	0.92 (0.2-5.6)	0.85 (0.1-6.7)	0.62 (0.1-3.1)	0.69 (0.1-15.5)
Median time since initial diagnosis (range) —months	49 (11-328)	52.9 (5-313)	43.9 (11-173)	61.0 (13-301)
Disease Stage Category at Study Entry, n (%)				
Metastasis	38 (84.4)	96 (67.1)	26 (83.9)	52 (78.8)
Lung	7 (15.6)	21 (14.7)	3 (9.7)	13 (19.7)
Liver	3 (6.7)	9 (6.3)	3 (9.7)	6 (9.1)
Peritoneal Cavity	12 (26.7)	35 (24.5)	10 (32.3)	16 (24.2)
Other	16 (35.6)	31 (21.7)	10 (32.3)	17 (25.8)
Primary/Extension Site of Study Entry Liposarcoma Lesion, n (%)				
Extremity (Lower + Upper)	1 (2.2)	8 (5.6)	0	3 (4.5)
Retroperitoneum	31 (68.9)	107 (74.8)	19 (61.3)	47 (71.2)

Other	10 (22.2)	23 (16.1)	11 (35.5)	11 (16.7)
Median Prior Antineoplastic Regimen — no. (range)	45 (100.0)	143 (100.0)	31 (100.0)	66 (100.0)
Number of prior antineoplastic regimen — no. (%)				
≤2	26 (57.8)	78 (54.5)	17 (54.8)	36 (54.5)
≥3	19 (42.2)	65 (45.5)	14 (45.2)	30 (45.5)
Previous Systemic Therapy				
Eribulin	13 (28.9)	53 (37.1)	12 (38.7)	23 (34.8)
Anthracyclines	37 (82.2)	128 (89.5)	25 (80.6)	59 (89.4)
Anthracyclines + Alkylating Agents	37 (82.2)	131 (91.6)	26 (83.9)	61 (92.4)
Gemcitabine + Taxanes	15 (33.3)	57 (39.9)	12 (38.7)	16 (24.2)
Trabectedin	19 (42.2)	50 (35.0)	10 (32.3)	26 (39.4)
Dacarbazine	5 (11.1)	20 (14.0)	2 (6.5)	5 (7.6)
MDM2 inhibitor	2 (4.4)	6 (4.2)	0	1 (1.5)
CDK4 inhibitor	9 (20.0)	24 (16.8)	9 (29.0)	12 (18.2)
Immune checkpoint inhibitor	4 (8.9)	9 (6.3)	6 (19.4)	7 (10.6)
Tyrosine kinase inhibitor	9 (20.0)	52 (36.4)	12 (38.7)	18 (27.3)
Others	2 (4.4)	7 (4.9)	3 (9.7)	6 (9.1)
Prior radiotherapy, n (%)				
Yes	23 (51.1)	63 (44.1)	63 (44.1)	33 (50.0)
Prior surgery, n (%)				
Yes	41 (91.1)	127 (88.8)	27 (87.1)	55 (83.3)
Number of Prior Surgeries				
Median (range)	2 (1-7)	2 (1-10)	2 (1-7)	2 (1-4)

\*Represents only patients from phase 3. The biomarker discovery in set 1 comparing patients with tumor growth vs shrinkage also contained patients from phase 2.

†Eastern Cooperative Oncology Group (ECOG) performance-status scores range from 0 to 5, with higher scores reflecting greater disability.

## 14. References

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## 15. Remark Checklist

Item to be reported	Page no.
<b>INTRODUCTION</b>	
<p><b>1 State the marker examined, the study objectives, and any pre-specified hypotheses.</b>            “The object of the molecular correlative studies was to identify predictive biomarkers of response to selinexor through assessment of RNA-levels of all expressed genes in tumor biopsies from treated patients. Studies were exploratory with no prespecified hypothesis.”</p>	S2
<b>MATERIALS AND METHODS</b>	
<i>Patients</i>	
<p><b>2 Describe the characteristics (e.g., disease stage or co-morbidities) of the study patients, including their source and inclusion and exclusion criteria.</b>            These are included in Table A1.</p>	Table A1
<p><b>3 Describe treatments received and how chosen (e.g., randomized or rule-based).</b>            “Patients were randomly assigned in a 2:1 ratio... Selinexor (60mg) or matching placebo was administered twice weekly in 6-week cycles. Patients were stratified by prior eribulin or trabectedin use and by the number of other (i.e., not eribulin or trabectedin) prior systemic therapies (<math>\leq 2</math> versus <math>\geq 3</math>). Supportive care measures included a 5HT3 antagonist (e.g., ondansetron), olanzapine and, if needed, low-dose steroids. Treatment was administered until disease progression, discontinuation, or unacceptable side effects. If radiographic progression was confirmed by central independent radiology review in the placebo arm, eligible patients were allowed to cross over to selinexor. Patients on selinexor with confirmed progression were permitted to continue selinexor if their treating physician considered them to be benefiting from the therapy.”</p>	12-13
<i>Specimen characteristics</i>	
<p><b>4 Describe type of biological material used (including control samples) and methods of preservation and storage.</b>            “RNA was extracted from formalin-fixed paraffin-embedded (FFPE) resected tumors or tumor biopsies of patients who were treated on study for at least one complete cycle. FFPE blocks and slides were stored at room temperature.”</p>	S2
<i>Assay methods</i>	
<p><b>5 Specify the assay method used and provide (or reference) a detailed protocol, including specific reagents or kits used, quality control procedures, reproducibility assessments, quantitation methods, and scoring and reporting protocols. Specify whether and how assays were performed blinded to the study endpoint.</b>            “Ribodepleted RNA sequencing was performed by HudsonAlpha Discovery Sequencing and Bioinformatics Division (Huntsville, AL) as follows: RNA was extracted using the HudsonAlpha Discovery proprietary dual DNA/RNA extraction protocol from FFPE. The concentration of extracted RNA was quantified using Ribogreen assays (Invitrogen). 20-500 ng RNA was used as input for library prep with the TruSeq™ Stranded Total RNA With Ribo-Zero™ Plus rRNA Depletion protocol (Illumina). Fragment size estimation was performed using the Caliper DNA-HS chip, and Kapa</p>	S2



qPCR quantification was performed to estimate the nanomolar concentration of the final libraries. RNA libraries were pooled and sequenced at 100 base pair read length with a target depth of 100M paired-end reads on NovaSeq 6000 instruments (Illumina). Samples with fewer than 30M pass-filter reads were removed. Hudson Alpha scientists were blinded to patient outcomes.”

*Study design*

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|--|---|
| <p><b>6 State the method of case selection, including whether prospective or retrospective and whether stratification or matching (e.g., by stage of disease or age) was used. Specify the time period from which cases were taken, the end of the follow-up period, and the median follow-up time.</b></p> <p>A full list of inclusion or exclusion criteria for the study is provided in Table A1. Patients who were included in the exploratory biomarker studies are described in Figure S1, and Tables A2-A3. Median follow-up was 14.6 months (IQR 8.2 to 23.5) as indicated on page 15.</p> | <p>14,<br/>Fig.<br/>S1<br/>Tables<br/>1, A1,<br/>A2,<br/>A3</p> |
| <p><b>7 Precisely define all clinical endpoints examined.</b></p> <p>“PFS, defined as the time from date of randomization until the first date of progression confirmed by central radiographic review, based on RECIST v1.1, or death due to any cause.”</p>  | <p>13</p>   |
| <p><b>8 List all candidate variables initially examined or considered for inclusion in models.</b></p> <p>“Differential expression analysis was performed for 58,395 genes in the human GRCh38.92.gtf reference”</p>   | <p>S2</p>   |
| <p><b>9 Give rationale for sample size; if the study was designed to detect a specified effect size, give the target power and effect size.</b></p> <p>“The sample size was designed to have 90% power to detect a hazard ratio of 0.6 between selinexor and placebo for the primary efficacy endpoint of PFS, using a one-sided test with a nominal level of 0.025”</p>   | <p>14</p>   |

*Statistical analysis methods*

- |  |  |
|--|--|
| <p><b>10 Specify all statistical methods, including details of any variable selection procedures and other model-building issues, how model assumptions were verified, and how missing data were handled.</b></p> <p>“Differential expression analysis was performed for 58,395 genes in the human GRCh38.92.gtf reference, using a negative binomial distribution with DeSeq2. P-values were calculated with Wald’s method and adjusted with Benjamini and Hochberg method. Visual examination of MA plots validated symmetry and examination of dispersion plots showed values generally scatter around the fitted curve, which decreases with increasing mean expression levels.”</p> | <p>S2,<br/>Fig.<br/>A3</p>                   |
| <p><b>11 Clarify how marker values were handled in the analyses; if relevant, describe methods used for cutpoint determination.</b></p> <p>“...gene-level expressions were determined with featurecounts.<sup>2</sup> Differential expression analysis was performed for 58,395 genes in the human GRCh38.92.gtf reference, using a negative binomial distribution with DeSeq2.”</p> <p>Marker Cutoff determination was based on detectable vs. no detectable expression of <i>CALB1</i>, as indicated throughout the manuscript.</p>  | <p>S2<br/><br/>16-17,<br/>Fig.<br/>3F-H,</p> |

		Fig. A2
<b>RESULTS</b>		
<i>Data</i>		
<b>12</b>	<b>Describe the flow of patients through the study, including the number of patients included in each stage of the analysis (a diagram may be helpful) and reasons for dropout. Specifically, both overall and for each subgroup extensively examined report the numbers of patients and the number of events.</b> Consort diagram is included as Figure 1.	Fig 1.
<b>13</b>	<b>Report distributions of basic demographic characteristics (at least age and sex), standard (disease-specific) prognostic variables, and tumor marker, including numbers of missing values.</b> Baseline demographic and clinical characteristics are provided in table 1.	Table 1.
<i>Analysis and presentation</i>		
<b>14</b>	<b>Show the relation of the marker to standard prognostic variables.</b> Table A8 shows the relationship of the marker to baseline demographic and clinical characteristics, including those associated with prognosis.	Table A8
<b>15</b>	<b>Present univariable analyses showing the relation between the marker and outcome, with the estimated effect (e.g., hazard ratio and survival probability). Preferably provide similar analyses for all other variables being analyzed. For the effect of a tumor marker on a time-to-event outcome, a Kaplan-Meier plot is recommended.</b> Hazard ratios, survival probabilities by time and Kaplan Meier plots are shown in Figure 3.	Fig. 3
<b>16</b>	<b>For key multivariable analyses, report estimated effects (e.g., hazard ratio) with confidence intervals for the marker and, at least for the final model, all other variables in the model.</b> No multivariable analyses are performed.	
<b>17</b>	<b>Among reported results, provide estimated effects with confidence intervals from an analysis in which the marker and standard prognostic variables are included, regardless of their statistical significance.</b> We are only reporting on a single molecular variable so are not including multivariable models.	
<b>18</b>	<b>If done, report results of further investigations, such as checking assumptions, sensitivity analyses, and internal validation.</b> N/A	
<b>DISCUSSION</b>		
<b>19</b>	<b>Interpret the results in the context of the pre-specified hypotheses and other relevant studies; include a discussion of limitations of the study.</b> “To better delineate which patients were more likely to benefit from selinexor, we conducted exploratory molecular biomarker studies using a representative subset of patients ( <b>Appendix Table A9, online only</b> ). These analyses revealed that expression of	20, Table A9

*CALB1* was strongly associated with resistance to selinexor. We confirmed that *CALB1* is not a prognostic marker in DD-LPS, as there was no association between *CALB1* expression and outcomes in the placebo arm or the TCGA data. *CALB1* was an unexpected discovery, as it encodes a calcium binding protein highly expressed in the central nervous system and kidneys, where it acts as a buffer and calcium sensor.<sup>28</sup> Although most human adult tissues do not express *CALB1*, its ectopic expression has been observed in several cancer types.<sup>29, 30</sup> Recent functional studies have demonstrated a novel oncogenic activity of *CALB1* where it binds MDM2 to enhance MDM2-mediated suppression of p53 signaling.<sup>29</sup> This is especially important in the context of DD-LPS, as MDM2 overexpression is a hallmark of this disease, and treatment with selinexor, which restores p53 activity. We speculate *CALB1* expression could prevent selinexor from overcoming MDM2-mediated suppression of p53 causing drug resistance and additional laboratory work is ongoing.”

**20 Discuss implications for future research and clinical value.**

“Further investigation is warranted for selinexor as a treatment for patients with DD-LPS with *CALB1* expression.”

21