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(73) 特許権者	599045903 学校法人　久留米大学 福岡県久留米市旭町６７番地
(74) 代理人	100062144 弁理士　青山　葆
(74) 代理人	100101454 弁理士　山田　卓二
(74) 代理人	100106518 弁理士　松谷　道子
(74) 代理人	100138911 弁理士　櫻井　陽子
(72) 発明者	伊東　恭悟 福岡県久留米市旭町６７番地　久留米大学内

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(54) 【発明の名称】 **癌患者に対する免疫療法の治療効果および／または免疫療法後の予後の予測方法、ならびに該方法に用いる遺伝子セットおよびキット**

(57) 【特許請求の範囲】

【請求項１】

前立腺癌患者に対する免疫療法の効果および／または免疫療法後の予後を予測する方法であって、以下の工程を含む方法：

（１）免疫療法前の前立腺癌患者から採取された試料において、以下の遺伝子：

No.	Illumina社プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc
1	3390368	PDP2	-	57546	NM_020786.1
2	1300687	NULL	NULL	731950	XR_016039.1
3	5860465	USP9Y	″ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)″	8287	NM_004654.3
4	4390576	DFFA	″DNA fragmentation factor, 45kDa, alpha polypeptide″	1676	NM_213566.1
5	4830255	DPP4	dipeptidyl-peptidase 4	1803	NM_001935.3
6	4570403	NULL	NULL	NULL	BX106581
7	1780719	PTGES3	prostaglandin E synthase 3 (cytosolic)	10728	NM_006601.4
8	3130477	C7orf28A	chromosome 7 open reading frame 28A	51622	XM_001133729.1
9	6110630	HIST1H2BK	″histone cluster 1, H2bk″	85236	NM_080593.1
10	3310309	CCDC135	coiled-coil domain containing 135	84229	NM_032269.4
11	4220731	P4HA1	″prolyl 4-hydroxylase, alpha polypeptide I″	5033	NM_000917.2
12	520706	UBE4A	″ubiquitination factor E4A (UFD2 homolog, yeast)″	9354	NM_004788.2
13	6420446	CMPK1	″cytidine monophosphate (UMP-CMP) kinase 1, cytosolic″	51727	NM_016308.1
14	1400240	LDHB	lactate dehydrogenase B	3945	NM_002300.4

No.	Illumina社プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc
15	7510379	SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	26278	NM_014363.3
16	2640025	HP	haptoglobin	3240	NM_005143.2
17	3130296	AMY2A	"amylase, alpha 2A (pancreatic)"	279	NM_000699.2
18	3520601	MPO	myeloperoxidase	4353	NM_000250.1
19	1110091	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	7073	NM_001033925.1
20	3130370	ZNF83	zinc finger protein 83	55769	NM_018300.2
21	2030332	PTPN18	"protein tyrosine phosphatase, non-receptor type 18 (brain-derived)"	26469	NM_014369.2
22	670209	ZNF700	zinc finger protein 700	90592	NM_144566.1
23	6560161	NULL	NULL	NULL	BX111675
24	1740647	FAM180B	"family with sequence similarity 180, member B"	399888	XM_941808.2
25	4880463	SEC24A	"SEC24 family, member A (S. cerevisiae)"	10802	NM_021982.1
26	990315	TCP1	t-complex 1	6950	NM_030752.2
27	240463	RNF216L	ring finger protein 216-like	441191	XR_001271.1
28	2000035	NULL	NULL	NULL	AL042883

No.	Illumina社プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc
29	1780709	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	10521	NM_030881.2
30	2680440	NULL	NULL	NULL	BF338665
31	150672	KLHL7	kelch-like 7 (Drosophila)	55975	NM_001031710.1
32	6940176	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	10096	NM_005721.3
33	6180497	GOLGA8C	"golgi autoantigen, golgin subfamily a, 8C"	400304	XM_375152.3
34	150706	UGP2	UDP-glucose pyrophosphorylase 2	7360	NM_006759.3
35	5900129	CROP	-	51747	NM_006107.2
36	6450437	NULL	NULL	NULL	BF445990
37	3990608	MAN2A1	"mannosidase, alpha, class 2A, member 1"	4124	NM_002372.2
38	3120075	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	7072	NM_022173.1
39	1500047	RIN1	Ras and Rab interactor 1	9610	NM_004292.2
40	840358	EXOSC10	exosome component 10	5394	NM_002685.2
41	6590484	NAP1L1	nucleosome assembly protein 1-like 1	4673	NM_139207.1
42	2100594	BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)	9184	NM_004725.2

No.	Illumina社プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc
43	6650056	ZNF566	zinc finger protein 566	84924	NM_032838.2
44	2120017	NOL8	nucleolar protein 8	55035	NM_017948.4
45	1780639	LOC645355	-	645355	XM_932842.1
46	6650594	ATP11B	"ATPase, class VI, type 11B"	23200	NM_014616.1
47	3420136	C6orf222	chromosome 6 open reading frame 222	389384	NM_001010903.3
48	6760017	YY1	YY1 transcription factor	7528	NM_003403.3
49	510209	LOC643310	-	643310	XM_926656.1
50	4220673	NULL	NULL	NULL	AA971450

からなる遺伝子セットの各遺伝子の発現レベルを測定する工程、および

（２）前立腺癌患者群における前記遺伝子セットの各遺伝子の発現レベルの測定結果から潜在変数３で構築されたPLS回帰モデルに、工程（１）の前立腺癌患者の各遺伝子の発現レベルをあてはめ、予測生存日数を算出する工程、

ここで、予測生存日数は、以下の回帰式：

予測生存日数＝ａ１ｇ１＋ａ２ｇ２＋ａ３ｇ３＋・・・＋ａ５０ｇ５０＋Ｅ（式１）

（式中、ａ１、ａ２、ａ３、・・・、ａ５０は、回帰モデル構築された各遺伝子の発現量にかかる係数であり、ｇ１、ｇ２、ｇ３、ｇ４、・・・、ｇ５０は、対象とする患者における各遺伝子の発現レベルであり、Ｅは回帰式の定数項である。）

により算出される。

【請求項２】

免疫療法がペプチドワクチン療法である、請求項１の方法。

【請求項３】

前立腺癌患者に対する免疫療法の効果および／または免疫療法後の予後を予測するための、以下の遺伝子：

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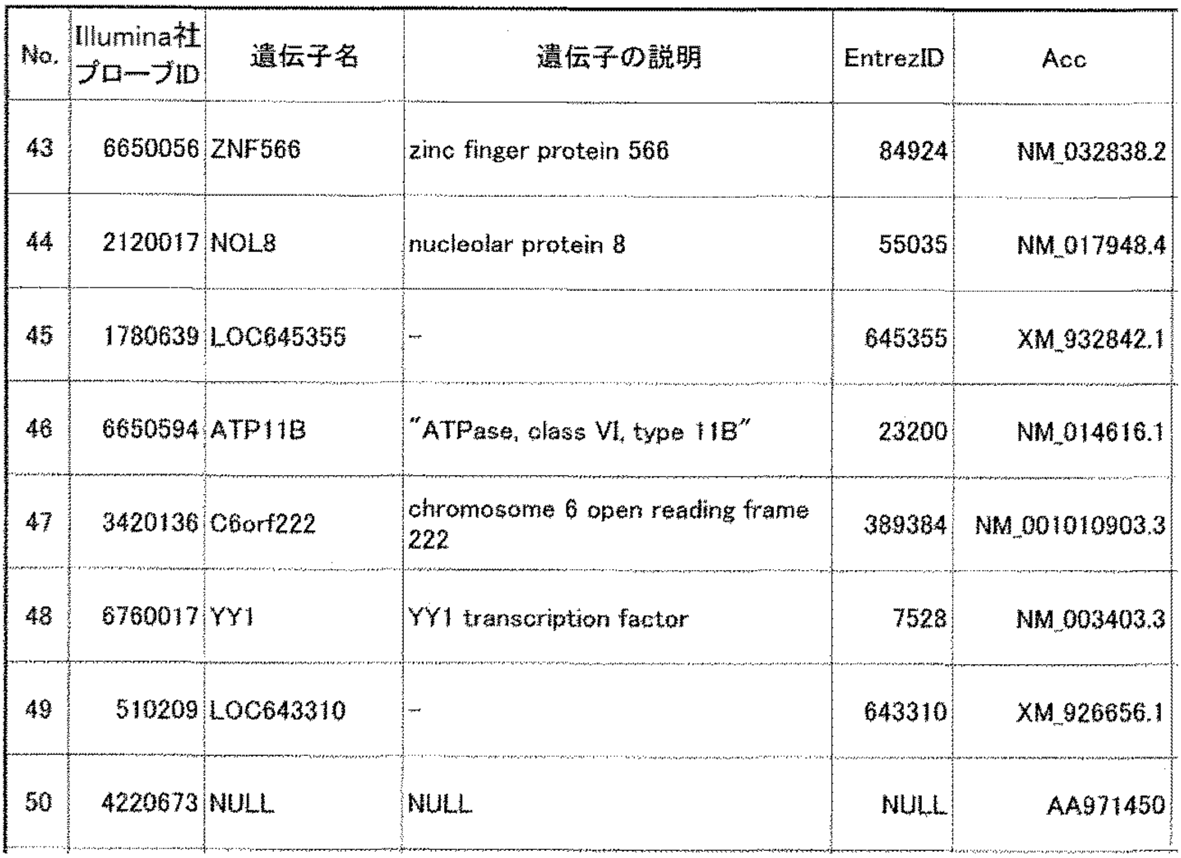
42	2100594	BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)	9184	NM_004725.2



No.	Illumina社プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc
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49	510209	LOC643310	-	643310	XM_926656.1
50	4220673	NULL	NULL	NULL	AA971450

からなる遺伝子セット。

【請求項４】

免疫療法がペプチドワクチン療法である、請求項３の遺伝子セット。

【請求項５】

前立腺癌患者に対する免疫療法の効果および／または免疫療法後の予後を予測するためのキットであって、請求項３の遺伝子セットの各遺伝子に対するプローブまたはプライマーを含むキット。

【請求項６】

ＤＮＡマイクロアレイ法に用いられる、請求項５のキット。

【発明の詳細な説明】

【技術分野】

【０００１】

本発明は、癌患者に対する免疫療法の治療効果および／または免疫療法後の予後の予測方法、ならびに前記方法に用いる遺伝子セットおよびキットに関する。なお、本願は、日本国特許出願第２００９−２３０２７９号に対して優先権を主張するものであり、参照により該日本国特許出願の内容を本願に一体化させる。

【背景技術】

【０００２】

各種がんに対する免疫療法は、一部奏効する症例があるものの、すべての患者にとって最適な治療法とはなりえていない。その原因の一つとして、免疫療法が、がん細胞の増殖を抑えるために個人差の大きい免疫能を介していることが上げられる。がんの免疫療法には、現在その効果を予測する方法がなく、治療を行ってみなければ有効性を判断することができない。これまでに、乳癌患者において遺伝子発現レベルを測定し化学療法の効果を予測する方法が知られているが、この方法は遺伝子発現と他の因子とを組み合わせる複雑な系であり、また、乳癌に対する化学療法の効果のみを対象としている（特許文献１）。がんの免疫療法の治療効果や、免疫療法後の患者の予後を予測する方法はこれまで知られ

ていない。

【特許文献１】特表２００８－５３６０９４号公報

【発明の開示】

【発明が解決しようとする課題】

【０００３】

本発明は、癌患者に対する免疫療法の治療効果を精度よく予測する方法を提供することを目的とする。

【課題を解決するための手段】

【０００４】

本発明者らは、長年におよぶ前立腺癌患者に対するペプチドワクチン療法で得られた結果に基づき、がん免疫療法の治療効果を予測することを試みた。まず、ペプチドワクチン療法前の前立腺癌患者における遺伝子発現プロファイルをＤＮＡマイクロアレイで解析した。次いで、治療後の生存日数を基準として患者を予後良好群と予後不良群に分類し、治療前の各遺伝子の発現レベルと治療後の生存日数との相関を調べたところ、両者の間に相関のある遺伝子が存在することが明らかとなった。そして、これら遺伝子の発現レベルから免疫療法後の患者の生存日数を予測できることを確認し、本発明を完成するにいたった。

【０００５】

すなわち、本発明は、癌患者に対する免疫療法の効果および／または免疫療法後の予後を予測する方法であって、

（１）免疫療法前の癌患者から採取された試料において、表１～５のいずれかに示す遺伝子の群から選択される少なくとも１の遺伝子からなる遺伝子セットの各遺伝子の発現レベルを測定する工程、および

（２）前記発現レベルを統計処理し、予測生存日数を算出する工程、

を含む方法を提供する。

【０００６】

また、本発明は、癌患者に対する免疫療法の効果および／または免疫療法後の予後を予測するための遺伝子セットであって、表１～５のいずれかに示す遺伝子の群から選択される少なくとも１の遺伝子からなる遺伝子セットを提供する。

【０００７】

さらに、本発明は、癌患者に対する免疫療法の効果および／または免疫療法後の予後を予測するためのキットであって、前記遺伝子セットの各遺伝子に対するプローブまたはプライマーを含むキットを提供する。

【発明の効果】

【０００８】

本発明により、癌患者の遺伝子発現プロファイルを免疫療法開始前に測定することで、その患者に対する免疫療法の治療効果および治療後の予後を予測することが可能となった。本発明は、癌患者に対する治療法の選択に有用な情報を提供する。

【図面の簡単な説明】

【０００９】

【図１】４０名の前立腺癌患者の生存日数の分布。

【図２】マイクロアレイデータの前処理。

【図３】Pearsonの積率相関係数による上位３００遺伝子の分布。

【図４】各遺伝子選択方法における生存日数予測率。

【図５】Pearsonの積率相関係数により選択された上位３００遺伝子（表１）の１番目の遺伝子から順に選択した遺伝子からなる３０の遺伝子セットによる生存日数予測精度。縦軸は予測が正解であった患者数を示す。

【図６】各患者の予測生存日数（Pearsonの積率相関係数、潜在変数３、上位５０遺伝子の遺伝子セットによる）と、実際の生存日数との比較。

【図７】生存日数予測結果を用いたKaplan-Meier生存曲線。

【図８】Pearsonの積率相関係数により選択された上位３００遺伝子（表１）の３００番目の遺伝子から順に選択した遺伝子からなる３０の遺伝子セットによる生存日数予測精度。縦軸は予測が正解であった患者数を示す。

【図９】Pearsonの積率相関係数により選択された上位３００遺伝子（表１）からランダムに選択した遺伝子からなる３０の遺伝子セットによる生存日数予測精度。縦軸は予測が正解であった患者数を示す。

【図１０】生存日数３００日で予後良好群と予後不良群を分類した場合の生存日数予測結果。

【図１１－１】Pearsonの積率相関係数により選択された上位３００遺伝子（表１）からランダムに選択した１の遺伝子による生存日数予測結果（１）（表１の順位をグラフ横に示す）。

【図１１－２】Pearsonの積率相関係数により選択された上位３００遺伝子（表１）からランダムに選択した１の遺伝子による生存日数予測結果（２）（表１の順位をグラフ横に示す）。

【図１１－３】Pearsonの積率相関係数により選択された上位３００遺伝子（表１）からランダムに選択した１の遺伝子による生存日数予測結果（３）（表１の順位をグラフ横に示す）。

【発明を実施するための最良の形態】

【００１０】

本発明の予測方法は、その発現レベルが癌患者の免疫療法後の生存日数と高い相関を示した遺伝子を利用する。本発明の遺伝子セットは、表１～５のいずれかに示す遺伝子の群から選択される少なくとも１の遺伝子から構成される。遺伝子は、表１～５の１番目から順に選択しても、３００番目から順に選択しても、あるいはランダムに選択してもよい。予測率を考慮すると、１番目から順に選択することが好ましい。

【００１１】

遺伝子セット中の遺伝子数は、１以上であれば特に制限はない。例えば、１、２、３、４、５、６、７、８、９、１０、２０、３０、４０、５０、６０、７０、８０、９０、１００、１１０、１２０、１３０、１４０、１５０、１６０、１７０、１８０、１９０、２００、２１０、２２０、２３０、２４０、２５０、２６０、２７０、２８０、２９０、３００の遺伝子を選択することができる。

【００１２】

本発明の対象となる癌患者は特に限定されず、例えば前立腺癌、膵臓癌、乳癌、肝臓癌などの患者が挙げられる。本発明は、なかでも前立腺癌患者に対して好適に用いられる。

【００１３】

本発明において、免疫療法とは、癌患者における腫瘍抗原タンパク質に対する免疫応答を賦活化することにより癌を治療する方法を意味する。本発明の免疫療法としては、腫瘍抗原ペプチドを用いるペプチドワクチン療法、細胞傷害性Ｔ細胞やナチュラルキラー細胞などのリンパ球を用いる養子免疫療法、腫瘍抗原タンパク質や腫瘍抗原ペプチドを発現するウイルスベクターを生体に導入するＤＮＡワクチン、腫瘍抗原ペプチドを提示する樹状細胞を投与する樹状細胞ワクチンなどが挙げられる。本発明は、ペプチドワクチン療法に特に好適である。

【００１４】

本発明の方法において、遺伝子の発現レベルは、常套的方法により測定すればよい。発現レベルの測定方法としては、ＤＮＡマイクロアレイ法、ＤＮＡチップ法、ＰＣＲ法、ノーザンブロット法などが挙げられるが、なかでもＤＮＡマイクロアレイ法が好適である。

【００１５】

ＤＮＡマイクロアレイ法では、測定対象とする遺伝子に対するプローブを含むマイクロアレイを使用する。かかるマイクロアレイとしては、llumina社製　HumanWG-6 v3.0 Expression BeadChipが挙げられる。あるいは、測定対象の遺伝子に対するプローブを合成し、スライドガラスなどの適当な基盤上に固定して、所望のマイクロアレイを作製してもよ

い。マイクロアレイの作製方法は、当業界にて周知である。マイクロアレイデータの解析も周知であり、例えば「統合ゲノミクスのためのマイクロアレイデータアナリシス」星田有人訳　シュプリンガー・フェアラーク東京社出版を参考に行うことができる。

【００１６】

遺伝子発現レベルの測定に用いる患者試料は、限定はされないが、例えば患者から採取した末梢血を使用することができる。

【００１７】

ＤＮＡマイクロアレイ法による発現レベルの測定は、例えば以下のとおりである。はじめに、患者の末梢血から全ＲＮＡを抽出し、精製する。次いで、Illumina TotalPrep RNA Amplification Kit（アンビオン社製）などを使用し、ビオチン化ｃＲＮＡを合成する。このビオチン化ｃＲＮＡをマイクロアレイにハイブリダイズさせ、次いでＣｙ３標識ストレプトアビジンと反応させる。反応後のマイクロアレイを専用のスキャナーでスキャンし、BeadStudioなどの専用ソフトウエアを用いて各スポットのＣｙ３の蛍光を数値化することで、各遺伝子の発現レベルを得ることができる。

【００１８】

患者の予測生存日数は、例えば、その患者における本発明の遺伝子セットの各遺伝子の発現レベルを以下の実施例に示すＰＬＳ回帰分析の回帰式にあてはめ、算出することができる。あるいは、実施例の癌患者群、または別の癌患者群における本発明の遺伝子セットの各遺伝子の発現レベルを測定し、ＳＶＭ（サポートベクターマシーン）、正則化最小二乗法、主成分分析法などにより算出することも可能である。

【００１９】

本発明の遺伝子セットは、癌患者に対する免疫療法の効果および／または免疫療法後の予後を予測するために使用されるものであり、本発明の予測方法に用いるＤＮＡマイクロアレイ用のプローブやＰＣＲ用プライマーなどを作製するために用いることができる。

【００２０】

本発明のキットは、本発明の遺伝子セットの各遺伝子の発現レベルを測定することができる、プローブまたはプライマーを含む。各遺伝子に対するプローブおよびプライマーは、その遺伝子の配列情報に基づき、常套的方法により合成することができる。キットは、測定方法に応じて、その他必要な試薬を含んでいてもよい。本発明のキットは、例えば、ＤＮＡマイクロアレイ法、ＤＮＡチップ法、ＰＣＲ法、ノーザンブロット法などに用いられるキットである。ＤＮＡマイクロアレイ法用のキットとしては、前記プローブが適当な基盤上に固定されたマイクロアレイを含むものが挙げられる。

【実施例】

【００２１】

実施例１

１：ＤＮＡマイクロアレイによるペプチドワクチン療法前の遺伝子発現プロファイルの検討

患者試料として、久留米大学倫理委員会により承認されたプロトコールに即してインフォームドコンセントを得た前立腺癌患者から過去の臨床試験において再燃前立腺癌と診断された時点に収集した末梢血を使用した。４０名の前立腺癌患者において、ＤＮＡマイクロアレイ（llumina社製　HumanWG-6 v3.0 Expression BeadChip）を用いて、ペプチドワクチン療法前の遺伝子発現プロファイルを調べた。前立腺癌患者は、予後良好群（ペプチドワクチン療法後の生存日数７００日以上）２０名、予後不良群（ペプチドワクチン療法後の生存日数７００日未満）２０名であった（図１）。

【００２２】

（Ｉ）患者末梢血からのＲＮＡ抽出・精製

１．患者末梢血サンプルにTRIzol LS（インビトロジェン社製）を１：３の比率になるように添加し、混濁した。

２．TRIzol LS溶液７５０μＬに対し、２００μＬのクロロホルムを加え、混濁後、遠心分離した。

３．上清を新しいチューブに移し、上清の０．５５倍量のエタノールを添加した。
４．SV Total RNA Isolation System（プロメガ社製）のカラムに上記３．の検体をのせ、フィルターを通した。
５．フィルターを５００μＬのWash Bufferで洗浄した。
６．全ＲＮＡを８０μＬのNuclease Free Waterで溶出した。
７．分光光度計を用いて、ＲＮＡの濃度を測定し、Experionシステム（バイオラッド社製）を用いて電気泳動によりＲＮＡのクオリティをチェックした。

【００２３】

（ＩＩ）Illumina TotalPrep RNA Amplification Kit（アンビオン社製）を用いたマイクロアレイ用ｃＲＮＡの合成

（１）逆転写による一本鎖ｃＤＮＡの合成
１．各５００μｇの全ＲＮＡにNuclease Free Waterを加え、１１μＬに調整した。
２．上記１．の溶液に９μＬのReverse Transcription Master Mixを加え、４２°Ｃで２時間インキュベートした。

【００２４】

（２）二本鎖ｃＤＮＡ合成
１．８０μＬの Second Strand Master Mixを、上記（１）２．の各々のチューブに添加した。
２．各チューブを１６°Ｃで２時間インキュベートした。

【００２５】

（３）ｃＤＮＡ精製
１．２５０μＬのcDNA Binding Bufferを各々のチューブに添加した。
２．上記１．の溶液を、cDNA Filter Cartridgeにのせ、遠心によりフィルターを通した。
３．フィルターを５００μＬのWash Bufferで洗浄した。
４．ｃＤＮＡを１９μＬの５０～５５°Ｃに予熱しておいたNuclease Free Waterで溶出した。

【００２６】

（４）インビトロ転写反応によるｃＲＮＡ合成
１．７．５μＬのIVT Master Mixを、上記（３）４．で得られたｃＤＮＡサンプルに添加した。
２．上記１．のチューブを３７℃で１４時間インキュベートした。
３．上記２．のチューブに７５μＬのNuclease Free Waterを添加した。

【００２７】

（５）ｃＲＮＡ精製
１．３５０μＬのcRNA Binding Bufferを各チューブに添加した。
２．２５０μＬの１００％エタノールを各チューブに加え、混濁した。
３．上記２．のサンプルをcRNA Filter Cartridgeにのせ、遠心によりフィルターを通した。
４．６５０μＬのWash Bufferでフィルターを洗浄した。
５．ｃＲＮＡを１００μＬの５０～５５°Ｃに予熱しておいたNuclease Free Waterで溶出した。
６．ｃＲＮＡ濃度をＯＤで測定後、ハイブリダイゼーションサンプルとした。

【００２８】

（ＩＩＩ）マイクロアレイハイブリダイゼーション

（１）ハイブリダイゼーション用ｃＲＮＡの調製
１．各５００μｇの全ＲＮＡにNuclease Free Waterを加え、１０μＬに調整した。
２．上記１．の溶液に２０μＬのGEX-HYBを加え、６５℃で５分インキュベートした。

（２）ハイブリダイゼーション
１．専用チャンバーにセットしたHumanWG-6 v3.0 Expression BeadChipに、調製済みの

ｃＲＮＡサンプルをアプライした。

２．専用チャンバーのふたを閉め、５５℃で１８時間インキュベートした。

【００２９】

（ＩＶ）マイクロアレイ洗浄・染色

（１）アレイの洗浄

１．Wash E1BC溶液中で、マイクロアレイのカバーを外した。

２．アレイを速やかにスライドラックにセットし、５５℃に予熱しておいた1×High-Temp Wash buffer内で１０分間洗浄した。

３．アレイをWash E1BC溶液中で５分間洗浄した。

４．アレイをエタノール中で５分間洗浄した。

５．アレイをWash E1BC溶液中で５分間洗浄した。

６．染色専用トレイに４ｍｌのブロックE1バッファーを準備し、アレイを一枚ずつセットし、室温で１０分間ブロッキングを行った。

７．染色専用トレイに２ｍｌのブロックE1バッファーに対して２μＬのストレプトアビジン－Ｃｙ３を加え、アレイを一枚ずつセットし、室温で１０分間染色を行った。

８．アレイをWash E1BC溶液中で５分間洗浄後、遠心により乾燥した。

【００３０】

（Ｖ）スキャニング、数値化

１．Illumina社専用スキャナーにアレイをセットし、標準モードでスキャンを行った。

２．スキャン終了後、専用ソフトウエアBeadStudioを用いて、マイクロアレイ上の各スポットの数値化を行った。

【００３１】

得られたマイクロアレイデータは、VST（Variance Stabilizing Transformation）、及びRSN（robust spline normalization）を用いて正規化を行なった。陰性対照（マイクロアレイ上に存在しない遺伝子に対するプローブにより測定される遺伝子発現量）に対するPresence Probability < 0.05の遺伝子発現量を有意と判断した（図２）。４０名中、７０％以上の患者でPresence Probability < 0.05の遺伝子を以下の実験に使用した。

【００３２】

２：ＰＬＳ回帰モデル構築に用いる遺伝子セットの選択

実施例１の前立腺癌患者を、ペプチドワクチン療法後の生存日数を基準として予後良好群（生存日数７００日以上）または予後不良群（生存日数７００日未満）に分類し、各遺伝子の遺伝子発現レベルと生存日数との間の相関、および予後良好群と予後不良群との間の発現変動を基準として遺伝子を選択した。発現変動は、予後良好群の平均発現レベルを対照とした、予後不良群の平均発現レベルの増加または減少として表した。

【００３３】

解析には、以下の５種類の統計学的方法を用いた（Ａ：生存日数と遺伝子発現レベルとの相関を解析、Ｂ：予後良好群と予後不良群との間の発現変動を解析）。

Pearsonの積率相関係数	（Ａ）
Limma[b]	（Ｂ）
SAM[a]	（Ｂ）
Rank Prod[c]	（Ｂ）
Spearmanの順位和係数	（Ａ）

（参考文献）

[a] Tusher et al. Significance analysis of microarrays applied to the ionizing radiation response. Proc Natl Acad Sci USA (2001) vol. 98 (9) pp. 5116-21.

[b] Smyth. Linear models and empirical bayes methods for assessing differential expression in microarray experiments. Statistical applications in genetics and molecular biology (2004) vol. 3 pp. Article.

[c] Breitling et al. Rank products: a simple, yet powerful, new method to detect differentially regulated genes in replicated microarray experiments. FEBS Letters (2004) vol. 573 (1-3) pp. 83-92.

これらの参考文献は、出典明示により本願明細書の一部とする。

【００３４】

３：ＰＬＳ回帰モデルの評価

各患者のペプチドワクチン療法後の生存日数を予測するため、ＰＬＳ（Partial Least Square）回帰モデルを構築した。具体的には、上記５種類の方法で選択された上位３００の遺伝子（表１～５、図３）からなる５つの遺伝子セットから、上位から１０遺伝子ずつを含む（すなわち、それぞれ１０、２０、・・・または３００の遺伝子を含む）３０セットの遺伝子セットを抽出し、潜在変数１～１０でＰＬＳ回帰モデルを構築した。

【００３５】

回帰モデルの評価は、Leave One Out Cross Validation（LOOCV）形式で行った。すなわち、全４０名の前立腺癌患者について、３９名の結果を用いて回帰モデルを構築し、構築された回帰モデルを用いて残りの１名の患者の生存日数を予測した。

【００３６】

例として、上位５０遺伝子からなる遺伝子セットによる生存日数の算出方法を説明する。予測生存日数は、以下の回帰式により算出した。

予測生存日数＝ａ１ｇ１＋ａ２ｇ２＋ａ３ｇ３＋・・・＋ａ５０ｇ５０＋Ｅ（式１）

（式中、ａ１、ａ２、ａ３、・・・、ａ５０は、回帰モデル構築された各遺伝子の発現量にかかる係数であり、ｇ１、ｇ２、ｇ３、ｇ４、・・・、ｇ５０は、対象とする患者における各遺伝子の発現レベルであり、Ｅは回帰式の定数項である。）

Pearsonの積率相関係数、潜在変数３、上位５０遺伝子の遺伝子セットによる各患者の生存日数予測に使用した係数を表６に示す。

（参考文献）

[1] Bjrn-Helge Mevik and Ron Wehrens Journal of Statistical Software: Vol 18, Issue 2 (2007), "The pls Package: Principal Componentand Partial Least Squares Regression in R"

[2] Geladi, P. and B. Kowalski (1986) Partial least-squares regression: Atutorial. Analytica Chimica Acta 185:1-17.

これらの参考文献は、出典明示により本願明細書の一部とする。

【００３７】

予測生存日数が、予後良好患者の場合は７００日以上、予後不良患者の場合は７００日未満であった場合に正解とし、各回帰モデルの正解率（予測率）を計算した。回帰モデルの評価の結果、上記５種類の統計学的方法により選択された３００遺伝子は、いずれも最高で８０％以上の予測率を示した（図４）。なかでも、Pearsonの積率相関係数、潜在変数３、上位５０遺伝子の遺伝子セットが最も予測率がよく、９５％であった。この遺伝子セットによる生存日数予測精度、および予測生存日数と実際の生存日数の比較を図５および６に示す。図６の右上枠内および左下枠内の患者は、予測生存日数と実際の生存日数が一致した患者に相当する。左上枠内は、免疫療法後の予後が良好と予測されたにもかかわらず、実際の生存日数が短かった患者を示す。一方、本方法により予後不良と予測されたにもかかわらず、実際の生存日数が長かった患者は存在しなかった（図６、右下枠内）。このことは、本方法により、免疫療法開始前に免疫療法の治療効果が低い患者を予測できることを示す。

【００３８】

また、Pearsonの積率相関係数、潜在変数３、上位５０遺伝子の遺伝子セットを用いて分類された予後良好群および不良群と、実際の生存日数を用いてKaplan-Meier曲線を描き

、ログランク検定を行なったところ、本方法で分類された患者群は、p＝1.6e-10の確率で予後良好群と予後不良群に分類できることが示された。（図７）。

【００３９】

次いで、表１の遺伝子セットにおいて、下位から順に１０遺伝子ずつを含む（すなわち、それぞれ１０、２０、・・・または３００の遺伝子を含む）３０セットの遺伝子セットを抽出し、潜在変数３でＰＬＳ回帰モデルを構築した（図８）。この場合の予測率は６５～８５％であった。また、同じ３００遺伝子のセットから、ランダムに３０セットの遺伝子セットを抽出し（表７）、潜在変数３でＰＬＳ回帰モデルを構築した（図９）。この場合の予測率は６２．５～８５％であった。以上の結果から、いずれの選択方法でも治療後の生存日数が予測可能であることが明らかとなった。

【００４０】

実施例２

実施例１の４０名の前立腺癌患者にさらに９名の前立腺癌患者の遺伝子発現データを加え、生存日数３００日以上を予後良好群、生存日数３００日未満を予後不良群と分類し、Pearsonの積率相関係数、潜在変数３、上位５０遺伝子の遺伝子セットを用いてＰＬＳ回帰モデルを構築し、新たな９名の前立腺癌患者の生存日数を予測した（図１０）。本方法においても、９名中８名で予測が正解であった。

【００４１】

実施例３

実施例１の４０名の前立腺癌患者について、Pearsonの積率相関係数で選択された上位３００遺伝子（表１）の各遺伝子の発現レベルと生存日数より、一次線形回帰式を作成した。次いで、得られた式と各患者における発現レベルから各患者の予測生存日数を算出し、実際の生存日数をｘ軸、算出された予測生存日数をｙ軸にとりグラフ化した（図１１）。グラフには、１から３００の間で乱数をとり、これを順位と仮定して表１から選択した１０の遺伝子の結果を示す。その結果、１の遺伝子の発現レベルに基づいた場合でも、生存日数が予測可能であることが明らかとなった。

【００４２】

表１　Pearsonの積率相関係数で選択された上位３００の遺伝子のリスト

【表１－１】

Pearson
表1-1

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
1	3390368	PDP2	–	57546	NM_020786.1	0.068777448	−0.640094678	0.640094678	8.68E−06	0.0806
2	1300687	NULL	NULL	731950	XR_016039.1	−0.061135983	0.631326974	0.631326974	1.25E−05	0.0806
3	5860465	USP9Y	"ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)"	8287	NM_004654.3	−0.094524102	0.628214485	0.628214485	1.42E−05	0.0806
4	4390576	DFFA	"DNA fragmentation factor, 45kDa, alpha polypeptide"	1676	NM_213566.1	0.121909434	−0.601015195	0.601015195	4.12E−05	0.1137
5	4830255	DPP4	dipeptidyl-peptidase 4	1803	NM_001935.3	−0.307400655	0.598684997	0.598684997	4.49E−05	0.1137
6	4570403	NULL	NULL	NULL	BX106581	0.112837902	−0.591426067	0.591426067	5.85E−05	0.1137
7	1780719	PTGES3	prostaglandin E synthase 3 (cytosolic)	10728	NM_006601.4	−0.528677962	0.586249078	0.586249078	7.04E−05	0.1137
8	3130477	C7orf28A	chromosome 7 open reading frame 28A	51622	XM_001133729.1	−0.383441629	0.585296251	0.585296251	7.28E−05	0.1137
9	6110630	HIST1H2BK	"histone cluster 1, H2bk"	85236	NM_080593.1	0.379122401	−0.583688805	0.583688805	7.70E−05	0.1137
10	3310309	CCDC135	coiled-coil domain containing 135	84229	NM_032269.4	0.099558313	−0.582768194	0.582768194	7.96E−05	0.1137
11	4220731	P4HA1	"prolyl 4-hydroxylase, alpha polypeptide I"	5033	NM_000917.2	−0.307837835	0.582543435	0.582543435	8.02E−05	0.1137
12	520706	UBE4A	"ubiquitination factor E4A (UFD2 homolog, yeast)"	9354	NM_004788.2	−0.230502672	0.582455331	0.582455331	8.04E−05	0.1137
13	6420446	CMPK1	"cytidine monophosphate (UMP-CMP) kinase 1, cytosolic"	51727	NM_016308.1	−0.398631213	0.576832021	0.576832021	9.78E−05	0.1276
14	1400240	LDHB	lactate dehydrogenase B	3945	NM_002300.4	−0.605485777	0.573136201	0.573136201	0.000110918	0.1341

【表１－２】

Pearson
表1-2

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
15	7510379	SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	26278	NM_014363.3	−0.121241812	0.571175816	0.571175816	0.000118529	0.1341
16	2640025	HP	haptoglobin	3240	NM_005143.2	0.40681683	−0.565414687	0.565414687	0.000143707	0.1412
17	3130296	AMY2A	"amylase, alpha 2A (pancreatic)"	279	NM_000699.2	−0.282794372	0.562912837	0.562912837	0.000156073	0.1412
18	3520601	MPO	myeloperoxidase	4353	NM_000250.1	0.96554979	−0.560650984	0.560650984	0.000168071	0.1412
19	1110091	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	7073	NM_001033925.1	−0.233908998	0.560267499	0.560267499	0.000170186	0.1412
20	3130370	ZNF83	zinc finger protein 83	55769	NM_018300.2	−0.30567958	0.557785556	0.557785556	0.000184463	0.1412
21	2030332	PTPN18	"protein tyrosine phosphatase, non-receptor type 18 (brain-derived)"	26469	NM_014369.2	0.083763446	−0.556808508	0.556808508	0.000190373	0.1412
22	670209	ZNF700	zinc finger protein 700	90592	NM_144566.1	−0.134476397	0.556120039	0.556120039	0.00019464	0.1412
23	6560161	NULL	NULL	NULL	BX111675	0.054993081	−0.555033755	0.555033755	0.000201547	0.1412
24	1740647	FAM180B	"family with sequence similarity 180, member B"	399888	XM_941808.2	0.083819707	−0.552949574	0.552949574	0.000215422	0.1412
25	4880463	SEC24A	"SEC24 family, member A (S. cerevisiae)"	10802	NM_021982.1	−0.069649892	0.551748217	0.551748217	0.000223805	0.1412
26	990315	TCP1	t-complex 1	6950	NM_030752.2	−0.256767834	0.548462787	0.548462787	0.00024825	0.1412
27	240463	RNF216L	ring finger protein 216-like	441191	XR_001271.1	0.162378967	−0.546624738	0.546624738	0.000262951	0.1412
28	2000035	NULL	NULL	NULL	AL042883	0.08373784	−0.545628461	0.545628461	0.000271242	0.1412

【表１－３】

Pearson
表1-3

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
29	1780709	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	10521	NM_030881.2	-0.443292451	0.54494961	0.54494961	0.000277025	0.1412
30	2680440	NULL	NULL	NULL	BF338665	0.061724508	-0.544896308	0.544896308	0.000277484	0.1412
31	150672	KLHL7	kelch-like 7 (Drosophila)	55975	NM_001031710.1	-0.155913324	0.544163441	0.544163441	0.000283861	0.1412
32	6940176	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	10096	NM_005721.3	-0.459963089	0.543431629	0.543431629	0.00029036	0.1412
33	6180497	GOLGA8C	"golgi autoantigen, golgin subfamily a, 8C"	400304	XM_375152.3	-0.242008817	0.542516269	0.542516269	0.000298677	0.1412
34	150706	UGP2	UDP-glucose pyrophosphorylase 2	7360	NM_006759.3	-0.347146055	0.542493196	0.542493196	0.000298889	0.1412
35	5900129	CROP	-	51747	NM_006107.2	-0.443849065	0.541743162	0.541743162	0.000305867	0.1412
36	6450437	NULL	NULL	NULL	BF445990	0.102742584	-0.541344228	0.541344228	0.000309638	0.1412
37	3990608	MAN2A1	"mannosidase, alpha, class 2A, member 1"	4124	NM_002372.2	-0.327379686	0.540749807	0.540749807	0.000315334	0.1412
38	3120075	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	7072	NM_022173.1	-0.154497679	0.540658588	0.540658588	0.000316217	0.1412
39	1500047	RIN1	Ras and Rab interactor 1	9610	NM_004292.2	0.132155916	-0.537690388	0.537690388	0.000346168	0.1475
40	840358	EXOSC10	exosome component 10	5394	NM_002685.2	-0.226165883	0.53626305	0.53626305	0.000361457	0.1475
41	6590484	NAP1L1	nucleosome assembly protein 1-like 1	4673	NM_139207.1	-0.357418466	0.535985012	0.535985012	0.000364505	0.1475
42	2100594	BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)	9184	NM_004725.2	-0.303162523	0.535031257	0.535031257	0.000375136	0.1475

【表１－４】

Pearson
表1-4

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
43	6650056	ZNF566	zinc finger protein 566	84924	NM_032838.2	−0.051770571	0.534725261	0.534725261	0.000378605	0.1475
44	2120017	NOL8	nucleolar protein 8	55035	NM_017948.4	−0.189491166	0.534382962	0.534382962	0.00038252	0.1475
45	1780639	LOC645355	-	645355	XM_932842.1	0.036028447	−0.532604561	0.532604561	0.000403449	0.1481
46	6650594	ATP11B	"ATPase, class VI, type 11B"	23200	NM_014616.1	−0.252853775	0.531209574	0.531209574	0.000420578	0.1481
47	3420136	C6orf222	chromosome 6 open reading frame 222	389384	NM_001010903.3	0.050501562	−0.531038639	0.531038639	0.000422721	0.1481
48	6760017	YY1	YY1 transcription factor	7528	NM_003403.3	−0.328869705	0.530931836	0.530931836	0.000424065	0.1481
49	510209	LOC643310	-	643310	XM_926656.1	−0.395581648	0.530359688	0.530359688	0.00043133	0.1481
50	4220673	NULL	NULL	NULL	AA971450	0.072927449	−0.529035258	0.529035258	0.000448577	0.1481
51	7650497	ELA2	"elastase 2, neutrophil"	1991	NM_001972.2	1.319902836	−0.527751453	0.527751453	0.000465881	0.1481
52	2650601	GPBP1L1	GC-rich promoter binding protein 1-like 1	60313	NM_021639.3	−0.185092124	0.526741783	0.526741783	0.000479908	0.1481
53	4880521	CDC16	cell division cycle 16 homolog (S. cerevisiae)	8881	NM_003903.3	−0.34380491	0.526389836	0.526389836	0.000484886	0.1481
54	5720300	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	10146	NM_005754.2	−0.241645343	0.526197011	0.526197011	0.000487632	0.1481
55	7210279	NULL	NULL	NULL	AA431552	0.088033112	−0.52587792	0.52587792	0.000492208	0.1481
56	840064	LOC645489	-	645489	XM_928514.1	−0.199041088	0.525473195	0.525473195	0.000498067	0.1481

【表１－５】

Pearson
表1-5

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
57	5960072	NULL	NULL	NULL	BY797688	−0.097047292	0.525204521	0.525204521	0.00050199	0.1481
58	3610521	PCDHGB6	"protocadherin gamma subfamily B, 6"	56100	NM_018926.2	0.176789549	−0.524908903	0.524908903	0.00050634	0.1481
59	770441	DOPEY1	dopey family member 1	23033	NM_015018.2	−0.10084509	0.520195136	0.520195136	0.000580393	0.1577
60	5810619	TADA1L	"transcriptional adaptor 1 (HFI1 homolog, yeast)-like"	117143	NM_053053.2	−0.16203449	0.519513067	0.519513067	0.000591874	0.1577
61	4260767	GP1BA	"glycoprotein Ib (platelet), alpha polypeptide"	2811	NM_000173.4	0.13089936	−0.519405182	0.519405182	0.000593708	0.1577
62	5290358	CPT1A	carnitine palmitoyltransferase 1A (liver)	1374	NM_001031847.1	0.165571989	−0.518549295	0.518549295	0.000608441	0.1577
63	3440189	ZBTB20	zinc finger and BTB domain containing 20	26137	NM_015642.3	−0.287117754	0.518214913	0.518214913	0.000614286	0.1577
64	4050195	FAM10A4	"family with sequence similarity 10, member A4 pseudogene"	145165	NR_002183.1	−0.370567771	0.517317921	0.517317921	0.000630211	0.1577
65	160253	MBNL1	muscleblind-like (Drosophila)	4154	NM_207295.1	−0.320695796	0.517296744	0.517296744	0.000630591	0.1577
66	6550164	DEFA4	"defensin, alpha 4, corticostatin"	1669	NM_001925.1	1.278228028	−0.516993333	0.516993333	0.000636064	0.1577
67	2710653	FBXO38	F-box protein 38	81545	NM_030793.3	−0.149047116	0.51550975	0.51550975	0.000663438	0.1577
68	7200433	NULL	NULL	NULL	BF434110	0.123387473	−0.515143069	0.515143069	0.000670364	0.1577
69	4210129	ELOVL5	"ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like,	60481	NM_021814.3	−0.284710319	0.515004341	0.515004341	0.000673001	0.1577
70	270544	NR2C1	"nuclear receptor subfamily 2, group C, member 1"	7181	NM_003297.1	−0.155303368	0.514911933	0.514911933	0.000674763	0.1577

【表１－６】

Pearson
表1-6

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
71	1710646	C11orf63	chromosome 11 open reading frame 63	79864	NM_024806.2	−0.036113925	0.513815279	0.513815279	0.000695986	0.1577
72	4250154	NULL	NULL	648749	XM_937834.2	−0.061658345	0.513627958	0.513627958	0.00069967	0.1577
73	5670739	AZU1	azurocidin 1	566	NM_001700.3	0.606626505	−0.513100443	0.513100443	0.000710138	0.1577
74	3990563	IFNA10	"interferon, alpha 10"	3446	NM_002171.1	0.151388979	−0.512771949	0.512771949	0.000716727	0.1577
75	6200678	NULL	NULL	NULL	AA889171	0.058541514	−0.512743528	0.512743528	0.000717299	0.1577
76	2320577	SSR2	"signal sequence receptor, beta (translocon-associated protein beta)"	6746	XM_945427.1	0.064320484	−0.512114597	0.512114597	0.000730076	0.1577
77	7160332	NULL	NULL	NULL	CF552427	0.054930882	−0.512069207	0.512069207	0.000731006	0.1577
78	1570392	IL21R	interleukin 21 receptor	50615	NM_181078.1	0.057079914	−0.512060675	0.512060675	0.000731181	0.1577
79	450195	Sept7	septin 7	989	NM_001788.4	−0.31815245	0.511500444	0.511500444	0.000742747	0.1577
80	6590278	CBX2	"chromobox homolog 2 (Pc class homolog, Drosophila)"	84733	NM_005189.1	0.077041967	−0.511473889	0.511473889	0.0007433	0.1577
81	6280521	NULL	NULL	648399	XM_937448.1	−0.092941768	0.509883609	0.509883609	0.000777049	0.1621
82	4810072	TUSC2	tumor suppressor candidate 2	11334	NM_007275.1	0.162628207	−0.509587506	0.509587506	0.000783482	0.1621
83	2600204	SACM1L	SAC1 suppressor of actin mutations 1-like (yeast)	22908	NM_014016.2	−0.262966982	0.508788843	0.508788843	0.000801069	0.1638
84	2360672	TNFRSF19	"tumor necrosis factor receptor superfamily, member 19"	55504	NM_148957.2	0.070969941	−0.507699006	0.507699006	0.000825635	0.1661

【表１－７】

Pearson
表1-7

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
85	4010195	COL6A2	"collagen, type VI, alpha 2"	1292	NM_058175.2	0.063152686	-0.507000048	0.507000048	0.00084174	0.1661
86	4850093	NULL	NULL	649596	XM_938659.1	0.101165023	-0.506996656	0.506996656	0.000841819	0.1661
87	3930561	PRKCI	"protein kinase C, iota"	5584	NM_002740.5	-0.105841727	0.506274935	0.506274935	0.000858744	0.1675
88	2970196	DEFB125	"defensin, beta 125"	245938	NM_153325.2	0.07618092	-0.505487341	0.505487341	0.000877558	0.1684
89	2850379	NULL	NULL	NULL	BC032017	0.065153173	-0.504716304	0.504716304	0.00089633	0.1684
90	7320424	HNRPA1L-2	-	664709	NR_002944.2	-0.432630765	0.504548219	0.504548219	0.00090047	0.1684
91	2070019	UBA6	ubiquitin-like modifier activating enzyme 6	55236	NM_018227.5	-0.194843638	0.504433181	0.504433181	0.000903313	0.1684
92	2940767	CEBPE	"CCAAT/enhancer binding protein (C/EBP), epsilon"	1053	NM_001805.2	0.145286933	-0.503471709	0.503471709	0.000927387	0.171
93	5910463	PKIA	"protein kinase (cAMP-dependent, catalytic) inhibitor alpha"	5569	NM_006823.2	-0.254561014	0.501973023	0.501973023	0.000966051	0.1714
94	6550750	ARMC8	armadillo repeat containing 8	25852	NM_014154.2	-0.087200394	0.501272073	0.501272073	0.000984621	0.1714
95	4010632	LQK1	-	642946	XM_927142.1	0.072739876	-0.500272952	0.500272952	0.001011638	0.1714
96	2350288	NULL	NULL	NULL	CA429430	0.061870864	-0.500162546	0.500162546	0.001014664	0.1714
97	5420053	CCT6P1	"chaperonin containing TCP1, subunit 6 (zeta) pseudogene 1"	643253	NR_003110.2	-0.281922881	0.49954008	0.49954008	0.001031872	0.1714
98	4590692	PCDH24	protocadherin 24	54825	NM_017675.3	0.053628265	-0.499137989	0.499137989	0.001043126	0.1714

【表１－８】

Pearson
表1-8

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
99	840601	MEGF10	multiple EGF-like-domains 10	84466	NM_032446.1	0.047723662	−0.499051274	0.499051274	0.001045567	0.1714
100	1500735	CTSG	cathepsin G	1511	NM_001911.2	1.254662256	−0.498929923	0.498929923	0.001048992	0.1714
101	7650524	BCAT1	"branched chain aminotransferase 1, cytosolic"	586	NM_005504.4	0.161097122	−0.498874361	0.498874361	0.001050563	0.1714
102	4570170	KIAA0947	–	23379	NM_015325.1	−0.180354486	0.498739242	0.498739242	0.001054393	0.1714
103	2370041	LRRN3	leucine rich repeat neuronal 3	54674	NM_018334.3	−0.383213794	0.498520298	0.498520298	0.001060626	0.1714
104	2120537	SPOCD1	SPOC domain containing 1	90853	NM_144569.4	0.09473433	−0.498432827	0.498432827	0.001063125	0.1714
105	7560300	TCTEX1D1	Tctex1 domain containing 1	200132	NM_152665.1	0.124259481	−0.498376405	0.498376405	0.001064739	0.1714
106	5550711	SYNE1	"spectrin repeat containing, nuclear envelope 1"	23345	NM_182961.2	0.075512374	−0.497880756	0.497880756	0.001079019	0.1714
107	3060288	NAIP	"NLR family, apoptosis inhibitory protein"	4671	NM_004536.2	0.073560957	−0.497822596	0.497822596	0.001080705	0.1714
108	6380673	TUBE1	"tubulin, epsilon 1"	51175	NM_016262.3	−0.138726153	0.496861389	0.496861389	0.00110892	0.1742
109	990044	KIAA1147	KIAA1147	57189	XM_001130020.1	−0.162506963	0.496349996	0.496349996	0.001124197	0.175
110	7380707	ZFAND1	"zinc finger, AN1-type domain 1"	79752	NM_024699.1	−0.254784176	0.495918538	0.495918538	0.00113723	0.1751
111	5720703	AKTIP	AKT interacting protein	64400	NM_022476.2	−0.132110131	0.495659163	0.495659163	0.001145129	0.1751
112	6520315	NULL	NULL	NULL	BC033504	0.0764326	−0.494719268	0.494719268	0.001174163	0.1779

【表１－９】

Pearson
表1-9

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
113	270091	C19orf68	chromosome 19 open reading frame 68	374920	NM_199341.1	0.052642885	−0.494044806	0.494044806	0.001195398	0.1787
114	580014	C12orf43	chromosome 12 open reading frame 43	64897	NM_022895.1	−0.20852646	0.493884539	0.493884539	0.001200494	0.1787
115	1170288	PRMT1	protein arginine methyltransferase 1	3276	NM_198319.2	0.067974089	−0.493547647	0.493547647	0.001211268	0.1787
116	4180142	KIAA1370	KIAA1370	56204	NM_019600.1	−0.224539294	0.492945505	0.492945505	0.001230739	0.18
117	6860148	SLC9A6	"solute carrier family 9 (sodium/hydrogen exchanger), member 6"	10479	NM_001042537.1	−0.17456976	0.491943559	0.491943559	0.001263753	0.1827
118	1990487	XRN1	5'−3' exoribonuclease 1	54464	NM_019001.2	−0.23813416	0.491542716	0.491542716	0.001277179	0.1827
119	1230270	WTIP	Wilms tumor 1 interacting protein	126374	XM_059037.7	0.07763865	−0.49141535	0.49141535	0.001281471	0.1827
120	7510164	SCAMP5	secretory carrier membrane protein 5	192683	NM_138967.2	0.0612925	−0.490826456	0.490826456	0.001301484	0.183
121	4760243	NULL	NULL	648210	XR_018923.1	−0.404442095	0.490196486	0.490196486	0.001323199	0.183
122	3290689	C14orf166	chromosome 14 open reading frame 166	51637	NM_016039.1	−0.321385016	0.490154831	0.490154831	0.001324646	0.183
123	3780465	SMARCA5	"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	8467	NM_003601.2	−0.115124978	0.489947033	0.489947033	0.001331886	0.183
124	730379	LOC388621	−	388621	XM_941195.2	−0.448108038	0.48978157	0.48978157	0.001337675	0.183
125	3990561	LY6H	"lymphocyte antigen 6 complex, locus H"	4062	NM_002347.2	0.197994096	−0.48850596	0.48850596	0.001383063	0.1843
126	6760326	ZNF658	zinc finger protein 658	26149	NM_033160.4	−0.078993442	0.487877369	0.487877369	0.001405927	0.1843

【表１－１０】

Pearson
表1-10

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
127	2340091	NULL	NULL	646135	XM_933437.1	0.111295385	−0.487712861	0.487712861	0.001411965	0.1843
128	4220114	NULL	NULL	NULL	DA160411	0.070349309	−0.487568568	0.487568568	0.00141728	0.1843
129	5910131	PDE6H	"phosphodiesterase 6H, cGMP-specific, cone, gamma"	5149	NM_006205.1	0.060610886	−0.487328442	0.487328442	0.001426165	0.1843
130	4610138	CAPZA1	"capping protein (actin filament) muscle Z-line, alpha 1"	829	NM_006135.1	−0.36644329	0.487145738	0.487145738	0.001432958	0.1843
131	160537	KDSR	3-ketodihydrosphingosine reductase	2531	NM_002035.1	−0.165230376	0.487124003	0.487124003	0.001433768	0.1843
132	4540138	NGB	neuroglobin	58157	NM_021257.3	0.062540263	−0.487061726	0.487061726	0.001436091	0.1843
133	3440670	NULL	NULL	402251	XM_377933.3	−0.279019599	0.48643729	0.48643729	0.00145957	0.1843
134	2000162	C5orf20	chromosome 5 open reading frame 20	140947	NM_130848.2	0.086688645	−0.486295653	0.486295653	0.001464943	0.1843
135	520215	UBE2V1	ubiquitin-conjugating enzyme E2 variant 1	7335	NM_001032288.1	0.104438712	−0.48626056	0.48626056	0.001466277	0.1843
136	4150553	TAF13	"TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa"	6884	NM_005645.3	0.061312413	−0.485315546	0.485315546	0.001502601	0.1857
137	4640739	NULL	NULL	NULL	AL120241	−0.069719279	0.485027915	0.485027915	0.001513814	0.1857
138	60053	RPL11	ribosomal protein L11	6135	NM_000975.2	−0.156372832	0.484070445	0.484070445	0.001551674	0.1857
139	6180463	CNNM3	cyclin M3	26505	NM_017623.4	0.168754951	−0.484039615	0.484039615	0.001552907	0.1857
140	2710020	NULL	NULL	NULL	BX093329	0.068337239	−0.483771626	0.483771626	0.00156366	0.1857

【表１－１１】

Pearson
表1-11

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
141	1090692	GPBP1	GC-rich promoter binding protein 1	65056	NM_022913.1	-0.264875927	0.483664554	0.483664554	0.001567975	0.1857
142	5360719	MAPK9	mitogen-activated protein kinase 9	5601	NM_002752.3	-0.123212945	0.483410076	0.483410076	0.001578271	0.1857
143	7550066	MERTK	c-mer proto-oncogene tyrosine kinase	10461	NM_006343.2	0.178168499	-0.483308071	0.483308071	0.001582415	0.1857
144	1980626	SMARCA5	"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	8467	NM_003601.2	-0.146115776	0.483245604	0.483245604	0.001584958	0.1857
145	6980253	PTPLB	"protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b"	201562	NM_198402.2	-0.336175973	0.483199931	0.483199931	0.001586819	0.1857
146	5560465	NOP56	NOP56 ribonucleoprotein homolog (yeast)	10528	NM_006392.2	-0.266935568	0.482908033	0.482908033	0.00159876	0.1858
147	730288	COG3	component of oligomeric golgi complex 3	83548	NM_031431.2	-0.128112796	0.482057164	0.482057164	0.001634022	0.1881
148	6110747	GIMAP2	"GTPase, IMAP family member 2"	26157	NM_015660.2	-0.45531031	0.481664524	0.481664524	0.001650524	0.1881
149	1500201	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	3183	NM_031314.1	-0.397999182	0.481642829	0.481642829	0.00165144	0.1881
150	1570491	hCG_2015956	-	648000	XM_371757.5	-0.31840088	0.481241081	0.481241081	0.001668486	0.1887
151	4540356	UFM1	ubiquitin-fold modifier 1	51569	NM_016617.1	-0.290998607	0.480702355	0.480702355	0.001691587	0.1901
152	7000474	GARNL1	GTPase activating Rap/RanGAP domain-like 1	253959	NM_194301.2	-0.175348366	0.480353096	0.480353096	0.001706713	0.1905
153	7380382	RNF115	ring finger protein 115	27246	NM_014455.1	0.278371033	-0.479876191	0.479876191	0.001727561	0.1916
154	3060040	PABPC1	"poly(A) binding protein, cytoplasmic 1"	26986	NM_002568.3	-0.393451244	0.479514498	0.479514498	0.001743522	0.1919

【表１－１２】

Pearson
表1-12

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
155	2570132	CLEC2D	"C-type lectin domain family 2, member D"	29121	NM_001004419.2	-0.163087579	0.479273474	0.479273474	0.00175423	0.1919
156	5900731	SFRS12	"splicing factor, arginine/serine-rich 12"	140890	NM_001077199.1	-0.290167988	0.47882202	0.47882202	0.001774443	0.1919
157	2360754	LSM14B	"LSM14B, SCD6 homolog B (S. cerevisiae)"	149986	NM_144703.2	0.096185097	-0.47854662	0.47854662	0.001786874	0.1919
158	840403	TSPAN17	tetraspanin 17	26262	NM_130465.3	0.154915647	-0.478510302	0.478510302	0.001788519	0.1919
159	3990564	CCDC89	coiled-coil domain containing 89	220388	NM_152723.1	0.204429972	-0.478138699	0.478138699	0.001805428	0.1919
160	1990093	NULL	NULL	NULL	BC042493	0.047968793	-0.477656393	0.477656393	0.001827585	0.1919
161	3990441	ABCC13	"ATP-binding cassette, sub-family C (CFTR/MRP), member 13"	150000	NR_003087.1	0.143863548	-0.477586579	0.477586579	0.001830812	0.1919
162	6940433	STAT5B	signal transducer and activator of transcription 5B	6777	NM_012448.3	-0.24015242	0.477561066	0.477561066	0.001831992	0.1919
163	6060553	RBP5	"retinol binding protein 5, cellular"	83758	NM_031491.1	0.051243739	-0.47707584	0.47707584	0.001854572	0.1924
164	770021	PRKRA	"protein kinase, interferon-inducible double stranded RNA dependent activator"	8575	NM_003690.3	-0.229357783	0.476977269	0.476977269	0.001859189	0.1924
165	2360630	FDFT1	farnesyl-diphosphate farnesyltransferase 1	2222	NM_004462.3	-0.242595956	0.476367672	0.476367672	0.001887967	0.1942
166	5570161	KCNJ14	"potassium inwardly-rectifying channel, subfamily J, member 14"	3770	NM_170720.1	0.076087153	-0.475749323	0.475749323	0.001917559	0.1947
167	3120762	MSH5	mutS homolog 5 (E. coli)	4439	NM_002441.3	0.058093161	-0.475672606	0.475672606	0.001921258	0.1947
168	6280747	NULL	NULL	643240	XM_926602.1	0.057101502	-0.475541877	0.475541877	0.001927577	0.1947

【表１－１３】

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表1-13

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
169	4780767	FLJ40473	-	285226	XR_001031.1	-0.068012051	0.474724843	0.474724843	0.001967486	0.1968
170	290632	NULL	NULL	NULL	DB337375	0.05951249	-0.474639429	0.474639429	0.001971699	0.1968
171	3360100	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	3419	NM_005530.2	-0.146008756	0.474175832	0.474175832	0.001994709	0.1979
172	7150270	LRRC26	leucine rich repeat containing 26	389816	NM_001013653.2	0.105999587	-0.472964535	0.472964535	0.00205595	0.2028
173	7610113	SLC26A8	"solute carrier family 26, member 8"	116369	NM_138718.1	0.063661004	-0.472306817	0.472306817	0.002089891	0.2028
174	6650646	C4orf39	chromosome 4 open reading frame 39	152756	NM_153027.1	-0.056865183	0.472186172	0.472186172	0.00209617	0.2028
175	3390309	FAM74A4	"family with sequence similarity 74, member A4"	401508	NM_207507.1	0.052989269	-0.471884728	0.471884728	0.002111932	0.2028
176	5860327	PRPF18	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	8559	NM_003675.3	-0.26670234	0.471782594	0.471782594	0.002117296	0.2028
177	1090367	BIVM	"basic, immunoglobulin-like variable motif containing"	54841	NM_017693.2	-0.126644305	0.471623506	0.471623506	0.002125674	0.2028
178	2570725	PPCS	phosphopantothenoylcysteine synthetase	79717	NM_001077447.1	-0.310167811	0.471401485	0.471401485	0.002137416	0.2028
179	6110091	WSB1	WD repeat and SOCS box-containing 1	26118	NM_134265.2	-0.29256262	0.471357938	0.471357938	0.002139726	0.2028
180	1110102	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	9653	NM_012262.2	-0.075582168	0.470862477	0.470862477	0.002166161	0.2033
181	4010452	SLC38A6	"solute carrier family 38, member 6"	145389	NM_153811.1	-0.136358094	0.470802009	0.470802009	0.002169407	0.2033
182	3130543	RNASE3	"ribonuclease, RNase A family, 3 (eosinophil cationic protein)"	6037	NM_002935.2	0.573752609	-0.470400954	0.470400954	0.002191043	0.2033

【表１－１４】

Pearson
表1-14

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
183	4180709	SPAG5	sperm associated antigen 5	10615	NM_006461.3	0.043518097	−0.470381365	0.470381365	0.002192104	0.2033
184	2340601	AMMECR1	"Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region	9949	NM_015365.2	−0.137410703	0.469981776	0.469981776	0.002213859	0.2042
185	5870326	SLC2A8	"solute carrier family 2 (facilitated glucose transporter), member 8"	29988	NM_014580.3	0.183791974	−0.468266194	0.468266194	0.002309432	0.2118
186	610367	HECA	headcase homolog (Drosophila)	51696	NM_016217.2	−0.312188665	0.467582354	0.467582354	0.002348527	0.2142
187	6510619	NAE1	NEDD8 activating enzyme E1 subunit 1	8883	NM_001018160.1	−0.29276015	0.467293313	0.467293313	0.002365226	0.2146
188	6100170	NULL	NULL	NULL	AI004472	0.074355718	−0.466767709	0.466767709	0.002395858	0.2155
189	2570358	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	9987	NM_031372.1	−0.382998221	0.46668552	0.46668552	0.00240068	0.2155
190	1690600	FAM53B	"family with sequence similarity 53, member B"	9679	NM_014661.3	0.082502036	−0.465522685	0.465522685	0.002469813	0.2204
191	2230538	LRRN3	leucine rich repeat neuronal 3	54674	NM_001099660.1	−0.625504431	0.465045112	0.465045112	0.002498708	0.2204
192	4610519	NULL	NULL	NULL	BU753725	0.072652165	−0.464655359	0.464655359	0.002522509	0.2204
193	6200593	CCDC15	coiled-coil domain containing 15	80071	NM_025004.2	−0.055337923	0.464591132	0.464591132	0.002526451	0.2204
194	1580286	SEH1L	SEH1-like (S. cerevisiae)	81929	NM_031216.3	−0.083010039	0.464510779	0.464510779	0.002531389	0.2204
195	5050402	HIST1H2BK	"histone cluster 1, H2bk"	85236	NM_080593.1	0.379454337	−0.464481722	0.464481722	0.002533177	0.2204
196	1850300	TC2N	"tandem C2 domains, nuclear"	123036	NM_152332.3	−0.236871126	0.463622849	0.463622849	0.002586527	0.2232

【表１－１５】

Pearson
表1-15

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
197	3610376	NULL	NULL	NULL	BM717102	0.080470357	-0.463547722	0.463547722	0.00259124	0.2232
198	7400377	CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	4680	NM_002483.3	0.588920001	-0.462719693	0.462719693	0.002643687	0.2266
199	2030477	OTP	orthopedia homeobox	23440	NM_032109.2	0.058004572	-0.462346154	0.462346154	0.002667651	0.2271
200	3360215	NULL	NULL	NULL	BQ183460	0.053186883	-0.462195315	0.462195315	0.002677381	0.2271
201	6420730	RPL9	ribosomal protein L9	6133	NM_001024921.2	-0.56653985	0.462002078	0.462002078	0.002689892	0.2271
202	3780670	NGLY1	N-glycanase 1	55768	NM_018297.2	-0.197659111	0.46152437	0.46152437	0.002721041	0.2279
203	1230593	SP3	Sp3 transcription factor	6670	NM_001017371.3	-0.175703429	0.461118519	0.461118519	0.002747753	0.2279
204	5900128	NULL	NULL	391817	XM_936708.1	-0.044221454	0.461068597	0.461068597	0.002751055	0.2279
205	7400376	RABL2A	"RAB, member of RAS oncogene family-like 2A"	11159	NM_013412.1	-0.178370764	0.460558719	0.460558719	0.002784974	0.2279
206	6380768	EIF4E	eukaryotic translation initiation factor 4E	1977	NM_001968.2	-0.084050702	0.460244198	0.460244198	0.00280608	0.2279
207	5310747	PSIP1	PC4 and SFRS1 interacting protein 1	11168	NM_033222.2	-0.298779917	0.460104407	0.460104407	0.002815505	0.2279
208	110195	LOC646197	-	646197	XM_929153.1	-0.239784184	0.459988242	0.459988242	0.002823359	0.2279
209	7380068	CNBP	"CCHC-type zinc finger, nucleic acid binding protein"	7555	NM_003418.1	-0.327720874	0.45994846	0.45994846	0.002826053	0.2279
210	6020575	NNT	nicotinamide nucleotide transhydrogenase	23530	NM_012343.3	-0.191702435	0.459704691	0.459704691	0.00284261	0.2279

【表１－１６】

Pearson
表1-16

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
211	3180438	RPS3A	ribosomal protein S3A	6189	NM_001006.3	−0.215689394	0.459396504	0.459396504	0.002863663	0.2279
212	6590441	TRIP12	thyroid hormone receptor interactor 12	9320	NM_004238.1	−0.196624966	0.459371285	0.459371285	0.002865392	0.2279
213	4150408	P2RY2	"purinergic receptor P2Y, G-protein coupled, 2"	5029	NM_002564.2	0.182075591	−0.459094109	0.459094109	0.002884454	0.2279
214	6020598	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	5366	NM_021127.1	−0.206408928	0.458725976	0.458725976	0.002909942	0.2279
215	3780382	DKFZp761E198	−	91056	NM_138368.3	0.361999782	−0.458706675	0.458706675	0.002911284	0.2279
216	4570008	EXOG	"endo/exonuclease (5'-3'), endonuclease G-like"	9941	NM_005107.2	0.223001865	−0.458501321	0.458501321	0.002925593	0.2279
217	7550341	HIGD1A	"HIG1 domain family, member 1A"	25994	NM_014056.1	−0.279289648	0.458461556	0.458461556	0.002928371	0.2279
218	2640551	CMPK1	"cytidine monophosphate (UMP-CMP) kinase 1, cytosolic"	51727	NM_016308.1	−0.272595837	0.458061071	0.458061071	0.002956478	0.2279
219	1010315	LINS1	lines homolog 1 (Drosophila)	55180	NM_001040614.1	−0.286168405	0.458036973	0.458036973	0.002958177	0.2279
220	870040	ASCC3	activating signal cointegrator 1 complex subunit 3	10973	NM_006828.2	−0.10465835	0.457844382	0.457844382	0.002971785	0.2279
221	5820202	LOC644131	−	644131	XR_018325.1	−0.244724622	0.457679581	0.457679581	0.002983472	0.2279
222	130670	ZDHHC5	"zinc finger, DHHC-type containing 5"	25921	NM_015457.2	0.193270447	−0.457640394	0.457640394	0.002986257	0.2279
223	2370754	G3BP2	GTPase activating protein (SH3 domain) binding protein 2	9908	NM_012297.3	0.055347977	−0.457521539	0.457521539	0.002994718	0.2279
224	6250615	PGLYRP1	peptidoglycan recognition protein 1	8993	NM_005091.1	0.663365274	−0.456858765	0.456858765	0.003042283	0.2305

【表１－１７】

Pearson
表1-17

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
225	6450538	TCERG1	transcription elongation regulator 1	10915	NM_006706.3	-0.153163323	0.455894063	0.455894063	0.003112699	0.2315
226	4200022	MIRHG1	microRNA host gene 1 (non-protein coding)	407975	XM_931068.1	-0.087998961	0.455880766	0.455880766	0.003113679	0.2315
227	6510441	NULL	NULL	NULL	AW337309	0.053375479	-0.455703686	0.455703686	0.003126762	0.2315
228	1990132	USH1G	Usher syndrome 1G (autosomal recessive)	124590	NM_173477.2	0.052441261	-0.455661664	0.455661664	0.003129874	0.2315
229	3800647	UGCG	UDP-glucose ceramide glucosyltransferase	7357	NM_003358.1	0.348634208	-0.455608899	0.455608899	0.003133785	0.2315
230	6900044	AMN1	antagonist of mitotic exit network 1 homolog (S. cerevisiae)	196394	NM_207337.1	-0.126543905	0.45510482	0.45510482	0.003171363	0.2315
231	4560270	PTPLB	"protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b"	201562	NM_198402.2	-0.266540406	0.455059166	0.455059166	0.003174786	0.2315
232	3710681	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	10565	NM_006421.3	-0.094839399	0.454851268	0.454851268	0.003190414	0.2315
233	4540689	ANKRD10	ankyrin repeat domain 10	55608	NM_017664.2	-0.170575575	0.454839609	0.454839609	0.003191293	0.2315
234	4860762	INPP4B	"inositol polyphosphate-4-phosphatase, type II, 105kDa"	8821	NM_003866.1	-0.281061337	0.454820734	0.454820734	0.003192715	0.2315
235	2320594	NULL	NULL	NULL	BX119501	0.089280604	-0.454390975	0.454390975	0.003225254	0.2325
236	5690403	NULL	NULL	645550	XM_928570.1	-0.065705517	0.454284141	0.454284141	0.003233388	0.2325
237	3710682	NULL	NULL	642033	XM_936103.1	0.143366073	-0.453895065	0.453895065	0.003263162	0.2336
238	7570189	GAGE6	G antigen 6	2578	NM_001476.1	0.084017945	-0.453062273	0.453062273	0.003327698	0.2372

【表１－１８】

Pearson
表1-18

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
239	2120468	C10orf58	chromosome 10 open reading frame 58	84293	NM_032333.2	−0.327354271	0.451962933	0.451962933	0.003414595	0.2389
240	1410170	GOPC	golgi associated PDZ and coiled-coil motif containing	57120	NM_020399.2	−0.088182858	0.45162816	0.45162816	0.003441448	0.2389
241	3420068	HAT1	histone acetyltransferase 1	8520	NM_003642.2	−0.268653366	0.451449886	0.451449886	0.003455823	0.2389
242	4590349	ACVR2A	"activin A receptor, type IIA"	92	NM_001616.3	−0.105208688	0.45133743	0.45133743	0.003464917	0.2389
243	3370673	GUSBL2	"glucuronidase, beta-like 2"	375513	NM_206910.1	0.128073825	−0.451300153	0.451300153	0.003467937	0.2389
244	2640255	NULL	NULL	641848	XM_935588.1	−0.645965338	0.45124504	0.45124504	0.003472405	0.2389
245	5960332	SLC39A10	"solute carrier family 39 (zinc transporter), member 10"	57181	NM_020342.1	−0.147299889	0.451151515	0.451151515	0.003479999	0.2389
246	4120056	IQSEC2	IQ motif and Sec7 domain 2	23096	NM_015075.1	0.077724109	−0.450780113	0.450780113	0.003510299	0.2389
247	5820392	CCT6A	"chaperonin containing TCP1, subunit 6A (zeta 1)"	908	NM_001009186.1	−0.24460782	0.450747413	0.450747413	0.003512977	0.2389
248	2570112	ABLIM1	actin binding LIM protein 1	3983	NM_006720.3	−0.4799407	0.450454564	0.450454564	0.003537047	0.2389
249	2710735	RASD1	"RAS, dexamethasone-induced 1"	51655	NM_016084.3	0.176270502	−0.450334284	0.450334284	0.003546974	0.2389
250	3390047	FREM2	FRAS1 related extracellular matrix protein 2	341640	NM_207361.4	0.062120756	−0.450220577	0.450220577	0.003556381	0.2389
251	2900039	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break	7520	NM_021141.2	−0.210035123	0.450062106	0.450062106	0.003569529	0.2389
252	6550600	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	4609	NM_002467.3	−0.337363684	0.450052467	0.450052467	0.00357033	0.2389

【表１－１９】

Pearson
表1-19

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
253	7400343	STX2	syntaxin 2	2054	NM_001980.2	-0.258793675	0.449998887	0.449998887	0.003574785	0.2389
254	2190390	NCOA1	nuclear receptor coactivator 1	8648	NM_147223.2	-0.208822548	0.449989658	0.449989658	0.003575553	0.2389
255	3710465	C6orf211	chromosome 6 open reading frame 211	79624	NM_024573.1	-0.114858487	0.449508458	0.449508458	0.003615794	0.2397
256	6620356	ARPP-19	-	10776	NM_006628.4	-0.261668585	0.449498501	0.449498501	0.003616631	0.2397
257	5900100	BCR	breakpoint cluster region	613	NM_021574.2	0.074331836	-0.449183958	0.449183958	0.003643153	0.2398
258	5360204	NMD3	NMD3 homolog (S. cerevisiae)	51068	NM_015938.3	-0.201253758	0.449147407	0.449147407	0.003646246	0.2398
259	7320615	NULL	NULL	NULL	DR731427	0.097655571	-0.448768392	0.448768392	0.003678454	0.241
260	1070475	RPL11	ribosomal protein L11	6135	NM_000975.2	-0.145832491	0.448285553	0.448285553	0.003719844	0.2419
261	1430477	CTSL2	cathepsin L2	1515	NM_001333.2	0.048311832	-0.448097229	0.448097229	0.003736097	0.2419
262	6560609	CNOT8	"CCR4-NOT transcription complex, subunit 8"	9337	NM_004779.4	-0.206326635	0.448051554	0.448051554	0.003740048	0.2419
263	430100	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	2547	NM_001469.3	-0.202101353	0.447948393	0.447948393	0.003748986	0.2419
264	7150685	CBX5	"chromobox homolog 5 (HP1 alpha homolog, Drosophila)"	23468	NM_012117.1	0.077258047	-0.447723533	0.447723533	0.003768532	0.2422
265	460682	CCDC132	coiled-coil domain containing 132	55610	NM_017667.2	-0.123015026	0.447052981	0.447052981	0.003827349	0.2429
266	160047	LOC389787	-	389787	XM_497072.2	-0.49206406	0.446705007	0.446705007	0.003858186	0.2429

【表１－２０】

Pearson
表1-20

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
267	2900255	ZBTB45	zinc finger and BTB domain containing 45	84878	NM_032792.2	0.124641218	−0.446554684	0.446554684	0.003871574	0.2429
268	5360168	NULL	NULL	652324	XM_941748.1	−0.08742157	0.446262544	0.446262544	0.003897708	0.2429
269	4390398	LCN2	lipocalin 2	3934	NM_005564.3	0.939054288	−0.446256107	0.446256107	0.003898286	0.2429
270	6620402	NUDT16	nudix (nucleoside diphosphate linked moiety X)-type motif 16	131870	NM_152395.1	0.177581106	−0.446234853	0.446234853	0.003900194	0.2429
271	5900482	HMGB2	high-mobility group box 2	3148	NM_002129.2	−0.440289057	0.446075441	0.446075441	0.003914527	0.2429
272	1740709	NULL	NULL	NULL	CB052724	0.070777262	−0.446031691	0.446031691	0.003918469	0.2429
273	5310736	FAM162A	"family with sequence similarity 162, member A"	26355	NM_014367.3	−0.324511803	0.445941038	0.445941038	0.003926647	0.2429
274	770128	L3MBTL3	l(3)mbt-like 3 (Drosophila)	84456	NM_032438.1	−0.161561418	0.445836872	0.445836872	0.003936064	0.2429
275	7320022	NULL	NULL	NULL	AL832228	0.086273286	−0.445654736	0.445654736	0.003952575	0.2429
276	6980328	ANP32C	"acidic (leucine-rich) nuclear phosphoprotein 32 family, member C"	23520	NM_012403.1	−0.074417224	0.445406089	0.445406089	0.003975214	0.2429
277	510050	LOC652837	-	652837	XM_942529.1	−0.036184103	0.445136212	0.445136212	0.003999913	0.2429
278	1300746	NULL	NULL	647971	XM_937029.2	0.038761564	−0.44462162	0.44462162	0.004047379	0.2429
279	5910241	ZBBX	"zinc finger, B-box domain containing"	79740	NM_024687.2	0.067673114	−0.444458165	0.444458165	0.004062559	0.2429
280	4860066	NULL	NULL	647346	XM_936495.2	−0.209955699	0.44434344	0.44434344	0.004073242	0.2429

【表１－２１】

Pearson
表1-21

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
281	5220204	C19orf66	chromosome 19 open reading frame 66	55337	NM_018381.2	0.15331761	−0.444184486	0.444184486	0.004088085	0.2429
282	6480600	THUMPD1	THUMP domain containing 1	55623	NM_017736.3	−0.123219301	0.444044022	0.444044022	0.004101241	0.2429
283	5390433	DICER1	"dicer 1, ribonuclease type III"	23405	NM_030621.2	−0.111116126	0.443842864	0.443842864	0.004120145	0.2429
284	2570020	CTR9	"Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)"	9646	NM_014633.3	−0.109638771	0.443761854	0.443761854	0.004127779	0.2429
285	50563	DOK7	docking protein 7	285489	NM_173660.3	0.047906163	−0.443751623	0.443751623	0.004128744	0.2429
286	6380747	ANKRD32	ankyrin repeat domain 32	84250	NM_032290.2	−0.104537188	0.443725202	0.443725202	0.004131237	0.2429
287	5310270	GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14	79623	NM_024572.2	0.073549787	−0.443580709	0.443580709	0.004144895	0.2429
288	2900445	IQGAP3	IQ motif containing GTPase activating protein 3	128239	NM_178229.3	−0.047779237	0.443165428	0.443165428	0.004184367	0.2429
289	4250048	CMTM7	CKLF-like MARVEL transmembrane domain containing 7	112616	NM_138410.2	0.263133293	−0.44312946	0.44312946	0.004187801	0.2429
290	3940358	OSBPL8	oxysterol binding protein-like 8	114882	NM_001003712.1	−0.261246813	0.443098374	0.443098374	0.004190771	0.2429
291	2450487	KLRG2	"killer cell lectin-like receptor subfamily G, member 2"	346689	NM_198508.2	0.048222142	−0.443079336	0.443079336	0.004192591	0.2429
292	6420309	FAM134B	"family with sequence similarity 134, member B"	54463	NM_001034850.1	−0.358481173	0.442988596	0.442988596	0.004201274	0.2429
293	4900343	MORF4L1	mortality factor 4 like 1	10933	NM_206839.1	−0.24904666	0.442917936	0.442917936	0.004208046	0.2429
294	1570292	NULL	NULL	NULL	AI807878	−0.087151047	0.442699765	0.442699765	0.004229016	0.2429

【表１－２２】

Pearson
表1-22

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Pearson_R	Cor_Pearson_absR	Cor_Pearson_Pval	Cor_Pearson_adPval
295	7650669	TBC1D4	"TBC1 domain family, member 4"	9882	NM_014832.2	-0.247692111	0.44262335	0.44262335	0.004236383	0.2429
296	2760553	UBA3	ubiquitin-like modifier activating enzyme 3	9039	NM_198197.1	-0.187898967	0.442606739	0.442606739	0.004237986	0.2429
297	4670605	MGC40489	-	146880	XR_016048.1	-0.029223716	0.442250835	0.442250835	0.004272453	0.2437
298	3460132	PAQR4	progestin and adipoQ receptor family member IV	124222	NM_152341.2	0.235239034	-0.442151094	0.442151094	0.004282157	0.2437
299	6200747	LOC220433	-	220433	XM_941684.2	-0.448374765	0.442031781	0.442031781	0.004293789	0.2437
300	4120438	RABGGTA	"Rab geranylgeranyltransferase, alpha subunit"	5875	NM_182836.1	0.121605116	-0.441511876	0.441511876	0.004344798	0.2448

【００４３】
表２　Limmaで選択された上位３００の遺伝子のリスト

【表２－１】

Limma
表2－1

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
1	HIST1H2BK	"histone cluster 1, H2bk"	85236	NM_080593.1	0.379122401	10.56860754	4.621075111	3.96E-05	0.194083013
2	LDHB	lactate dehydrogenase B	3945	NM_002300.4	−0.605485777	11.14389182	−4.582736357	4.47E-05	0.194083013
3	DPP4	dipeptidyl-peptidase 4	1803	NM_001935.3	−0.307400655	7.025297744	−4.581722797	4.48E-05	0.194083013
4	PCDHGB6	"protocadherin gamma subfamily B, 6"	56100	NM_018926.2	0.176789549	6.795139553	4.467413408	6.40E-05	0.194083013
5	PTPN18	"protein tyrosine phosphatase, non-receptor type 18 (brain-derived)"	26469	NM_014369.2	0.083763446	6.656468326	4.431096493	7.16E-05	0.194083013
6	P2RY2	"purinergic receptor P2Y, G-protein coupled, 2"	5029	NM_002564.2	0.182075591	6.769555976	4.414689685	7.54E-05	0.194083013
7	MAN2A1	"mannosidase, alpha, class 2A, member 1"	4124	NM_002372.2	−0.327379686	8.689610458	−4.395157644	8.01E-05	0.194083013
8	ZNF83	zinc finger protein 83	55769	NM_018300.2	−0.30567958	7.621524008	−4.252369567	0.000124289	0.248550702
9	PTGES3	prostaglandin E synthase 3 (cytosolic)	10728	NM_006601.4	−0.528677962	8.635339	−4.175586605	0.000157174	0.248550702
10	ZBTB20	zinc finger and BTB domain containing 20	26137	NM_015642.3	−0.287117754	7.696970778	−4.105392785	0.000194573	0.248550702
11	TUSC2	tumor suppressor candidate 2	11334	NM_007275.1	0.162628207	7.290633004	4.10064263	0.000197396	0.248550702
12	P4HA1	"prolyl 4-hydroxylase, alpha polypeptide I"	5033	NM_000917.2	−0.307837835	8.037416362	−4.091284705	0.000203075	0.248550702
13	PDP2	−	57546	NM_020786.1	0.068777448	6.597619521	4.058263335	0.000224413	0.248550702

【表２－２】

Limma
表2−2

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
14	C7orf28A	chromosome 7 open reading frame 28A	51622	XM_001133729.1	−0.383441629	7.951155828	−4.03783508	0.000238691	0.248550702
15	USP9Y	"ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)"	8287	NM_004654.3	−0.094524102	6.676560456	−4.036753411	0.000239471	0.248550702
16	DFFA	"DNA fragmentation factor, 45kDa, alpha polypeptide"	1676	NM_213566.1	0.121909434	6.810258539	4.008160095	0.000261017	0.248550702
17	NAIP	"NLR family, apoptosis inhibitory protein"	4671	NM_004536.2	0.073560957	6.62992199	3.957213679	0.000304171	0.248550702
18	MBNL1	muscleblind-like (Drosophila)	4154	NM_207295.1	−0.320695796	9.005728482	−3.947528218	0.000313125	0.248550702
19	CPT1A	carnitine palmitoyltransferase 1A (liver)	1374	NM_001031847.1	0.165571989	6.885159727	3.947282501	0.000313355	0.248550702
20	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	7073	NM_001033925.1	−0.233908998	7.770315033	−3.945464543	0.000315066	0.248550702
21	ZBTB45	zinc finger and BTB domain containing 45	84878	NM_032792.2	0.124641218	6.816614376	3.938104816	0.000322082	0.248550702
22	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	10521	NM_030881.2	−0.443292451	8.856378817	−3.877227352	0.000386238	0.248550702
23	LOC645489	-	645489	XM_928514.1	−0.199041088	7.339931356	−3.865849564	0.000399531	0.248550702
24	LOC643310	-	643310	XM_926656.1	−0.395581648	9.491360136	−3.862341614	0.000403718	0.248550702
25	CROP	-	51747	NM_006107.2	−0.443849065	8.126025421	−3.823023431	0.000453658	0.248550702
26	GP1BA	"glycoprotein Ib (platelet), alpha polypeptide"	2811	NM_000173.4	0.13089936	6.982468215	3.821325354	0.000455945	0.248550702

【表２－３】

Limma
表2−3

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
27	RIN1	Ras and Rab interactor 1	9610	NM_004292.2	0.132155916	6.826236745	3.815491484	0.000463885	0.248550702
28	HNRPA1L-2	-	664709	NR_002944.2	−0.432630765	9.53229527	−3.813682717	0.000466374	0.248550702
29	NULL	NULL	NULL	BY797688	−0.097047292	6.728704366	−3.798342261	0.000488009	0.248550702
30	NAP1L1	nucleosome assembly protein 1-like 1	4673	NM_139207.1	−0.357418466	7.704201529	−3.786307558	0.000505658	0.248550702
31	BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)	9184	NM_004725.2	−0.303162523	7.95184304	−3.766258332	0.000536441	0.248550702
32	BCAT1	"branched chain aminotransferase 1, cytosolic"	586	NM_005504.4	0.161097122	6.846191463	3.760614109	0.000545429	0.248550702
33	CMPK1	"cytidine monophosphate (UMP-CMP) kinase 1, cytosolic"	51727	NM_016308.1	−0.398631213	8.439255099	−3.756013453	0.000552862	0.248550702
34	UBE4A	"ubiquitination factor E4A (UFD2 homolog, yeast)"	9354	NM_004788.2	−0.230502672	7.842924308	−3.753787092	0.000556494	0.248550702
35	ALKBH4	"alkB, alkylation repair homolog 4 (E. coli)"	54784	NM_017621.2	0.120660698	6.880124992	3.743909631	0.000572889	0.248550702
36	TSPAN17	tetraspanin 17	26262	NM_130465.3	0.154915647	7.039678231	3.741571832	0.000576837	0.248550702
37	AMY2A	"amylase, alpha 2A (pancreatic)"	279	NM_000699.2	−0.282794372	7.393714088	−3.736503685	0.000585487	0.248550702
38	IQSEC2	IQ motif and Sec7 domain 2	23096	NM_015075.1	0.077724109	6.596496017	3.736312891	0.000585815	0.248550702
39	UGP2	UDP-glucose pyrophosphorylase 2	7360	NM_006759.3	−0.347146055	8.140532242	−3.729235851	0.00059811	0.248550702

【表２－４】

Limma
表2－4

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
40	STAT5B	signal transducer and activator of transcription 5B	6777	NM_012448.3	−0.24015242	8.701273034	−3.715107247	0.000623404	0.248550702
41	IFNA10	"interferon, alpha 10"	3446	NM_002171.1	0.151388979	6.956915233	3.697947469	0.000655515	0.248550702
42	NULL	NULL	NULL	BX106581	0.112837902	6.659739953	3.696828765	0.000657663	0.248550702
43	TCP1	t−complex 1	6950	NM_030752.2	−0.256767834	8.217718732	−3.695651035	0.000659932	0.248550702
44	RASD1	"RAS, dexamethasone−induced 1"	51655	NM_016084.3	0.176270502	6.830608498	3.690572246	0.000669802	0.248550702
45	EXOSC10	exosome component 10	5394	NM_002685.2	−0.226165883	7.858330385	−3.680867853	0.000689058	0.248550702
46	LQK1	−	642946	XM_927142.1	0.072739876	6.577138215	3.676653685	0.000697586	0.248550702
47	NULL	NULL	646135	XM_933437.1	0.111295385	6.809297621	3.670589619	0.000710035	0.248550702
48	RPS20	ribosomal protein S20	6224	NM_001023.2	−0.162977591	14.67218734	−3.670408202	0.000710411	0.248550702
49	HP	haptoglobin	3240	NM_005143.2	0.40681683	7.165541368	3.666877322	0.000717762	0.248550702
50	ACTR3	ARP3 actin−related protein 3 homolog (yeast)	10096	NM_005721.3	−0.459963089	8.761151473	−3.653066998	0.000747224	0.253578052
51	hCG_2015956	−	648000	XM_371757.5	−0.31840088	13.43073634	−3.643230911	0.000768915	0.255822595
52	C14orf166	chromosome 14 open reading frame 166	51637	NM_016039.1	−0.321385016	9.613544794	−3.613732377	0.000837664	0.26384555

【表２－５】

Limma
表2−5

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
53	WSB1	WD repeat and SOCS box-containing 1	26118	NM_134265.2	−0.29256262	8.293125883	−3.612814725	0.000839894	0.26384555
54	CNNM3	cyclin M3	26505	NM_017623.4	0.168754951	7.079276404	3.609952443	0.000846889	0.26384555
55	KLHL7	kelch-like 7 (Drosophila)	55975	NM_001031710.1	−0.155913324	7.054179324	−3.605822463	0.000857081	0.26384555
56	SYNE1	"spectrin repeat containing, nuclear envelope 1"	23345	NM_182961.2	0.075512374	6.64747449	3.594518134	0.000885585	0.26384555
57	CDC16	cell division cycle 16 homolog (S. cerevisiae)	8881	NM_003903.3	−0.34380491	9.005265989	−3.594228701	0.000886327	0.26384555
58	ESRRAP2	estrogen-related receptor alpha pseudogene 2	144832	NR_000033.2	0.169761171	6.944028851	3.578018474	0.000928831	0.268633114
59	ZDHHC5	"zinc finger, DHHC-type containing 5"	25921	NM_015457.2	0.193270447	7.893569537	3.57606895	0.000934073	0.268633114
60	FAM10A4	"family with sequence similarity 10, member A4 pseudogene"	145165	NR_002183.1	−0.370567771	9.471949409	−3.560823632	0.000976057	0.276028841
61	ELOVL5	"ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like,	60481	NM_021814.3	−0.284710319	8.617781544	−3.519828721	0.001098134	0.278705103
62	LINS1	lines homolog 1 (Drosophila)	55180	NM_001040614.1	−0.286168405	7.802936078	−3.51832105	0.001102893	0.278705103
63	CCT6P1	"chaperonin containing TCP1, subunit 6 (zeta) pseudogene 1"	643253	NR_003110.2	−0.281922881	8.987022794	−3.517147156	0.001106611	0.278705103
64	GOLGA8C	"golgi autoantigen, golgin subfamily a, 8C"	400304	XM_375152.3	−0.242008817	6.988112539	−3.501558507	0.001157143	0.278705103
65	RPS3A	ribosomal protein S3A	6189	NM_001006.3	−0.215689394	13.27274226	−3.480011693	0.001230644	0.278705103

【表２－６】

Limma
表2－6

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
66	LRRC26	leucine rich repeat containing 26	389816	NM_001013653.2	0.105999587	6.599170468	3.476732331	0.001242216	0.278705103
67	SLC9A6	"solute carrier family 9 (sodium/hydrogen exchanger), member 6"	10479	NM_001042537.1	−0.17456976	8.079094525	−3.468474071	0.00127182	0.278705103
68	NULL	NULL	648749	XM_937834.2	−0.061658345	6.590715595	−3.467954326	0.001273705	0.278705103
69	MPO	myeloperoxidase	4353	NM_000250.1	0.96554979	7.646263192	3.467107562	0.001276783	0.278705103
70	FDFT1	farnesyl-diphosphate farnesyltransferase 1	2222	NM_004462.3	−0.242595956	8.794891033	−3.459119586	0.00130617	0.278705103
71	NULL	NULL	NULL	U43604	0.301411554	7.199165409	3.453864806	0.001325853	0.278705103
72	IL21R	interleukin 21 receptor	50615	NM_181078.1	0.057079914	6.591538699	3.45178774	0.001333712	0.278705103
73	XRN1	5'-3' exoribonuclease 1	54464	NM_019001.2	−0.23813416	8.508548219	−3.441864471	0.001371875	0.278705103
74	EXOG	"endo/exonuclease (5'-3'), endonuclease G-like"	9941	NM_005107.2	0.223001865	7.264760612	3.441155154	0.001374642	0.278705103
75	G3BP2	GTPase activating protein (SH3 domain) binding protein 2	9908	NM_012297.3	0.055347977	6.583384068	3.439083684	0.001382755	0.278705103
76	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	4609	NM_002467.3	−0.337363684	7.745340453	−3.43222232	0.001409956	0.278705103
77	RPL11	ribosomal protein L11	6135	NM_000975.2	−0.156372832	14.69523285	−3.421668194	0.001452799	0.278705103
78	SLC2A8	"solute carrier family 2 (facilitated glucose transporter), member 8"	29988	NM_014580.3	0.183791974	7.48215931	3.419438233	0.001462008	0.278705103

【表２－７】

Limma
表2－7

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
79	THOC2	THO complex 2	57187	NM_001081550.1	0.168129085	6.922775737	3.418506601	0.001465873	0.278705103
80	NULL	NULL	NULL	AV730797	0.146406334	6.702252803	3.415196196	0.001479683	0.278705103
81	TNFRSF19	"tumor necrosis factor receptor superfamily, member 19"	55504	NM_148957.2	0.070969941	6.600503679	3.412998956	0.001488918	0.278705103
82	RNF115	ring finger protein 115	27246	NM_014455.1	0.278371033	8.827361643	3.410923159	0.001497693	0.278705103
83	LEF1	lymphoid enhancer-binding factor 1	51176	NM_016269.2	−0.599827856	9.374949765	−3.410373939	0.001500023	0.278705103
84	NELL2	NEL-like 2 (chicken)	4753	NM_006159.1	−0.537157632	8.635324105	−3.406582362	0.001516203	0.278705103
85	TUBE1	"tubulin, epsilon 1"	51175	NM_016262.3	−0.138726153	6.918780573	−3.405525994	0.00152074	0.278705103
86	GPBP1L1	GC-rich promoter binding protein 1-like 1	60313	NM_021639.3	−0.185092124	6.99451945	−3.40453954	0.001524989	0.278705103
87	NULL	NULL	645609	XM_928619.1	0.215115706	6.93283128	3.402248419	0.001534902	0.278705103
88	RNF216L	ring finger protein 216-like	441191	XR_001271.1	0.162378967	7.075767146	3.391284261	0.001583195	0.278705103
89	LOC388621	-	388621	XM_941195.2	−0.448108038	12.6172039	−3.381059183	0.001629539	0.278705103
90	SNORA33	"small nucleolar RNA, H/ACA box 33"	594839	NR_002436.1	−0.186113851	7.237748956	−3.378911416	0.001639437	0.278705103
91	FAM53B	"family with sequence similarity 53, member B"	9679	NM_014661.3	0.082502036	6.720712848	3.378900914	0.001639485	0.278705103

【表２－８】

Limma
表2－8

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
92	TCTEX1D1	Tctex1 domain containing 1	200132	NM_152665.1	0.124259481	6.947438013	3.378852115	0.001639711	0.278705103
93	CBX2	"chromobox homolog 2 (Pc class homolog, Drosophila)"	84733	NM_005189.1	0.077041967	6.586068418	3.37584138	0.001653684	0.278705103
94	SLC26A2	"solute carrier family 26 (sulfate transporter), member 2"	1836	NM_000112.3	0.078282552	6.63165789	3.374992231	0.001657646	0.278705103
95	TADA1L	"transcriptional adaptor 1 (HFI1 homolog, yeast)-like"	117143	NM_053053.2	−0.16203449	7.226654736	−3.373370577	0.001665237	0.278705103
96	PTPLB	"protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b"	201562	NM_198402.2	−0.336175973	9.255647124	−3.373281148	0.001665656	0.278705103
97	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	3183	NM_031314.1	−0.397999182	8.413292708	−3.361986141	0.001719468	0.278705103
98	NULL	NULL	NULL	BF338665	0.061724508	6.594937826	3.36186306	0.001720063	0.278705103
99	NULL	NULL	731950	XR_016039.1	−0.061135983	6.603654541	−3.361179911	0.001723372	0.278705103
100	PKIA	"protein kinase (cAMP-dependent, catalytic) inhibitor alpha"	5569	NM_006823.2	−0.254561014	7.229052236	−3.360304127	0.001727622	0.278705103
101	PAQR4	progestin and adipoQ receptor family member IV	124222	NM_152341.2	0.235239034	7.212347489	3.360042242	0.001728895	0.278705103
102	ELA2	"elastase 2, neutrophil"	1991	NM_001972.2	1.319902836	8.282120812	3.357180559	0.001742862	0.278705103
103	ZNF276	zinc finger protein 276	92822	NM_152287.2	0.130599764	6.992968715	3.356571932	0.001745846	0.278705103
104	SLC26A8	"solute carrier family 26, member 8"	116369	NM_138718.1	0.063661004	6.612090652	3.356315889	0.001747103	0.278705103

【表２－９】

Limma
表2−9

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
105	NULL	NULL	NULL	BM932227	−0.116682268	6.661300061	−3.347803068	0.00178939	0.278705103
106	HDAC2	histone deacetylase 2	3066	NM_001527.2	−0.308059644	9.194835902	−3.344717795	0.001804956	0.278705103
107	NULL	NULL	NULL	AA971450	0.072927449	6.644971089	3.340652054	0.001825665	0.278705103
108	HNRPDL	heterogeneous nuclear ribonucleoprotein D−like	9987	NM_031372.1	−0.382998221	8.609895867	−3.339735723	0.001830363	0.278705103
109	DSC1	desmocollin 1	1823	NM_004948.2	−0.247522067	6.842109462	−3.337976177	0.001839418	0.278705103
110	FAM134B	"family with sequence similarity 134, member B"	54463	NM_001034850.1	−0.358481173	7.824193291	−3.332078062	0.001870082	0.278705103
111	NULL	NULL	NULL	AA431552	0.088033112	6.60564995	3.331235614	0.001874502	0.278705103
112	NOP56	NOP56 ribonucleoprotein homolog (yeast)	10528	NM_006392.2	−0.266935568	7.752420168	−3.32920812	0.001885179	0.278705103
113	SACM1L	SAC1 suppressor of actin mutations 1−like (yeast)	22908	NM_014016.2	−0.262966982	8.037968043	−3.320589417	0.001931216	0.278705103
114	C12orf43	chromosome 12 open reading frame 43	64897	NM_022895.1	−0.20852646	7.657143361	−3.318702024	0.00194144	0.278705103
115	SMARCA5	"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	8467	NM_003601.2	−0.115124978	7.082731596	−3.318505294	0.001942508	0.278705103
116	GIMAP2	"GTPase, IMAP family member 2"	26157	NM_015660.2	−0.45531031	8.473264716	−3.316388313	0.001954043	0.278705103
117	NUDT16	nudix (nucleoside diphosphate linked moiety X)−type motif 16	131870	NM_152395.1	0.177581106	7.017862529	3.314837959	0.001962531	0.278705103

【表２－１０】

Limma
表2－10

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
118	LRRN3	leucine rich repeat neuronal 3	54674	NM_018334.3	−0.383213794	6.977063895	−3.311837127	0.001979062	0.278705103
119	PRKCI	″protein kinase C, iota″	5584	NM_002740.5	−0.105841727	6.824866958	−3.311134682	0.00198295	0.278705103
120	RPL11	ribosomal protein L11	6135	NM_000975.2	−0.145832491	14.51015798	−3.31068699	0.001985432	0.278705103
121	NULL	NULL	NULL	AL120241	−0.069719279	6.594134665	−3.308246033	0.001999018	0.278705103
122	NULL	NULL	NULL	CX782759	−0.206252167	6.710163433	−3.305733304	0.002013095	0.278705103
123	AMN1	antagonist of mitotic exit network 1 homolog (S. cerevisiae)	196394	NM_207337.1	−0.126543905	6.727686827	−3.304450826	0.002020316	0.278705103
124	FAM180B	″family with sequence similarity 180, member B″	399888	XM_941808.2	0.083819707	6.625010712	3.296734176	0.00206429	0.279340342
125	HAT1	histone acetyltransferase 1	8520	NM_003642.2	−0.268653366	8.011690033	−3.295875016	0.002069242	0.279340342
126	NULL	NULL	649088	XM_938168.1	−0.257637488	6.821077074	−3.294997835	0.002074309	0.279340342
127	NULL	NULL	NULL	AL042883	0.08373784	6.721750094	3.288131695	0.002114385	0.280973338
128	SOX15	SRY (sex determining region Y)-box 15	6665	NM_006942.1	0.08255695	6.609101503	3.28725522	0.002119554	0.280973338
129	NULL	NULL	649555	XM_945579.1	−0.269621337	8.007087043	−3.284266937	0.002137266	0.281124998
130	NULL	NULL	NULL	BF445990	0.102742584	6.676471028	3.276579261	0.002183481	0.283914285

【表２－１１】

Limma
表2－11

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
131	GOSR1	golgi SNAP receptor complex member 1	9527	NM_001007024.1	0.092600962	6.795254442	3.271571079	0.002214098	0.283914285
132	GAGE6	G antigen 6	2578	NM_001476.1	0.084017945	6.682459172	3.264048516	0.002260854	0.283914285
133	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	328	NM_080649.1	−0.205907613	10.29653222	−3.263741347	0.002262783	0.283914285
134	DEFA4	"defensin, alpha 4, corticostatin"	1669	NM_001925.1	1.278228028	8.166305327	3.261061773	0.002279678	0.283914285
135	NULL	NULL	654161	XM_944884.1	0.104968986	6.718195712	3.257061934	0.002305119	0.283914285
136	NUDT15	nudix (nucleoside diphosphate linked moiety X)-type motif 15	55270	NM_018283.1	0.123752342	6.885930043	3.255768591	0.002313403	0.283914285
137	NULL	NULL	NULL	BF434110	0.123387473	6.780690807	3.249401682	0.002354598	0.283914285
138	UFM1	ubiquitin-fold modifier 1	51569	NM_016617.1	−0.290998607	7.377470679	−3.247199714	0.002369006	0.283914285
139	PPCS	phosphopantothenoylcysteine synthetase	79717	NM_001077447.1	−0.310167811	8.568975401	−3.246841442	0.002371358	0.283914285
140	NOL8	nucleolar protein 8	55035	NM_017948.4	−0.189491166	7.101045922	−3.245977565	0.002377039	0.283914285
141	ARHGAP26	Rho GTPase activating protein 26	23092	NM_015071.3	0.134940814	6.848659921	3.24444167	0.002387172	0.283914285
142	LOC284757	-	284757	NM_001004305.1	0.123817908	6.718141693	3.240499839	0.002413364	0.283914285
143	OSTCL	oligosaccharyltransferase complex subunit-like	202459	NM_145303.2	0.060154691	6.581023808	3.238217924	0.00242865	0.283914285

【表２－１２】

Limma
表2－12

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
144	MGC2752	–	65996	NM_023939.3	0.119350056	6.792942939	3.237415006	0.002434051	0.283914285
145	NULL	NULL	648399	XM_937448.1	−0.092941768	6.644024172	−3.234527246	0.00245357	0.283914285
146	ZNF700	zinc finger protein 700	90592	NM_144566.1	−0.134476397	7.002962787	−3.234466743	0.00245398	0.283914285
147	C6orf222	chromosome 6 open reading frame 222	389384	NM_001010903.3	0.050501562	6.569327079	3.231679197	0.002472965	0.283914285
148	CCDC135	coiled−coil domain containing 135	84229	NM_032269.4	0.099558313	6.682670608	3.231179152	0.002476386	0.283914285
149	PCDH17	protocadherin 17	27253	NM_014459.2	−0.527638621	7.136230311	−3.222695445	0.002535104	0.284452992
150	ZDHHC9	"zinc finger, DHHC−type containing 9"	51114	NM_016032.2	0.119706025	6.997375053	3.217216624	0.002573725	0.284452992
151	LRRN3	leucine rich repeat neuronal 3	54674	NM_001099660.1	−0.625504431	7.682637114	−3.214775054	0.002591115	0.284452992
152	BPTF	bromodomain PHD finger transcription factor	2186	NM_004459.6	0.091882838	6.908904599	3.213818559	0.002597958	0.284452992
153	ABLIM1	actin binding LIM protein 1	3983	NM_006720.3	−0.4799407	9.683313038	−3.211379067	0.002615488	0.284452992
154	DNAJA2	"DnaJ (Hsp40) homolog, subfamily A, member 2"	10294	NM_005880.2	−0.266568167	10.14561262	−3.210741465	0.002620088	0.284452992
155	ESRRA	estrogen−related receptor alpha	2101	NM_004451.3	0.246532485	7.560235207	3.209923275	0.002626002	0.284452992
156	C10orf58	chromosome 10 open reading frame 58	84293	NM_032333.2	−0.327354271	12.01556757	−3.208768803	0.002634369	0.284452992

【表２－１３】

Limma
表2−13

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
157	Sept7	septin 7	989	NM_001788.4	−0.31815245	7.233902696	−3.207967599	0.002640191	0.284452992
158	NULL	NULL	NULL	CA847896	−0.142130207	6.698943452	−3.206384308	0.002651731	0.284452992
159	YY1	YY1 transcription factor	7528	NM_003403.3	−0.328869705	8.107148479	−3.204275996	0.002667172	0.284452992
160	DSC1	desmocollin 1	1823	NM_004948.2	−0.207019876	6.793195915	−3.200364719	0.002696043	0.284452992
161	CLEC2D	"C−type lectin domain family 2, member D"	29121	NM_001004419.2	−0.163087579	6.794369704	−3.198257031	0.002711724	0.284452992
162	PRPF18	PRP18 pre−mRNA processing factor 18 homolog (S. cerevisiae)	8559	NM_003675.3	−0.26670234	7.878626332	−3.197713488	0.002715782	0.284452992
163	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	10146	NM_005754.2	−0.241645343	7.052446591	−3.185861616	0.002805707	0.292068911
164	MST150	−	85027	NM_032947.3	0.146021285	6.865433004	3.176860762	0.002875877	0.296708297
165	TBC1D4	"TBC1 domain family, member 4"	9882	NM_014832.2	−0.247692111	7.386975828	−3.174355605	0.002895701	0.296708297
166	NULL	NULL	641848	XM_935588.1	−0.645965338	9.336735576	−3.173470885	0.002902733	0.296708297
167	LOC646197	−	646197	XM_929153.1	−0.239784184	7.328222264	−3.166981614	0.002954807	0.300222595
168	NULL	NULL	NULL	BX111675	0.054993081	6.598572236	3.162436409	0.002991807	0.302172471
169	STX2	syntaxin 2	2054	NM_001980.2	−0.258793675	8.129855454	−3.160200443	0.003010169	0.302228045

【表２－１４】

Limma
表2－14

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
170	MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	4552	NM_024010.1	-0.355492388	8.577705624	-3.152664579	0.003072842	0.306705797
171	RPS3A	ribosomal protein S3A	6189	NM_001006.3	-0.224696704	13.45225898	-3.146532931	0.003124746	0.308412922
172	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	3419	NM_005530.2	-0.146008756	7.834975506	-3.146351122	0.003126298	0.308412922
173	ABCC13	"ATP-binding cassette, sub-family C (CFTR/MRP), member 13"	150000	NR_003087.1	0.143863548	6.975180019	3.143481172	0.003150887	0.309041948
174	PFN2	profilin 2	5217	NM_053024.2	-0.101946483	6.657579392	-3.139339792	0.003186693	0.310064384
175	UBE2Q1	ubiquitin-conjugating enzyme E2Q family member 1	55585	NM_017582.5	0.154304568	7.337098311	3.138057327	0.003197859	0.310064384
176	AMMECR1	"Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region	9949	NM_015365.2	-0.137410703	7.232010532	-3.13384834	0.003234765	0.310661839
177	C1orf116	chromosome 1 open reading frame 116	79098	NM_023938.5	0.160946362	7.087582262	3.131317441	0.00325715	0.310661839
178	NULL	NULL	NULL	AI807878	-0.087151047	6.620513943	-3.13111503	0.003258947	0.310661839
179	SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	26278	NM_014363.3	-0.121241812	6.762655646	-3.11937001	0.003364815	0.313968641
180	LSM14B	"LSM14B, SCD6 homolog B (S. cerevisiae)"	149986	NM_144703.2	0.096185097	6.699394363	3.118872143	0.003369373	0.313968641
181	XAF1	XIAP associated factor 1	54739	NM_199139.1	0.524120564	8.118813402	3.118616591	0.003371715	0.313968641
182	C19orf10	chromosome 19 open reading frame 10	56005	NM_019107.3	0.409044609	8.364952884	3.11477554	0.003407106	0.313968641

【表２－１５】

Limma
表2−15

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
183	LY6H	"lymphocyte antigen 6 complex, locus H"	4062	NM_002347.2	0.197994096	7.625459259	3.11379814	0.003416167	0.313968641
184	PTPLB	"protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b"	201562	NM_198402.2	−0.266540406	8.55593686	−3.113403603	0.003419831	0.313968641
185	GPBP1	GC-rich promoter binding protein 1	65056	NM_022913.1	−0.264875927	7.600558229	−3.111547981	0.003437115	0.313968641
186	RPLP2	"ribosomal protein, large, P2"	6181	NM_001004.2	−0.118887297	15.00311102	−3.11020746	0.003449652	0.313968641
187	RNF11	ring finger protein 11	26994	NM_014372.3	0.225580915	7.461433616	3.109081409	0.003460217	0.313968641
188	INPP4B	"inositol polyphosphate-4-phosphatase, type II, 105kDa"	8821	NM_003866.1	−0.281061337	7.795763622	−3.104207785	0.003506294	0.313968641
189	FAM162A	"family with sequence similarity 162, member A"	26355	NM_014367.3	−0.324511803	7.752271827	−3.10396735	0.003508582	0.313968641
190	MORF4L1	mortality factor 4 like 1	10933	NM_206839.1	−0.24904666	10.34569001	−3.102150665	0.003525916	0.313968641
191	SCAMP5	secretory carrier membrane protein 5	192683	NM_138967.2	0.0612925	6.631370252	3.098618399	0.003559852	0.313968641
192	CCDC89	coiled-coil domain containing 89	220388	NM_152723.1	0.204429972	7.482187696	3.09753939	0.003570279	0.313968641
193	MEGF10	multiple EGF-like-domains 10	84466	NM_032446.1	0.047723662	6.628265945	3.096096662	0.003584267	0.313968641
194	SATB1	SATB homeobox 1	6304	NM_002971.2	−0.216171431	7.186778766	−3.09531339	0.003591883	0.313968641
195	ABCA10	"ATP-binding cassette, sub-family A (ABC1), member 10"	10349	NM_080282.3	−0.111376806	6.625364772	−3.093640769	0.003608197	0.313968641

【表２－１６】

Limma
表2−16

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
196	MRPL9	mitochondrial ribosomal protein L9	65005	NM_031420.2	−0.156554264	8.221670276	−3.087455651	0.003669133	0.31454873
197	TAPBPL	TAP binding protein-like	55080	NM_018009.3	0.214867322	8.1474735	3.086165839	0.003681962	0.31454873
198	COL6A2	"collagen, type VI, alpha 2"	1292	NM_058175.2	0.063152686	6.561772793	3.085397873	0.003689621	0.31454873
199	LOC439949	−	439949	XM_001129241.1	−0.469330965	9.557830109	−3.085250381	0.003691093	0.31454873
200	KIAA0947	−	23379	NM_015325.1	−0.180354486	7.294868393	−3.078574853	0.003758327	0.31454873
201	ZBP1	Z-DNA binding protein 1	81030	NM_030776.1	0.273696455	8.206083343	3.075164636	0.003793118	0.31454873
202	ZFAND1	"zinc finger, AN1-type domain 1"	79752	NM_024699.1	−0.254784176	7.600944243	−3.071364143	0.003832248	0.31454873
203	CTSG	cathepsin G	1511	NM_001911.2	1.254662256	8.153662815	3.066769075	0.003880067	0.31454873
204	WIPI1	"WD repeat domain, phosphoinositide interacting 1"	55062	NM_017983.4	0.224176607	7.728118352	3.066646213	0.003881354	0.31454873
205	NULL	NULL	NULL	AA532505	−0.182665342	6.801109687	−3.064162052	0.003907447	0.31454873
206	CETP	"cholesteryl ester transfer protein, plasma"	1071	NM_000078.1	0.23667459	7.0432678	3.063834245	0.003910903	0.31454873
207	PNN	"pinin, desmosome associated protein"	5411	NM_002687.3	−0.314789132	8.884666033	−3.062982207	0.003919898	0.31454873
208	HMGB2	high-mobility group box 2	3148	NM_002129.2	−0.440289057	9.197446056	−3.062831664	0.00392149	0.31454873

【表２－１７】

Limma
表2－17

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
209	KIAA0495	-	57212	NM_207306.1	0.103342047	6.804792712	3.054813009	0.004007139	0.31454873
210	INADL	InaD-like (Drosophila)	10207	NM_176878.1	-0.241811563	7.411681346	-3.052446632	0.00403275	0.31454873
211	NULL	NULL	402251	XM_377933.3	-0.279019599	13.20844854	-3.05231587	0.004034169	0.31454873
212	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	5366	NM_021127.1	-0.206408928	6.932806262	-3.051907227	0.004038609	0.31454873
213	ERVWE1	"endogenous retroviral family W, env(C7), member 1"	30816	NM_014590.3	-0.11912978	6.669466439	-3.051740881	0.004040418	0.31454873
214	DEFB125	"defensin, beta 125"	245938	NM_153325.2	0.07618092	6.649380002	3.050659019	0.004052199	0.31454873
215	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6	11226	NM_007210.3	0.080267134	6.753373034	3.050508823	0.004053837	0.31454873
216	PABPC1	"poly(A) binding protein, cytoplasmic 1"	26986	NM_002568.3	-0.393451244	8.998065664	-3.049628157	0.004063455	0.31454873
217	TFIP11	tuftelin interacting protein 11	24144	NM_001008697.1	-0.334180963	7.760123364	-3.049354132	0.004066452	0.31454873
218	NAE1	NEDD8 activating enzyme E1 subunit 1	8883	NM_001018160.1	-0.29276015	7.771592744	-3.044929903	0.004115128	0.31454873
219	ANKRD10	ankyrin repeat domain 10	55608	NM_017664.2	-0.170575575	7.64901735	-3.039743162	0.004172892	0.31454873
220	GM2A	GM2 ganglioside activator	2760	NM_000405.3	0.266114128	7.061105638	3.038262899	0.004189517	0.31454873
221	NULL	NULL	NULL	AW510851	0.206747428	7.083271693	3.038237159	0.004189807	0.31454873

【表２－１８】

Limma
表2－18

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
222	NULL	NULL	NULL	BC032017	0.065153173	6.608790075	3.036217154	0.004212596	0.31454873
223	MERTK	c-mer proto-oncogene tyrosine kinase	10461	NM_006343.2	0.178168499	6.954953554	3.0358305	0.004216971	0.31454873
224	AP3M2	"adaptor-related protein complex 3, mu 2 subunit"	10947	NM_006803.2	−0.269660186	7.913987405	−3.035147683	0.004224709	0.31454873
225	DKFZp761E198	–	91056	NM_138368.3	0.361999782	7.249752149	3.033989667	0.004237861	0.31454873
226	ADD3	adducin 3 (gamma)	120	NM_001121.2	−0.331309202	10.1268842	−3.032530689	0.004254487	0.31454873
227	CDC16	cell division cycle 16 homolog (S. cerevisiae)	8881	NM_001078645.1	−0.262987116	9.820606346	−3.030775491	0.004274569	0.31454873
228	KIAA1147	KIAA1147	57189	XM_001130020.1	−0.162506963	7.004494336	−3.030736896	0.004275012	0.31454873
229	UQCRC2	ubiquinol-cytochrome c reductase core protein II	7385	NM_003366.2	−0.306901413	9.073083441	−3.029625432	0.004287776	0.31454873
230	UBA6	ubiquitin-like modifier activating enzyme 6	55236	NM_018227.5	−0.194843638	7.532537393	−3.028380957	0.00430211	0.31454873
231	ROM1	retinal outer segment membrane protein 1	6094	NM_000327.2	0.090241562	6.729914462	3.028098053	0.004305375	0.31454873
232	NR2C1	"nuclear receptor subfamily 2, group C, member 1"	7181	NM_003297.1	−0.155303368	6.991172468	−3.0280023	0.004306481	0.31454873
233	F12	coagulation factor XII (Hageman factor)	2161	NM_000505.3	0.095388359	6.762822694	3.026085058	0.004328674	0.31454873
234	ARMC8	armadillo repeat containing 8	25852	NM_014154.2	−0.087200394	6.632486359	−3.025296236	0.004337836	0.31454873

【表２－１９】

Limma
表2－19

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
235	ATP11B	"ATPase, class VI, type 11B"	23200	NM_014616.1	−0.252853775	7.626141524	−3.008423755	0.004538234	0.32615798
236	NGLY1	N−glycanase 1	55768	NM_018297.2	−0.197659111	8.023132987	−3.007062614	0.004554774	0.32615798
237	SFRS12	"splicing factor, arginine/serine−rich 12"	140890	NM_001077199.1	−0.290167988	7.753512191	−3.003361465	0.004600037	0.32615798
238	NULL	NULL	643272	XM_926633.1	−0.171519101	6.729150181	−3.002858425	0.004606221	0.32615798
239	SNN	stannin	8303	NM_003498.4	0.236846461	7.364580648	3.002384307	0.004612057	0.32615798
240	NULL	NULL	NULL	BU753725	0.072652165	6.618401869	3.001859946	0.00461852	0.32615798
241	HIGD1A	"HIG1 domain family, member 1A"	25994	NM_014056.1	−0.279289648	8.999208769	−2.995323082	0.004699801	0.32615798
242	KCTD5	potassium channel tetramerisation domain containing 5	54442	NM_018992.2	0.23125854	8.529271571	2.995052196	0.004703198	0.32615798
243	KIAA1370	KIAA1370	56204	NM_019600.1	−0.224539294	7.456650271	−2.994813967	0.004706187	0.32615798
244	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	328	NM_001641.2	−0.196094396	9.738672442	−2.992976895	0.0047293	0.32615798
245	RABGGTA	"Rab geranylgeranyltransferase, alpha subunit"	5875	NM_182836.1	0.121605116	6.86888209	2.992774267	0.004731856	0.32615798
246	C2orf18	chromosome 2 open reading frame 18	54978	NM_017877.3	0.137500886	6.87955857	2.992710778	0.004732657	0.32615798
247	AK5	adenylate kinase 5	26289	NM_012093.2	−0.119581494	6.636155047	−2.988854547	0.004781554	0.32615798

【表２－２０】

Limma
表2－20

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
248	HERC2P3	hect domain and RLD 2 pseudogene 3	283755	XM_001128358.1	−0.175308013	6.682973877	−2.988111751	0.004791027	0.32615798
249	ATP5C1	"ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1"	509	NM_005174.2	−0.369186445	10.44337548	−2.98421357	0.00484103	0.32615798
250	IMMT	"inner membrane protein, mitochondrial (mitofilin)"	10989	NM_001100169.1	−0.221779779	8.555082028	−2.983540607	0.004849711	0.32615798
251	XIAP	X−linked inhibitor of apoptosis	331	NM_001167.2	0.07202812	6.621201373	2.981911934	0.004870783	0.32615798
252	C14orf4	chromosome 14 open reading frame 4	64207	NM_024496.2	0.29452834	7.653210546	2.979013545	0.004908495	0.32615798
253	NULL	NULL	645550	XM_928570.1	−0.065705517	6.590349507	−2.978667878	0.00491301	0.32615798
254	RPL9	ribosomal protein L9	6133	NM_001024921.2	−0.56653985	11.40544642	−2.975268779	0.004957625	0.32615798
255	NULL	NULL	NULL	BM717102	0.080470357	6.717739236	2.975115397	0.004959647	0.32615798
256	ZBBX	"zinc finger, B−box domain containing"	79740	NM_024687.2	0.067673114	6.679035963	2.97421524	0.00497153	0.32615798
257	UPK3A	uroplakin 3A	7380	NM_006953.2	0.082445237	6.698973174	2.971686744	0.005005051	0.32615798
258	NULL	NULL	NULL	AI479380	0.091888829	6.633620699	2.968887484	0.00504241	0.32615798
259	CAPZA1	"capping protein (actin filament) muscle Z−line, alpha 1"	829	NM_006135.1	−0.36644329	7.449870807	−2.968385028	0.005049143	0.32615798
260	FBXO38	F−box protein 38	81545	NM_030793.3	−0.149047116	6.882751518	−2.96757563	0.005060008	0.32615798

【表２－２１】

Limma
表2－21

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
261	NBPF14	"neuroblastoma breakpoint family, member 14"	25832	NM_015383.1	−0.189228519	7.28417605	−2.967517575	0.005060788	0.32615798
262	MYC	v−myc myelocytomatosis viral oncogene homolog (avian)	4609	NM_002467.3	−0.38321124	8.439937979	−2.965923374	0.005082253	0.32615798
263	UBA3	ubiquitin−like modifier activating enzyme 3	9039	NM_198197.1	−0.187898967	7.02054307	−2.964535444	0.005101011	0.32615798
264	TRIOBP	TRIO and F−actin binding protein	11078	NM_138632.2	0.133302598	7.129841312	2.963553212	0.005114326	0.32615798
265	RPL7	ribosomal protein L7	6129	NM_000971.3	−0.354882331	10.11769817	−2.962843057	0.005123972	0.32615798
266	CNOT7	"CCR4−NOT transcription complex, subunit 7"	29883	NM_013354.5	−0.212744803	8.998078077	−2.962376643	0.005130317	0.32615798
267	ALDH7A1	"aldehyde dehydrogenase 7 family, member A1"	501	NM_001182.2	−0.068559518	6.611321514	−2.960459925	0.005156468	0.32615798
268	OR11L1	"olfactory receptor, family 11, subfamily L, member 1"	391189	NM_001001959.1	0.101699642	6.879400128	2.960040266	0.005162211	0.32615798
269	GUSBL2	"glucuronidase, beta−like 2"	375513	NM_206910.1	0.128073825	6.907202924	2.958648625	0.005181296	0.32615798
270	AZU1	azurocidin 1	566	NM_001700.3	0.606626505	7.0491903	2.957871261	0.005191986	0.32615798
271	DUSP26	dual specificity phosphatase 26 (putative)	78986	NM_024025.1	0.086230095	6.832117186	2.956626422	0.005209147	0.32615798
272	TIA1	TIA1 cytotoxic granule−associated RNA binding protein	7072	NM_022173.1	−0.154497679	7.045284603	−2.951573346	0.005279357	0.328639571
273	RPL23	ribosomal protein L23	9349	NM_000978.3	−0.338815803	11.96776242	−2.949718357	0.005305352	0.328639571

【表２－２２】

Limma
表2－22

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
274	FKRP	fukutin related protein	79147	NM_024301.3	0.120111732	6.815052027	2.944636349	0.005377187	0.328639571
275	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	54552	NM_019067.4	0.338634328	7.473595121	2.94338078	0.005395075	0.328639571
276	NULL	NULL	NULL	CF552427	0.054930882	6.640898885	2.941052051	0.005428399	0.328639571
277	LOC642934	–	642934	XM_942991.2	−0.452151346	9.850733599	−2.938312313	0.005467851	0.328639571
278	RPL5	ribosomal protein L5	6125	NM_000969.3	−0.250479654	13.11440201	−2.936873997	0.005488671	0.328639571
279	TMEM189	transmembrane protein 189	387521	NM_199129.1	0.148299783	7.711569894	2.936068915	0.005500356	0.328639571
280	EIF1AX	"eukaryotic translation initiation factor 1A, X-linked"	1964	NM_001412.3	−0.259913717	7.91454554	−2.935272494	0.005511939	0.328639571
281	TCERG1	transcription elongation regulator 1	10915	NM_006706.3	−0.153163323	7.597318359	−2.934764583	0.005519338	0.328639571
282	TNIP2	TNFAIP3 interacting protein 2	79155	NM_024309.2	0.160957185	7.341463538	2.934623572	0.005521394	0.328639571
283	FLVCR1	feline leukemia virus subgroup C cellular receptor 1	28982	NM_014053.1	0.133852915	6.983247308	2.934521625	0.005522881	0.328639571
284	OSBPL1A	oxysterol binding protein-like 1A	114876	NM_080597.2	0.088316231	6.818536942	2.932343132	0.00555474	0.328639571
285	DHX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15	1665	NM_001358.2	−0.188453408	9.249900465	−2.931629933	0.005565207	0.328639571
286	PLEKHN1	"pleckstrin homology domain containing, family N member 1"	84069	NM_032129.1	0.124659553	6.987594206	2.929799098	0.005592163	0.328639571

【表２－２３】

Limma
表2－23

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
287	ATM	ataxia telangiectasia mutated	472	NM_000051.3	−0.361381652	8.817161402	−2.926480737	0.005641331	0.328639571
288	AKTIP	AKT interacting protein	64400	NM_022476.2	−0.132110131	7.173375215	−2.926408412	0.005642407	0.328639571
289	MGC10997	−	84741	NR_001565.1	−0.229371406	10.57230382	−2.926241638	0.005644889	0.328639571
290	NULL	NULL	648210	XR_018923.1	−0.404442095	10.47351845	−2.925088264	0.005662083	0.328639571
291	GRB14	growth factor receptor−bound protein 14	2888	NM_004490.2	0.107052844	6.780507016	2.924443935	0.00567171	0.328639571
292	UGCG	UDP−glucose ceramide glucosyltransferase	7357	NM_003358.1	0.348634208	7.672012128	2.923971985	0.005678771	0.328639571
293	BCR	breakpoint cluster region	613	NM_021574.2	0.074331836	6.624980953	2.923844748	0.005680676	0.328639571
294	KCNJ14	″potassium inwardly−rectifying channel, subfamily J, member 14″	3770	NM_170720.1	0.076087153	6.618374084	2.922939338	0.00569425	0.328639571
295	NDFIP1	Nedd4 family interacting protein 1	80762	NM_030571.2	−0.171766084	7.624592155	−2.921558194	0.005715014	0.328719859
296	LOC644131	−	644131	XR_018325.1	−0.244724622	7.573926707	−2.919946228	0.005739338	0.329003667
297	SPN	sialophorin	6693	NM_001030288.1	0.34574151	8.247211489	2.914907743	0.005815992	0.332014809
298	RBPJ	recombination signal binding protein for immunoglobulin kappa J region	3516	NM_203284.1	0.254681218	8.653397128	2.913617187	0.00583578	0.332014809
299	NULL	NULL	NULL	BM677010	−0.224636988	6.908713574	−2.911624953	0.00586645	0.332014809

【表２－２４】

Limma
表2－24

No.	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	AveExpr	limma_t	limma_pvalue	limma_adjpvalue
300	SEH1L	SEH1-like (S. cerevisiae)	81929	NM_031216.3	−0.083010039	6.697203672	−2.911306261	0.005871371	0.332014809

【００４４】

表３　SAMで選択された上位３００の遺伝子のリスト

【表３－１】

SAM
表3-1

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
1	1400240	LDHB	lactate dehydrogenase B	3945	NM_002300.4	−0.605485777	0.657250037	0	7.20E−05
2	4830255	DPP4	dipeptidyl-peptidase 4	1803	NM_001935.3	−0.307400655	0.808096419	0	9.00E−05
3	3990608	MAN2A1	"mannosidase, alpha, class 2A, member 1"	4124	NM_002372.2	−0.327379686	0.796982701	0	0.00010897
4	1780719	PTGES3	prostaglandin E synthase 3 (cytosolic)	10728	NM_006601.4	−0.528677962	0.693189659	0	0.000118989
5	3130370	ZNF83	zinc finger protein 83	55769	NM_018300.2	−0.30567958	0.809061019	0	0.000143446
6	3130477	C7orf28A	chromosome 7 open reading frame 28A	51622	XM_001133729.1	−0.383441629	0.766606625	0	0.000185113
7	4220731	P4HA1	"prolyl 4-hydroxylase, alpha polypeptide I"	5033	NM_000917.2	−0.307837835	0.807851578	0	0.00019578
8	3440189	ZBTB20	zinc finger and BTB domain containing 20	26137	NM_015642.3	−0.287117754	0.819537713	0	0.000201968
9	1780709	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	10521	NM_030881.2	−0.443292451	0.735454273	0	0.000244932
10	160253	MBNL1	muscleblind-like (Drosophila)	4154	NM_207295.1	−0.320695796	0.800683623	0	0.000260019
11	510209	LOC643310	−	643310	XM_926656.1	−0.395581648	0.760182834	0	0.000271806
12	5900129	CROP	−	51747	NM_006107.2	−0.443849065	0.735170578	0	0.000277699
13	7320424	HNRPA1L-2	−	664709	NR_002944.2	−0.432630765	0.740909499	0	0.000287011

【表３－２】

SAM
表3-2

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
14	6110630	HIST1H2BK	"histone cluster 1, H2bk"	85236	NM_080593.1	0.379122401	1.300550483	2.69772513	7.89E-05
15	6420446	CMPK1	"cytidine monophosphate (UMP-CMP) kinase 1, cytosolic"	51727	NM_016308.1	-0.398631213	0.758577658	4.54353706	0.000348715
16	6590484	NAP1L1	nucleosome assembly protein 1-like 1	4673	NM_139207.1	-0.357418466	0.780560051	4.54353706	0.000349599
17	1110091	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	7073	NM_001033925.1	-0.233908998	0.850327795	4.54353706	0.000350012
18	150706	UGP2	UDP-glucose pyrophosphorylase 2	7360	NM_006759.3	-0.347146055	0.786137702	4.54353706	0.000409771
19	6940176	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	10096	NM_005721.3	-0.459963089	0.727004859	4.54353706	0.000412423
20	2100594	BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)	9184	NM_004725.2	-0.303162523	0.810473813	4.54353706	0.000416549
21	3130296	AMY2A	"amylase, alpha 2A (pancreatic)"	279	NM_000699.2	-0.282794372	0.821997339	4.54353706	0.000476957
22	840064	LOC645489	-	645489	XM_928514.1	-0.199041088	0.871129382	4.54353706	0.000500236
23	1570491	hCG_2015956	-	648000	XM_371757.5	-0.31840088	0.801958296	4.54353706	0.00054479
24	520706	UBE4A	"ubiquitination factor E4A (UFD2 homolog, yeast)"	9354	NM_004788.2	-0.230502672	0.852337864	4.54353706	0.000554868
25	990315	TCP1	t-complex 1	6950	NM_030752.2	-0.256767834	0.83696092	4.54353706	0.000575613
26	4880521	CDC16	cell division cycle 16 homolog (S. cerevisiae)	8881	NM_003903.3	-0.34380491	0.787960431	4.54353706	0.000582037

【表３－３】

SAM
表3-3

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
27	3290689	C14orf166	chromosome 14 open reading frame 166	51637	NM_016039.1	−0.321385016	0.800301204	4.54353706	0.000582449
28	6940433	STAT5B	signal transducer and activator of transcription 5B	6777	NM_012448.3	−0.24015242	0.846655859	4.54353706	0.000583746
29	4050195	FAM10A4	"family with sequence similarity 10, member A4 pseudogene"	145165	NR_002183.1	−0.370567771	0.773478035	4.54353706	0.000601073
30	6110091	WSB1	WD repeat and SOCS box-containing 1	26118	NM_134265.2	−0.29256262	0.816450531	4.54353706	0.000625825
31	840358	EXOSC10	exosome component 10	5394	NM_002685.2	−0.226165883	0.854903874	4.54353706	0.000671087
32	4570255	LEF1	lymphoid enhancer-binding factor 1	51176	NM_016269.2	−0.599827856	0.659832683	4.54353706	0.000692126
33	7550358	NELL2	NEL-like 2 (chicken)	4753	NM_006159.1	−0.537157632	0.689127277	4.54353706	0.000734795
34	1010315	LINS1	lines homolog 1 (Drosophila)	55180	NM_001040614.1	−0.286168405	0.820077178	4.54353706	0.000818423
35	4210129	ELOVL5	"ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like,	60481	NM_021814.3	−0.284710319	0.820906424	4.54353706	0.0008186
36	5420053	CCT6P1	"chaperonin containing TCP1, subunit 6 (zeta) pseudogene 1"	643253	NR_003110.2	−0.281922881	0.822494034	4.54353706	0.000831565
37	730379	LOC388621	-	388621	XM_941195.2	−0.448108038	0.733003485	4.54353706	0.000873114
38	6550600	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	4609	NM_002467.3	−0.337363684	0.791486318	4.54353706	0.000906648
39	5860465	USP9Y	"ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)"	8287	NM_004654.3	−0.094524102	0.936581144	4.886445518	0.000963284

【表３－４】

SAM
表3-4

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
40	1500201	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	3183	NM_031314.1	−0.397999182	0.758910057	4.886445518	0.000981436
41	6180497	GOLGA8C	"golgi autoantigen, golgin subfamily a, 8C"	400304	XM_375152.3	−0.242008817	0.84556712	4.886445518	0.000987093
42	3360228	RPS20	ribosomal protein S20	6224	NM_001023.2	−0.162977591	0.893179726	4.886445518	0.000998468
43	6110747	GIMAP2	"GTPase, IMAP family member 2"	26157	NM_015660.2	−0.45531031	0.729353278	4.886445518	0.001029408
44	6980253	PTPLB	"protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b"	201562	NM_198402.2	−0.336175973	0.792138184	4.886445518	0.001054809
45	2570358	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	9987	NM_031372.1	−0.382998221	0.766842276	4.886445518	0.001060879
46	2360630	FDFT1	farnesyl-diphosphate farnesyltransferase 1	2222	NM_004462.3	−0.242595956	0.845223066	4.886445518	0.001090582
47	6420309	FAM134B	"family with sequence similarity 134, member B"	54463	NM_001034850.1	−0.358481173	0.779985293	4.886445518	0.001129538
48	2370041	LRRN3	leucine rich repeat neuronal 3	54674	NM_018334.3	−0.383213794	0.7667277	4.886445518	0.001144625
49	3180438	RPS3A	ribosomal protein S3A	6189	NM_001006.3	−0.215689394	0.861134567	4.886445518	0.001155882
50	1990487	XRN1	5'-3' exoribonuclease 1	54464	NM_019001.2	−0.23813416	0.847841118	4.886445518	0.001159241
51	2230538	LRRN3	leucine rich repeat neuronal 3	54674	NM_001099660.1	−0.625504431	0.6481931	4.886445518	0.001186233
52	6900750	HDAC2	histone deacetylase 2	3066	NM_001527.2	−0.308059644	0.807727384	4.886445518	0.001210868

【表３－５】

SAM
表3-5

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
53	150672	KLHL7	kelch-like 7 (Drosophila)	55975	NM_001031710.1	−0.155913324	0.897563974	4.886445518	0.001219177
54	2970370	PCDH17	protocadherin 17	27253	NM_014459.2	−0.527638621	0.693689224	4.886445518	0.001244342
55	2640255	NULL	NULL	641848	XM_935588.1	−0.645965338	0.639065035	4.886445518	0.001318364
56	2570112	ABLIM1	actin binding LIM protein 1	3983	NM_006720.3	−0.4799407	0.717007095	4.886445518	0.0013407
57	5910463	PKIA	"protein kinase (cAMP-dependent, catalytic) inhibitor alpha"	5569	NM_006823.2	−0.254561014	0.838242158	4.886445518	0.001347006
58	5560465	NOP56	NOP56 ribonucleoprotein homolog (yeast)	10528	NM_006392.2	−0.266935568	0.831082978	4.886445518	0.001404762
59	2600204	SACM1L	SAC1 suppressor of actin mutations 1-like (yeast)	22908	NM_014016.2	−0.262966982	0.83337228	4.886445518	0.00145079
60	4050328	DSC1	desmocollin 1	1823	NM_004948.2	−0.247522067	0.842341957	4.886445518	0.001456801
61	6860148	SLC9A6	"solute carrier family 9 (sodium/hydrogen exchanger), member 6"	10479	NM_001042537.1	−0.17456976	0.886031712	5.912822202	0.001472713
62	5960072	NULL	NULL	NULL	BY797688	−0.097047292	0.934944549	5.912822202	0.0015
63	3420068	HAT1	histone acetyltransferase 1	8520	NM_003642.2	−0.268653366	0.830094007	5.912822202	0.00151491
64	2570725	PPCS	phosphopantothenoylcysteine synthetase	79717	NM_001077447.1	−0.310167811	0.806547938	5.912822202	0.001552275
65	2680102	NULL	NULL	649555	XM_945579.1	−0.269621337	0.829537245	5.912822202	0.001556695

【表３－６】

SAM
表3-6

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
66	1690605	NULL	NULL	649088	XM_938168.1	−0.257637488	0.836456553	5.912822202	0.001568541
67	2650601	GPBP1L1	GC−rich promoter binding protein 1−like 1	60313	NM_021639.3	−0.185092124	0.879592907	5.912822202	0.001609618
68	4540356	UFM1	ubiquitin−fold modifier 1	51569	NM_016617.1	−0.290998607	0.817336118	5.912822202	0.001621405
69	2120468	C10orf58	chromosome 10 open reading frame 58	84293	NM_032333.2	−0.327354271	0.79699674	5.912822202	0.001658475
70	6760017	YY1	YY1 transcription factor	7528	NM_003403.3	−0.328869705	0.79616	5.912822202	0.001672796
71	450195	Sept7	septin 7	989	NM_001788.4	−0.31815245	0.802096404	5.912822202	0.001692185
72	6510433	SNORA33	"small nucleolar RNA, H/ACA box 33"	594839	NR_002436.1	−0.186113851	0.878970194	5.912822202	0.001704385
73	580014	C12orf43	chromosome 12 open reading frame 43	64897	NM_022895.1	−0.20852646	0.865420704	5.912822202	0.001772749
74	5340487	MTRR	5−methyltetrahydrofolate−homocysteine methyltransferase reductase	4552	NM_024010.1	−0.355492388	0.781602839	5.912822202	0.001833805
75	2370372	NULL	NULL	NULL	CX782759	−0.206252167	0.866786046	5.912822202	0.001846299
76	60053	RPL11	ribosomal protein L11	6135	NM_000975.2	−0.156372832	0.897278139	5.912822202	0.00185231
77	4050609	DNAJA2	"DnaJ (Hsp40) homolog, subfamily A, member 2"	10294	NM_005880.2	−0.266568167	0.831294651	5.912822202	0.001899988
78	4560088	LOC439949	−	439949	XM_001129241.1	−0.469330965	0.722299479	5.912822202	0.001914722

【表３－７】

SAM
表3-7

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
79	5860327	PRPF18	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	8559	NM_003675.3	−0.26670234	0.831217343	5.912822202	0.001963873
80	5810619	TADA1L	"transcriptional adaptor 1 (HFI1 homolog, yeast)-like"	117143	NM_053053.2	−0.16203449	0.893763795	5.912822202	0.001994991
81	6510053	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	328	NM_080649.1	−0.205907613	0.866993082	5.912822202	0.002050743
82	5900482	HMGB2	high-mobility group box 2	3148	NM_002129.2	−0.440289057	0.736986932	5.912822202	0.002095945
83	5720300	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	10146	NM_005754.2	−0.241645343	0.84578018	7.047118706	0.002177393
84	7650669	TBC1D4	"TBC1 domain family, member 4"	9882	NM_014832.2	−0.247692111	0.84224268	7.047118706	0.002197843
85	6380673	TUBE1	"tubulin, epsilon 1"	51175	NM_016262.3	−0.138726153	0.908320815	7.047118706	0.00219802
86	5310736	FAM162A	"family with sequence similarity 162, member A"	26355	NM_014367.3	−0.324511803	0.79856857	7.047118706	0.002198491
87	7400343	STX2	syntaxin 2	2054	NM_001980.2	−0.258793675	0.835786479	7.047118706	0.00220633
88	3060040	PABPC1	"poly(A) binding protein, cytoplasmic 1"	26986	NM_002568.3	−0.393451244	0.761306212	7.047118706	0.002289604
89	110195	LOC646197	–	646197	XM_929153.1	−0.239784184	0.846871989	7.047118706	0.002296146
90	2120017	NOL8	nucleolar protein 8	55035	NM_017948.4	−0.189491166	0.876914952	7.047118706	0.002304809
91	6860259	DSC1	desmocollin 1	1823	NM_004948.2	−0.207019876	0.866324921	7.047118706	0.002379125

【表３－８】

SAM
表3-8

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
92	4860762	INPP4B	"inositol polyphosphate-4-phosphatase, type II, 105kDa"	8821	NM_003866.1	-0.281061337	0.822985355	7.047118706	0.002406412
93	6420730	RPL9	ribosomal protein L9	6133	NM_001024921.2	-0.56653985	0.675234325	7.047118706	0.002410655
94	4560270	PTPLB	"protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b"	201562	NM_198402.2	-0.266540406	0.831310647	7.047118706	0.002436292
95	1090692	GPBP1	GC-rich promoter binding protein 1	65056	NM_022913.1	-0.264875927	0.832270308	7.047118706	0.002457744
96	7150132	PNN	"pinin, desmosome associated protein"	5411	NM_002687.3	-0.314789132	0.803968492	7.047118706	0.002498645
97	2600600	TFIP11	tuftelin interacting protein 11	24144	NM_001008697.1	-0.334180963	0.793234338	7.047118706	0.002502416
98	6560164	RPS3A	ribosomal protein S3A	6189	NM_001006.3	-0.224696704	0.855774915	7.047118706	0.002545674
99	1070475	RPL11	ribosomal protein L11	6135	NM_000975.2	-0.145832491	0.903857666	7.047118706	0.002576674
100	1990468	ADD3	adducin 3 (gamma)	120	NM_001121.2	-0.331309202	0.794814886	7.047118706	0.002626355
101	4900343	MORF4L1	mortality factor 4 like 1	10933	NM_206839.1	-0.24904666	0.841452268	7.047118706	0.002631424
102	6510619	NAE1	NEDD8 activating enzyme E1 subunit 1	8883	NM_001018160.1	-0.29276015	0.816338752	7.047118706	0.002737683
103	3440670	NULL	NULL	402251	XM_377933.3	-0.279019599	0.824150889	7.047118706	0.002770038
104	5220195	UQCRC2	ubiquinol-cytochrome c reductase core protein II	7385	NM_003366.2	-0.306901413	0.808376108	7.047118706	0.002770156

【表３－９】

SAM
表3-9

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
105	7380707	ZFAND1	"zinc finger, AN1-type domain 1"	79752	NM_024699.1	−0.254784176	0.838112505	7.047118706	0.002804514
106	4780450	ATP5C1	"ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1"	509	NM_005174.2	−0.369186445	0.774218966	7.047118706	0.002824257
107	5420095	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	4609	NM_002467.3	−0.38321124	0.766729057	7.047118706	0.002915665
108	7040482	LOC642934	-	642934	XM_942991.2	−0.452151346	0.73095204	7.047118706	0.002919319
109	4610138	CAPZA1	"capping protein (actin filament) muscle Z-line, alpha 1"	829	NM_006135.1	−0.36644329	0.775692474	7.047118706	0.002961398
110	3420128	AP3M2	"adaptor-related protein complex 3, mu 2 subunit"	10947	NM_006803.2	−0.269660186	0.829514908	7.047118706	0.002963637
111	3130669	SATB1	SATB homeobox 1	6304	NM_002971.2	−0.216171431	0.860846891	7.047118706	0.002982438
112	2570132	CLEC2D	"C-type lectin domain family 2, member D"	29121	NM_001004419.2	−0.163087579	0.893111634	7.047118706	0.002982614
113	5360619	CDC16	cell division cycle 16 homolog (S. cerevisiae)	8881	NM_001078645.1	−0.262987116	0.833360649	7.047118706	0.003044024
114	2680082	RPL7	ribosomal protein L7	6129	NM_000971.3	−0.354882331	0.781933417	7.047118706	0.003051686
115	2340632	INADL	InaD-like (Drosophila)	10207	NM_176878.1	−0.241811563	0.845682739	7.047118706	0.003052275
116	2060050	NULL	NULL	NULL	BM932227	−0.116682268	0.92230622	7.047118706	0.003063178
117	6900044	AMN1	antagonist of mitotic exit network 1 homolog (S. cerevisiae)	196394	NM_207337.1	−0.126543905	0.916023233	7.047118706	0.003064298

【表３－１０】

SAM
表3-10

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
118	5900731	SFRS12	"splicing factor, arginine/serine-rich 12"	140890	NM_001077199.1	-0.290167988	0.817806827	7.047118706	0.003068423
119	4760243	NULL	NULL	648210	XR_018923.1	-0.404442095	0.755528407	7.047118706	0.00317421
120	7550341	HIGD1A	"HIG1 domain family, member 1A"	25994	NM_014056.1	-0.279289648	0.823996635	7.047118706	0.003208746
121	380575	RPL23	ribosomal protein L23	9349	NM_000978.3	-0.338815803	0.790690062	7.047118706	0.003237093
122	6650594	ATP11B	"ATPase, class VI, type 11B"	23200	NM_014616.1	-0.252853775	0.839234694	7.047118706	0.00330976
123	3780465	SMARCA5	"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	8467	NM_003601.2	-0.115124978	0.923302323	7.047118706	0.003318835
124	6840605	ATM	ataxia telangiectasia mutated	472	NM_000051.3	-0.361381652	0.77841874	7.047118706	0.003336162
125	670209	ZNF700	zinc finger protein 700	90592	NM_144566.1	-0.134476397	0.911000407	7.047118706	0.003349717
126	2120307	NULL	NULL	NULL	CA847896	-0.142130207	0.90618015	7.047118706	0.003364274
127	110332	NULL	NULL	NULL	XM_378421	-0.394864244	0.760560941	7.047118706	0.003414781
128	6020598	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	5366	NM_021127.1	-0.206408928	0.866691867	9.763195707	0.003445073
129	4220307	NULL	NULL	647673	XM_936731.1	-0.504764306	0.704775508	9.763195707	0.003546617
130	3180131	hCG_1984468	-	389672	XM_933893.1	-0.387113765	0.764657839	9.763195707	0.003585337

【表３－１１】

SAM
表3-11

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
131	4570170	KIAA0947	–	23379	NM_015325.1	−0.180354486	0.882486133	9.763195707	0.003614274
132	5260161	NULL	NULL	NULL	AA532505	−0.182665342	0.881073731	9.763195707	0.003699434
133	4180142	KIAA1370	KIAA1370	56204	NM_019600.1	−0.224539294	0.855868293	9.763195707	0.003726839
134	3930561	PRKCI	"protein kinase C, iota"	5584	NM_002740.5	−0.105841727	0.929262615	9.763195707	0.003727074
135	3360100	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	3419	NM_005530.2	−0.146008756	0.903747242	9.763195707	0.003758487
136	6200747	LOC220433	–	220433	XM_941684.2	−0.448374765	0.732867979	9.763195707	0.003766914
137	2070019	UBA6	ubiquitin-like modifier activating enzyme 6	55236	NM_018227.5	−0.194843638	0.873667581	9.763195707	0.003822136
138	2810601	LEF1	lymphoid enhancer-binding factor 1	51176	NM_016269.2	−0.524099452	0.695393047	9.763195707	0.00384512
139	1010477	ADD3	adducin 3 (gamma)	120	NM_016824.3	−0.307853518	0.807842797	9.763195707	0.003857496
140	3190059	IMMT	"inner membrane protein, mitochondrial (mitofilin)"	10989	NM_001100169.1	−0.221779779	0.857506921	9.763195707	0.003863449
141	3930296	EIF1AX	"eukaryotic translation initiation factor 1A, X-linked"	1964	NM_001412.3	−0.259913717	0.835137865	9.763195707	0.00391702
142	3780670	NGLY1	N-glycanase 1	55768	NM_018297.2	−0.197659111	0.871964248	9.763195707	0.00397731
143	3930382	NMT2	N-myristoyltransferase 2	9397	NM_004808.1	−0.314300806	0.804240667	9.763195707	0.003985738

【表３－１２】

SAM
表3-12

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
144	830609	RPL5	ribosomal protein L5	6125	NM_000969.3	−0.250479654	0.840616888	9.763195707	0.003996346
145	1410603	RAB3IP	RAB3A interacting protein (rabin3)	117177	NM_001024647.2	−0.350434199	0.784348002	9.763195707	0.004009135
146	4010735	MRPL9	mitochondrial ribosomal protein L9	65005	NM_031420.2	−0.156554264	0.897165305	9.763195707	0.004017975
147	2340601	AMMECR1	"Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region	9949	NM_015365.2	−0.137410703	0.9091494	9.763195707	0.004106848
148	7610608	RP11-122C9.1	–	653702	NM_001093763.1	−0.316189323	0.803188588	9.763195707	0.004139616
149	3120309	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	328	NM_001641.2	−0.196094396	0.872910474	9.763195707	0.004145863
150	4540689	ANKRD10	ankyrin repeat domain 10	55608	NM_017664.2	−0.170575575	0.888488141	9.763195707	0.004158887
151	4590241	CNOT7	"CCR4-NOT transcription complex, subunit 7"	29883	NM_013354.5	−0.212744803	0.862893968	9.763195707	0.004202793
152	5820202	LOC644131	–	644131	XR_018325.1	−0.244724622	0.843976877	9.763195707	0.004242928
153	1450471	FAM153B	"family with sequence similarity 153, member B"	202134	XM_371783.3	−0.346939529	0.786250247	9.763195707	0.00428542
154	6770673	SOCS2	suppressor of cytokine signaling 2	8835	NM_003877.3	−0.524515864	0.695192362	9.763195707	0.004300625
155	160047	LOC389787	–	389787	XM_497072.2	−0.49206406	0.711007134	9.763195707	0.00434571
156	160079	MGC10997	–	84741	NR_001565.1	−0.229371406	0.853006473	9.763195707	0.004359913

【表３－１３】

SAM
表3-13

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
157	460386	PTMA	"prothymosin, alpha"	5757	NM_001099285.1	−0.590989351	0.66388748	9.763195707	0.004434111
158	990044	KIAA1147	KIAA1147	57189	XM_001130020.1	−0.162506963	0.893471142	9.763195707	0.004435761
159	780402	RTN4	reticulon 4	57142	NM_020532.4	−0.274156562	0.826933624	9.763195707	0.00448562
160	4040113	NULL	NULL	643272	XM_926633.1	−0.171519101	0.887907258	9.763195707	0.004516914
161	4860431	NBPF14	"neuroblastoma breakpoint family, member 14"	25832	NM_015383.1	−0.189228519	0.877074612	9.763195707	0.004533652
162	4830100	HSP90AB1	"heat shock protein 90kDa alpha (cytosolic), class B member 1"	3326	NM_007355.2	−0.346277597	0.786611074	9.763195707	0.004560644
163	3440709	NULL	NULL	NULL	BM677010	−0.224636988	0.855810338	9.763195707	0.004581447
164	460196	HERC2P3	hect domain and RLD 2 pseudogene 3	283755	XM_001128358.1	−0.175308013	0.88557843	9.763195707	0.004591702
165	2760553	UBA3	ubiquitin-like modifier activating enzyme 3	9039	NM_198197.1	−0.187898967	0.877883274	9.763195707	0.004591761
166	5130674	CSE1L	CSE1 chromosome segregation 1-like (yeast)	1434	NM_001316.2	−0.226954625	0.854436614	9.763195707	0.004607379
167	5310747	PSIP1	PC4 and SFRS1 interacting protein 1	11168	NM_033222.2	−0.298779917	0.812939606	9.763195707	0.004616219
168	270544	NR2C1	"nuclear receptor subfamily 2, group C, member 1"	7181	NM_003297.1	−0.155303368	0.897943535	9.763195707	0.004649104
169	430577	DDX50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	79009	NM_024045.1	−0.230181634	0.852527552	9.763195707	0.004696605

【表３－１４】

SAM
表3-14

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
170	5890661	GIMAP2	"GTPase, IMAP family member 2"	26157	NM_015660.2	−0.289089079	0.818418647	9.763195707	0.004754008
171	5360692	LY9	lymphocyte antigen 9	4063	NM_002348.2	−0.25013536	0.840817522	9.763195707	0.004774694
172	6510246	NULL	NULL	648210	XR_018923.1	−0.402275661	0.756663804	9.763195707	0.004787482
173	7510379	SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	26278	NM_014363.3	−0.121241812	0.919395932	9.763195707	0.004823904
174	1980201	WWP1	WW domain containing E3 ubiquitin protein ligase 1	11059	NM_007013.3	−0.293252037	0.816060469	9.763195707	0.004916018
175	4590333	DHX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15	1665	NM_001358.2	−0.188453408	0.87754596	9.763195707	0.004949375
176	770021	PRKRA	"protein kinase, interferon-inducible double stranded RNA dependent activator"	8575	NM_003690.3	−0.229357783	0.853014528	9.763195707	0.005003418
177	4850097	RPLP2	"ribosomal protein, large, P2"	6181	NM_001004.2	−0.118887297	0.920897635	9.763195707	0.005017739
178	4250154	NULL	NULL	648749	XM_937834.2	−0.061658345	0.958162101	9.763195707	0.005056518
179	1440121	tcag7.1261	-	645968	XM_928934.1	−0.360761142	0.778753613	9.763195707	0.005057756
180	4860066	NULL	NULL	647346	XM_936495.2	−0.209955699	0.864563779	9.763195707	0.005069543
181	6280521	NULL	NULL	648399	XM_937448.1	−0.092941768	0.937608941	9.763195707	0.005080504
182	7000377	PHIP	pleckstrin homology domain interacting protein	55023	NM_017934.4	−0.262231952	0.833796978	9.763195707	0.005190653

【表３－１５】

SAM
表3-15

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
183	6100288	Sept15	-	9403	NM_004261.3	−0.282927999	0.821921206	9.763195707	0.005198963
184	2600035	NCL	nucleolin	4691	NM_005381.2	−0.219773695	0.858700124	9.763195707	0.00521847
185	2260168	NULL	NULL	731640	XM_001133089.1	−0.328163712	0.796549701	9.763195707	0.005355375
186	6900634	CD69	CD69 molecule	969	NM_001781.1	−0.483558921	0.715211123	9.763195707	0.005374882
187	1780348	FH	fumarate hydratase	2271	NM_000143.2	−0.232880465	0.850934231	9.763195707	0.005384371
188	6280408	TTN	titin	7273	NM_003319.3	−0.519301868	0.697709379	9.763195707	0.005433758
189	60553	NDFIP1	Nedd4 family interacting protein 1	80762	NM_030571.2	−0.171766084	0.887755265	9.763195707	0.005457685
190	4880204	SPRYD5	SPRY domain containing 5	84767	NM_032681.1	−0.301606617	0.811348358	9.763195707	0.005479196
191	620450	RNASEH2B	″ribonuclease H2, subunit B″	79621	NM_024570.1	−0.267258493	0.830896974	9.763195707	0.005515794
192	2710653	FBXO38	F−box protein 38	81545	NM_030793.3	−0.149047116	0.901845925	9.763195707	0.005532001
193	4610681	LOC653658	-	653658	XM_939687.2	−0.384309209	0.766145757	9.763195707	0.005535596
194	4850133	SNRPN	small nuclear ribonucleoprotein polypeptide N	6638	NM_022806.2	−0.341806565	0.789052629	9.763195707	0.005543612
195	1850300	TC2N	″tandem C2 domains, nuclear″	123036	NM_152332.3	−0.236871126	0.848583701	9.763195707	0.005559111

【表３－１６】

SAM
表3-16

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
196	3120075	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	7072	NM_022173.1	−0.154497679	0.898445141	9.763195707	0.005559288
197	6130538	PFN2	profilin 2	5217	NM_053024.2	−0.101946483	0.931774993	9.763195707	0.005570898
198	3190541	ABCA10	"ATP-binding cassette, sub-family A (ABC1), member 10"	10349	NM_080282.3	−0.111376806	0.925704214	9.763195707	0.00557302
199	6590441	TRIP12	thyroid hormone receptor interactor 12	9320	NM_004238.1	−0.196624966	0.872589509	9.763195707	0.005598244
200	2190390	NCOA1	nuclear receptor coactivator 1	8648	NM_147223.2	−0.208822548	0.865243109	9.763195707	0.005617751
201	3610521	PCDHGB6	"protocadherin gamma subfamily B, 6"	56100	NM_018926.2	0.176789549	1.130365665	11.63540578	0.00016649
202	4150408	P2RY2	"purinergic receptor P2Y, G-protein coupled, 2"	5029	NM_002564.2	0.182075591	1.134514927	11.63540578	0.000175978
203	4810072	TUSC2	tumor suppressor candidate 2	11334	NM_007275.1	0.162628207	1.119324394	11.63540578	0.000383074
204	2640025	HP	haptoglobin	3240	NM_005143.2	0.40681683	1.325757427	11.63540578	0.000429338
205	3890315	ERVWE1	"endogenous retroviral family W, env(C7), member 1"	30816	NM_014590.3	−0.11912978	0.920742867	11.63540578	0.005684052
206	6860615	LOC147804	-	147804	NR_003148.2	−0.199498342	0.870853326	11.63540578	0.005685349
207	7380068	CNBP	"CCHC-type zinc finger, nucleic acid binding protein"	7555	NM_003418.1	−0.327720874	0.796794242	11.63540578	0.005735207
208	6660286	INTS8	integrator complex subunit 8	55656	NM_017864.2	−0.26616918	0.831524583	11.63540578	0.005746818

【表３－１７】

SAM
表3-17

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
209	6450538	TCERG1	transcription elongation regulator 1	10915	NM_006706.3	−0.153163323	0.899276502	11.63540578	0.00581695
210	3140047	CROP	−	51747	NM_016424.3	−0.279622544	0.823806524	11.63540578	0.005835278
211	3830136	NACAP1	nascent−polypeptide−associated complex alpha polypeptide pseudogene 1	83955	NR_002182.1	−0.386755375	0.764847816	11.63540578	0.005916077
212	3800707	XPO4	exportin 4	64328	NM_022459.3	−0.217365077	0.860134944	11.63540578	0.005991513
213	5700670	WIPF1	″WAS/WASL interacting protein family, member 1″	7456	NM_003387.3	−0.282049908	0.822421618	11.63540578	0.006078678
214	2230167	LOC653773	−	653773	XM_938755.2	−0.368995191	0.774321609	11.63540578	0.006078736
215	4640739	NULL	NULL	NULL	AL120241	−0.069719279	0.952823381	11.63540578	0.006097065
216	6650672	ZNF439	zinc finger protein 439	90594	NM_152262.2	−0.168089512	0.89002051	11.63540578	0.006187294
217	7400376	RABL2A	″RAB, member of RAS oncogene family−like 2A″	11159	NM_013412.1	−0.178370764	0.883700396	11.63540578	0.006256129
218	6020273	RPS4Y2	″ribosomal protein S4, Y−linked 2″	140032	NM_001039567.2	−0.29587893	0.814575919	11.63540578	0.006258428
219	6560564	PRKCA	″protein kinase C, alpha″	5578	NM_002737.2	−0.258004675	0.83624369	11.63540578	0.006276462
220	1300687	NULL	NULL	731950	XR_016039.1	−0.061135983	0.958509089	11.63540578	0.006280823
221	1980626	SMARCA5	″SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	8467	NM_003601.2	−0.146115776	0.903680204	11.63540578	0.006412188

【表３－１８】

SAM
表3-18

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
222	3370112	RPN2	ribophorin II	6185	NM_002951.2	−0.275150971	0.826363839	11.63540578	0.006430752
223	6270148	AK5	adenylate kinase 5	26289	NM_012093.2	−0.119581494	0.920454623	11.63540578	0.006481612
224	6620356	ARPP-19	–	10776	NM_006628.4	−0.261668585	0.834122636	11.63540578	0.006618753
225	6370435	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	2113	NM_005238.2	−0.467750348	0.723091264	11.63540578	0.006673916
226	1190064	UGT2B7	"UDP glucuronosyltransferase 2 family, polypeptide B7"	7364	XM_001128725.1	−0.170236569	0.888696943	11.63540578	0.006715523
227	1570292	NULL	NULL	NULL	AI807878	−0.087151047	0.941379899	11.63540578	0.006735266
228	2640551	CMPK1	"cytidine monophosphate (UMP-CMP) kinase 1, cytosolic"	51727	NM_016308.1	−0.272595837	0.827828695	11.63540578	0.006738036
229	2570328	TRIB2	tribbles homolog 2 (Drosophila)	28951	NM_021643.1	−0.296783847	0.814065144	11.63540578	0.006749057
230	5720703	AKTIP	AKT interacting protein	64400	NM_022476.2	−0.132110131	0.912495829	11.63540578	0.006757485
231	7000474	GARNL1	GTPase activating Rap/RanGAP domain-like 1	253959	NM_194301.2	−0.175348366	0.88555366	11.63540578	0.006769861
232	1990390	RAB3IP	RAB3A interacting protein (rabin3)	117177	NM_175624.2	−0.152503427	0.89968793	11.63540578	0.006809936
233	1410246	BBS2	Bardet-Biedl syndrome 2	583	NM_031885.2	−0.21311697	0.862671399	11.63540578	0.006841113
234	5910543	GLOD4	glyoxalase domain containing 4	51031	NM_016080.2	−0.177207323	0.884413331	11.63540578	0.006900106

【表３－１９】

SAM
表3-19

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
235	5360204	NMD3	NMD3 homolog (S. cerevisiae)	51068	NM_015938.3	−0.201253758	0.86979435	11.63540578	0.007013673
236	3710048	NULL	NULL	731895	XM_001133620.1	−0.292574951	0.816443553	11.63540578	0.007052393
237	2900039	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break	7520	NM_021141.2	−0.210035123	0.864516184	11.63540578	0.007062176
238	6770563	NULL	NULL	650215	XR_018889.1	−0.218802016	0.859278667	11.63540578	0.00715541
239	1820300	CTSO	cathepsin O	1519	NM_001334.2	−0.231977107	0.851467219	11.63540578	0.007180693
240	940398	EIF3M	"eukaryotic translation initiation factor 3, subunit M"	10480	NM_006360.3	−0.395462504	0.760245616	11.63540578	0.007189062
241	3940358	OSBPL8	oxysterol binding protein-like 8	114882	NM_001003712.1	−0.261246813	0.834366527	11.63540578	0.007193482
242	6650161	GNA13	"guanine nucleotide binding protein (G protein), alpha 13"	10672	NM_006572.3	−0.380533537	0.76815346	11.63540578	0.007222006
243	2100292	RBBP7	retinoblastoma binding protein 7	5931	NM_002893.2	−0.173081269	0.886946341	11.63540578	0.007230669
244	6020066	NULL	NULL	651202	XM_940333.2	−0.466560508	0.723687868	11.63540578	0.007345238
245	6770315	LOC391656	−	391656	XM_373027.4	−0.243291277	0.844815801	11.63540578	0.00737612
246	70753	C9orf123	chromosome 9 open reading frame 123	90871	NM_033428.1	−0.214876999	0.861619616	11.63540578	0.007418199
247	7330014	SNX4	sorting nexin 4	8723	NM_003794.2	−0.223828966	0.856289793	11.63540578	0.007451379

【表３－２０】

SAM
表3-20

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
248	6020575	NNT	nicotinamide nucleotide transhydrogenase	23530	NM_012343.3	−0.191702435	0.875571903	11.63540578	0.007520215
249	7200021	CUL4A	cullin 4A	8451	NM_003589.2	−0.244754746	0.843959254	11.63540578	0.007524576
250	7150554	LCOR	ligand dependent nuclear receptor corepressor	84458	NM_032440.1	−0.293176479	0.816103209	11.63540578	0.007535596
251	3850278	NULL	NULL	641849	XM_935589.1	−0.303375497	0.810354178	11.63540578	0.007557638
252	2190379	NULL	NULL	390856	XM_938867.1	−0.244649266	0.844020961	11.63540578	0.00755976
253	3990112	CAST	calpastatin	831	NM_001042445.1	−0.280052769	0.823560894	11.63540578	0.007623645
254	7000521	PRPS2	phosphoribosyl pyrophosphate synthetase 2	5634	NM_001039091.1	−0.203904286	0.868197825	11.63540578	0.007658416
255	620546	RRAS2	related RAS viral (r−ras) oncogene homolog 2	22800	NM_012250.3	−0.155953995	0.897538671	11.63540578	0.007705976
256	6760670	C7orf28B	chromosome 7 open reading frame 28B	221960	XM_001126212.1	−0.202393059	0.869107741	11.63540578	0.007751061
257	770128	L3MBTL3	l(3)mbt−like 3 (Drosophila)	84456	NM_032438.1	−0.161561418	0.894056916	11.63540578	0.007767798
258	6590646	FAM26F	"family with sequence similarity 26, member F"	441168	NM_001010919.1	−0.364528742	0.776722551	11.63540578	0.007768152
259	2030767	CD48	CD48 molecule	962	NM_001778.2	−0.244627443	0.844033729	11.63540578	0.007834807
260	3170020	DGKA	"diacylglycerol kinase, alpha 80kDa"	1606	NM_201554.1	−0.286024075	0.820159224	11.63540578	0.007836752

【表３－２１】

SAM
表3-21

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
261	5820392	CCT6A	"chaperonin containing TCP1, subunit 6A (zeta 1)"	908	NM_001009186.1	−0.24460782	0.844045209	13.42189746	0.007899045
262	2760068	NULL	NULL	NULL	AK023178	−0.17554108	0.885435376	13.42189746	0.008058286
263	2750367	PMAIP1	phorbol−12−myristate−13−acetate−induced protein 1	5366	NM_021127.1	−0.426578629	0.744024158	13.42189746	0.008127829
264	6580270	KRT18P31	keratin 18 pseudogene 31	646723	XR_017241.1	−0.149129275	0.901794568	13.42189746	0.008223008
265	4890292	TSHZ2	teashirt zinc finger homeobox 2	128553	NM_173485.4	−0.248756168	0.841621714	13.42189746	0.008259842
266	6400243	ABLIM1	actin binding LIM protein 1	3983	NM_001003407.1	−0.349061324	0.785094747	13.42189746	0.008281707
267	6550750	ARMC8	armadillo repeat containing 8	25852	NM_014154.2	−0.087200394	0.9413477	13.42189746	0.008333392
268	5290056	TRIM48	tripartite motif−containing 48	79097	NM_024114.2	−0.116938426	0.922142474	13.42189746	0.008404173
269	7000037	ZFAND1	"zinc finger, AN1−type domain 1"	79752	NM_024699.1	−0.243533327	0.844674072	13.42189746	0.008427098
270	1770546	ATIC	5−aminoimidazole−4−carboxamide ribonucleotide formyltransferase/IMP	471	NM_004044.4	−0.256334047	0.837212614	13.42189746	0.008437824
271	870181	LOC653314	−	653314	NM_001080544.1	−0.223215014	0.856654272	13.42189746	0.008476073
272	5550463	FARSB	"phenylalanyl−tRNA synthetase, beta subunit"	10056	NM_005687.2	−0.160949186	0.894436404	13.42189746	0.008580446
273	2690561	RPLP1	"ribosomal protein, large, P1"	6176	NM_001003.2	−0.685558024	0.621765286	13.42189746	0.008607143

【表３－２２】

SAM
表3-22

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
274	6860681	IER3IP1	immediate early response 3 interacting protein 1	51124	NM_016097.3	−0.206953948	0.866364511	13.42189746	0.008620934
275	5810435	SNAP23	"synaptosomal-associated protein, 23kDa"	8773	NM_003825.2	−0.266241158	0.831483098	13.42189746	0.008623291
276	5490403	CD1E	CD1e molecule	913	NM_001042586.1	−0.151209281	0.900495342	13.42189746	0.008811704
277	670195	NUDCD2	NudC domain containing 2	134492	NM_145266.4	−0.186890942	0.878496874	13.42189746	0.008826438
278	3460162	NULL	NULL	646900	XM_929862.1	−0.302886246	0.810629034	13.42189746	0.00883516
279	160537	KDSR	3-ketodihydrosphingosine reductase	2531	NM_002035.1	−0.165230376	0.891786103	13.42189746	0.0088971
280	1240450	CD27	CD27 molecule	939	NM_001242.4	−0.37061142	0.773454634	13.42189746	0.008948079
281	430100	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	2547	NM_001469.3	−0.202101353	0.869283488	13.42189746	0.008965229
282	360719	CD44	CD44 molecule (Indian blood group)	960	NM_000610.3	−0.236278041	0.848932621	13.42189746	0.00903041
283	520673	LRFN5	leucine rich repeat and fibronectin type III domain containing 5	145581	NM_152447.2	−0.181463688	0.881807903	13.42189746	0.009041077
284	3800678	NUP88	nucleoporin 88kDa	4927	NM_002532.3	−0.225702407	0.855178562	13.42189746	0.009061763
285	6370717	GNG10	"guanine nucleotide binding protein (G protein), gamma 10"	2790	NM_001017998.2	−0.296985545	0.81395134	13.42189746	0.00909789
286	2650653	ZNF75D	zinc finger protein 75D	7626	NM_007131.2	−0.135221715	0.910529892	13.42189746	0.009155705

【表３－２３】

SAM
表3-23

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
287	6020093	SARS	seryl-tRNA synthetase	6301	NM_006513.2	-0.201811182	0.869458346	13.42189746	0.009201968
288	5360592	NULL	NULL	729985	XM_001131964.1	-0.159755362	0.895176853	13.42189746	0.009231023
289	5960332	SLC39A10	"solute carrier family 39 (zinc transporter), member 10"	57181	NM_020342.1	-0.147299889	0.902938799	13.42189746	0.009245757
290	940500	CLDN14	claudin 14	23562	NM_012130.2	-0.153491707	0.899071834	13.42189746	0.009368576
291	7400047	LOC388344	-	388344	XM_371023.4	-0.327727336	0.796790672	13.42189746	0.009393152
292	3930689	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	1660	NM_001357.2	-0.143840193	0.905106716	13.42189746	0.009401285
293	6280524	CCNL1	cyclin L1	57018	NM_020307.2	-0.186663803	0.878635196	13.42189746	0.009567716
294	1820528	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	9061	NM_005443.4	-0.222706769	0.856956115	13.42189746	0.009667845
295	1050148	LOC653264	-	653264	XM_932721.2	-0.102751263	0.931255365	13.42189746	0.009778347
296	3830156	GTF3C3	"general transcription factor IIIC, polypeptide 3, 102kDa"	9330	NM_012086.2	-0.154434592	0.89848443	13.42189746	0.009781058
297	4590349	ACVR2A	"activin A receptor, type IIA"	92	NM_001616.3	-0.105208688	0.929670455	13.42189746	0.009897749
298	2260551	RAD21	RAD21 homolog (S. pombe)	5885	NM_006265.1	-0.356240374	0.781197711	13.42189746	0.009913602
299	6510600	MLLT10	"myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10"	8028	NM_004641.2	-0.211258659	0.863783307	13.42189746	0.009947313

【表３－２４】

SAM
表3-24

No.	プローブ ID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	SAM_FoldChange	SAM_qvalue	SAM_pvalue
300	3610348	FAM10A4	"family with sequence similarity 10, member A4 pseudogene"	145165	NR_002183.1	−0.192448279	0.875119368	13.42189746	0.009955446

【００４５】
表４　Rank Prodで選択された上位３００の遺伝子のリスト

【表４－１】

RankProd
表4-1

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
1	2480600	LOC728358	–	728358	NM_001042500.1	206.9319	0.3679	0	0
2	7150170	LOC728358	–	728358	NM_001042500.1	217.1554	0.3807	0	0
3	2970747	DEFA3	defensin, alpha 3, neutrophil-specific	1668	NM_005217.2	221.4639	0.3779	0	0
4	4540239	DEFA1	defensin, alpha 1	1667	NM_004084.2	226.007	0.387	0	0
5	5080692	HLA-A29.1	–	649853	NM_001080840.1	232.3536	0.3703	0	0
6	870477	LOC728358	–	728358	NM_001042500.1	249.17	0.3939	0	0
7	7650497	ELA2	elastase 2, neutrophil	1991	NM_001972.2	273.8273	0.4006	0	0
8	6550164	DEFA4	defensin, alpha 4, corticostatin	1669	NM_001925.1	309.0369	0.4123	0	0
9	770400	NULL	NULL	653600	XM_928349.1	324.4866	0.4475	0	0
10	1500735	CTSG	cathepsin G	1511	NM_001911.2	324.7636	0.4191	0	0
11	3890349	HIST1H4C	histone cluster 1, H4c	8364	NM_003542.3	342.3622	0.5327	0	0

【表４－２】

RankProd
表4-2

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
12	7330398	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	3126	NM_021983.4	395.251	1.5402	0	0
13	5860075	CAMP	cathelicidin antimicrobial peptide	820	NM_004345.3	426.4961	0.4888	0	0
14	7050021	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	5573	NM_002734.3	440.111	1.6574	0	0
15	4390398	LCN2	lipocalin 2	3934	NM_005564.3	468.6986	0.5216	0	0
16	4180768	ALAS2	aminolevulinate, delta-, synthase 2	212	NM_001037968.1	494.2717	0.6935	0	0
17	2690561	RPLP1	ribosomal protein, large, P1	6176	NM_001003.2	510.521	1.6083	0	0
18	4050717	MYOM2	myomesin (M-protein) 2, 165kDa	9172	NM_003970.1	521.0537	0.6829	0	0
19	3520601	MPO	myeloperoxidase	4353	NM_000250.1	552.0527	0.5121	0	0
20	1450358	HBD	hemoglobin, delta	3045	NM_000519.3	555.1003	0.636	0	0
21	620544	HLA-DRB6	major histocompatibility complex, class II, DR beta 6 (pseudogene)	3128	NR_001298.1	599.5065	1.2864	0	0
22	6660288	CCL3L1	chemokine (C-C motif) ligand 3-like 1	6349	NM_021006.4	608.9901	1.3171	0	0

【表４－３】

RankProd
表4-3

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
23	2350274	ERAF	erythroid associated factor	51327	NM_016633.2	624.2449	0.6242	0	0
24	6560376	RPS26L1	ribosomal protein S26-like 1	441502	NR_002309.1	627.4099	0.6128	0	0
25	6960195	NULL	NULL	650646	XM_942527.2	659.4889	0.6133	0	0
26	2230538	LRRN3	leucine rich repeat neuronal 3	54674	NM_001099660.1	663.6339	1.5428	0	0
27	6180743	LAIR2	leukocyte-associated immunoglobulin-like receptor 2	3904	NM_021270.2	674.7421	0.6789	0	0
28	2230601	UTS2	urotensin 2	10911	NM_021995.1	682.1642	1.3557	0	0
29	6590377	RPS26	ribosomal protein S26	6231	NM_001029.3	684.9927	0.6457	0	0
30	2640255	NULL	NULL	641848	XM_935588.1	694.3737	1.5648	0	0
31	5890730	RPS26L	-	400156	XR_017804.1	698.1257	0.6497	0	0
32	3520102	CCL4L1	chemokine (C-C motif) ligand 4-like 1	9560	NM_001001435.2	700.5086	1.4296	0	0
33	6860048	UTS2	urotensin 2	10911	NM_021995.1	717.5432	1.4062	0	0

【表４－４】

RankProd
表4-4

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
34	5260484	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	3123	NM_002124.1	718.7641	0.7652	0	0
35	50278	LAIR2	leukocyte-associated immunoglobulin-like receptor 2	3904	NM_002288.3	739.419	0.6969	0	0
36	4570255	LEF1	lymphoid enhancer-binding factor 1	51176	NM_016269.2	762.7748	1.5155	0	0
37	460386	PTMA	prothymosin, alpha	5757	NM_001099285.1	764.6714	1.5063	0	0
38	4670048	RPS26L	-	400156	NR_002225.2	796.2257	0.6646	0	0
39	6420730	RPL9	ribosomal protein L9	6133	NM_001024921.2	797.4422	1.481	0	0
40	6960022	5-Sep	septin 5	5413	NM_002688.4	812.1586	0.6894	0	0
41	6180427	G0S2	G0/G1switch 2	50486	NM_015714.2	832.1428	1.1905	0	0
42	5290762	UTS2	urotensin 2	10911	NM_006786.2	832.6698	1.2965	0	0
43	780403	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	3117	XM_936128.2	837.2042	1.3738	0	0
44	1010246	IFI6	interferon, alpha-inducible protein 6	2537	NM_022872.2	838.9897	0.6667	0	0

【表４－５】

RankProd
表4-5

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
45	6270307	LOC644934	-	644934	XM_930344.2	846.7408	0.6838	0	0
46	4780075	CEACAM8	carcinoembryonic antigen-related cell adhesion molecule 8	1088	NM_001816.2	851.5188	0.6171	0	0
47	1450139	FCGR3B	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	2215	NM_000570.3	852.2208	0.7809	0	0
48	1400240	LDHB	lactate dehydrogenase B	3945	NM_002300.4	869.5601	1.5215	0	0
49	2810601	LEF1	lymphoid enhancer-binding factor 1	51176	NM_016269.2	885.7056	1.438	0	0
50	4230121	RPS26L	-	400156	XR_017804.1	901.0353	0.6857	0	0
51	50689	C7orf28B	chromosome 7 open reading frame 28B	221960	NM_198097.1	901.4464	1.283	0	0
52	7160475	SNHG5	small nucleolar RNA host gene 5 (non-protein coding)	387066	XM_943699.1	915.2623	1.3754	0	0
53	1010546	NULL	NULL	649143	XM_944822.1	940.4695	1.2482	0	0
54	4120053	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	5209	NM_004566.2	949.932	0.7127	0	0
55	5870678	NULL	NULL	441763	XM_930284.1	959.3277	0.7098	0	0

【表４－６】

RankProd
表4-6

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
56	6250615	PGLYRP1	peptidoglycan recognition protein 1	8993	NM_005091.1	978.6937	0.6314	0	0
57	5310044	NBPF20	neuroblastoma breakpoint family, member 20	400818	NM_001037675.1	989.9365	0.6816	0	0
58	7160474	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	3119	NM_002123.2	993.2267	1.3788	0	0
59	1510424	S100P	S100 calcium binding protein P	6286	NM_005980.2	999.9308	0.776	0	0
60	7550358	NELL2	NEL-like 2 (chicken)	4753	NM_006159.1	1000.2823	1.4511	0	0
61	6370435	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	2113	NM_005238.2	1000.7099	1.383	0	0
62	4480730	HBM	hemoglobin, mu	3042	NM_001003938.3	1002.8748	0.7114	0	0
63	6770673	SOCS2	suppressor of cytokine signaling 2	8835	NM_003877.3	1008.5738	1.4385	0	0
64	3140242	KIR2DL3	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3	3804	NM_014511.3	1012.7829	0.7052	0	0
65	5390246	CCR7	chemokine (C-C motif) receptor 7	1236	NM_001838.2	1024.3788	1.3396	0	0
66	6280408	TTN	titin	7273	NM_003319.3	1040.0032	1.4333	0	0

【表４－７】

RankProd
表4-7

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
67	840685	IL1B	interleukin 1, beta	3553	NM_000576.2	1043.9839	0.9118	0	0
68	1440564	RUNX3	runt-related transcription factor 3	864	NM_004350.2	1045.6015	0.7504	0	0
69	2640301	TNF	tumor necrosis factor (TNF superfamily, member 2)	7124	NM_000594.2	1052.0345	0.9119	0	0
70	160047	LOC389787	-	389787	XM_497072.2	1058.0289	1.4065	0	0
71	1500280	IFIT3	interferon-induced protein with tetratricopeptide repeats 3	3437	NM_001031683.1	1067.6439	0.7336	0	0
72	1780719	PTGES3	prostaglandin E synthase 3 (cytosolic)	10728	NM_006601.4	1094.4413	1.4426	0	0
73	7610440	XAF1	XIAP associated factor 1	54739	NM_199139.1	1101.0267	0.6954	0	0
74	1260482	GZMK	granzyme K (granzyme 3; tryptase II)	3003	NM_002104.2	1101.0382	1.379	0	0
75	2570112	ABLIM1	actin binding LIM protein 1	3983	NM_006720.3	1109.2206	1.3947	0	0
76	5810685	THBS1	thrombospondin 1	7057	NM_003246.2	1112.0822	0.7981	0	0
77	1050292	GP9	glycoprotein IX (platelet)	2815	NM_000174.2	1121.2912	0.7089	0	0

【表４－８】

RankProd
表4-8

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
78	4010181	FOLR3	folate receptor 3 (gamma)	2352	NM_000804.2	1121.4294	0.7343	0	0
79	1580025	GNG11	guanine nucleotide binding protein (G protein), gamma 11	2791	NM_004126.3	1123.8896	0.7606	0	0
80	4220307	NULL	NULL	647673	XM_936731.1	1127.0089	1.4189	0	0
81	4220246	CCL20	chemokine (C-C motif) ligand 20	6364	NM_004591.1	1130.1869	0.8647	0	0
82	6270605	LOC649946	-	649946	NR_003040.1	1141.8104	1.3897	0	0
83	3370202	ANXA2P1	annexin A2 pseudogene 1	303	NR_001562.1	1148.68	1.3614	0	0
84	6020066	NULL	NULL	651202	XM_940333.2	1156.9854	1.3818	0	0
85	2970370	PCDH17	protocadherin 17	27253	NM_014459.2	1159.006	1.4416	0	0
86	2970575	CCL4L2	chemokine (C-C motif) ligand 4-like 2	388372	NM_207007.2	1160.5275	0.8619	0	0
87	3360615	FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	2205	NM_002001.2	1161.9701	1.3166	0	0
88	6900634	CD69	CD69 molecule	969	NM_001781.1	1185.7514	1.3982	0	0

【表４－９】

RankProd
表4-9

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
89	650349	RPS28	ribosomal protein S28	6234	NM_001031.4	1190.4157	1.3501	0	0
90	6650242	IFITM3	interferon induced transmembrane protein 3 (1-8U)	10410	NM_021034.2	1198.6619	0.7139	0	0
91	2000148	IFIT1	interferon-induced protein with tetratricopeptide repeats 1	3434	NM_001548.3	1201.038	0.728	0	0
92	2190139	CA1	carbonic anhydrase I	759	NM_001738.1	1216.0508	0.7338	0	0
93	2140753	RPL14	ribosomal protein L14	9045	NM_001034996.1	1216.4627	1.3673	0	0
94	5050162	CD83	CD83 molecule	9308	NM_001040280.1	1221.184	1.1247	0	0
95	4200746	BPI	bactericidal/permeability-increasing protein	671	NM_001725.1	1222.3488	0.676	0	0
96	2600747	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	3433	NM_001547.4	1226.2189	0.7229	0	0
97	3130543	RNASE3	ribonuclease, RNase A family, 3 (eosinophil cationic protein)	6037	NM_002935.2	1231.3433	0.6719	0	0
98	5670739	AZU1	azurocidin 1	566	NM_001700.3	1238.4609	0.6567	0	0
99	7400377	CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	4680	NM_002483.3	1240.5422	0.6648	0	0

【表４－１０】

RankProd
表4-10

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
100	4670390	CXCL2	chemokine (C-X-C motif) ligand 2	2920	NM_002089.3	1243.1968	1.0736	0	0
101	670010	NULL	NULL	650298	XM_939387.1	1255.7097	0.7673	0	0
102	6590682	CCL3	chemokine (C-C motif) ligand 3	6348	NM_002983.1	1258.8623	1.0301	0	0
103	4560088	LOC439949	-	439949	XM_001129241.1	1259.3189	1.3845	0	0
104	6220671	PLAUR	plasminogen activator, urokinase receptor	5329	NM_001005376.1	1269.8919	0.7674	0	0
105	3170152	IL2RB	interleukin 2 receptor, beta	3560	NM_000878.2	1271.1735	0.8008	0	0
106	6620026	CD83	CD83 molecule	9308	NM_004233.3	1287.9941	1.0467	0	0
107	2360164	KLRC2	killer cell lectin-like receptor subfamily C, member 2	3822	NM_002260.3	1288.636	0.8481	0	0
108	2650192	C6orf105	chromosome 6 open reading frame 105	84830	NM_032744.1	1289.3942	1.3412	0	0
109	2810010	CCL3L3	chemokine (C-C motif) ligand 3-like 3	414062	NM_001001437.3	1296.3404	1.2483	0	0
110	3190148	DDIT4	DNA-damage-inducible transcript 4	54541	NM_019058.2	1307.8573	0.7086	0	0

【表４－１１】

RankProd
表4-11

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
111	1770504	HLA-DRB3	major histocompatibility complex, class II, DR beta 3	3125	NM_022555.3	1317.7473	1.2121	0	0
112	6590594	HIST1H2AC	histone cluster 1, H2ac	8334	NM_003512.3	1319.1937	0.7494	0	0
113	2260129	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	64231	NM_022349.2	1320.1527	1.2241	0	0
114	2750367	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	5366	NM_021127.1	1322.9263	1.344	0	0
115	5890095	LILRA5	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5	353514	NM_021250.2	1328.6256	0.7741	0	0
116	2900360	KIR2DL4	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	3805	NM_002255.3	1329.4767	0.7459	0	0
117	6940176	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	10096	NM_005721.3	1331.182	1.3755	0	0
118	4010040	HBG2	hemoglobin, gamma G	3048	NM_000184.2	1331.5404	1.1022	0	0
119	270338	TRAT1	T cell receptor associated transmembrane adaptor 1	50852	NM_016388.2	1334.9472	1.2985	0	0
120	1070487	KLRC3	killer cell lectin-like receptor subfamily C, member 3	3823	NM_002261.2	1341.8253	0.8231	0	0
121	6770326	NLRP8	NLR family, pyrin domain containing 8	126205	NM_176811.2	1341.9389	1.2932	0	0

【表４－１２】

RankProd
表4-12

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
122	7160692	NULL	NULL	644250	XM_929199.1	1343.5684	1.3113	0	0
123	5870136	CLIC3	chloride intracellular channel 3	9022	NM_004669.2	1346.5828	0.7759	0	0
124	6200747	LOC220433	–	220433	XM_941684.2	1348.1888	1.3645	0	0
125	5260070	HES4	hairy and enhancer of split 4 (Drosophila)	57801	NM_021170.2	1348.7064	0.7167	0	0
126	4250053	CCL3L1	chemokine (C-C motif) ligand 3-like 1	6349	NM_021006.4	1356.1796	1.1002	0	0
127	6580041	GNLY	granulysin	10578	NM_006433.2	1356.7575	0.7782	0	0
128	7040482	LOC642934	–	642934	XM_942991.2	1359.7468	1.3681	0	0
129	3890523	IL7R	interleukin 7 receptor	3575	XM_937367.1	1362.7824	1.2775	0	0
130	1340600	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	23645	NM_014330.2	1373.0141	0.7984	0	0
131	5900129	CROP	–	51747	NM_006107.2	1375.3663	1.3602	0	0
132	1010592	CD36	CD36 molecule (thrombospondin receptor)	948	NM_001001548.1	1383.7856	1.1993	0	0

【表４－１３】

RankProd
表4-13

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
133	5720682	TMEM176A	transmembrane protein 176A	55365	NM_018487.2	1384.9828	0.7916	1.00E-04	0
134	610437	CD24	CD24 molecule	100133941	NM_013230.2	1388.7966	0.7457	1.00E-04	0
135	4180079	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	83716	NM_031476.2	1388.8351	0.72	1.00E-04	0
136	650112	LST1	leukocyte specific transcript 1	7940	NM_007161.2	1388.9553	0.7844	1.00E-04	0
137	520382	CLK1	CDC-like kinase 1	1195	NM_001024646.1	1395.6456	1.323	0	0
138	450537	HBG1	hemoglobin, gamma A	3047	NM_000559.2	1395.7174	1.0847	0	0
139	4490520	GPR183	G protein-coupled receptor 183	1880	NM_004951.3	1395.8256	1.273	0	0
140	4040398	MAL	mal, T-cell differentiation protein	4118	NM_022440.1	1396.4257	1.2775	0	0
141	5900482	HMGB2	high-mobility group box 2	3148	NM_002129.2	1396.9268	1.3569	0	0
142	510468	NFE2	nuclear factor (erythroid-derived 2), 45kDa	4778	NM_006163.1	1400.397	0.783	0	0
143	6330196	MAL	mal, T-cell differentiation protein	4118	NM_002371.2	1403.2124	1.2786	0	0

【表４－１４】

RankProd
表4-14

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
144	2100196	ISG15	ISG15 ubiquitin-like modifier	9636	NM_005101.1	1404.6098	0.7538	0	0
145	2260477	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	5743	NM_000963.1	1417.9779	1.1062	0	0
146	1780709	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	10521	NM_030881.2	1418.7298	1.3597	0	0
147	1400672	AMFR	autocrine motility factor receptor	267	NM_001144.4	1425.012	1.2953	0	0
148	6110747	GIMAP2	GTPase, IMAP family member 2	26157	NM_015660.2	1433.7316	1.3711	0	0
149	730379	LOC388621	-	388621	XM_941195.2	1434.8209	1.3642	0	0
150	870338	EGR1	early growth response 1	1958	NM_001964.2	1437.3716	0.8285	0	0
151	730528	PLAUR	plasminogen activator, urokinase receptor	5329	NM_002659.2	1448.22	0.7926	0	0
152	2060440	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	9935	NM_005461.3	1451.0344	0.7939	1.00E-04	0
153	3140750	RBM38	RNA binding motif protein 38	55544	NM_183425.1	1459.9844	0.7692	1.00E-04	0
154	4490176	RGS1	regulator of G-protein signaling 1	5996	NM_002922.3	1460.4038	1.0695	1.00E-04	0

【表４－１５】

RankProd
表4-15

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
155	2370010	GZMH	granzyme H (cathepsin G-like 2, protein h-CCPX)	2999	NM_033423.3	1464.3431	0.8085	1.00E-04	0
156	7210035	SNORD13	small nucleolar RNA, C/D box 13	692084	NR_003041.1	1465.3176	0.8786	1.00E-04	0
157	780465	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	6556	NM_000578.3	1465.5854	0.7539	1.00E-04	0
158	1410278	PF4V1	platelet factor 4 variant 1	5197	NM_002620.2	1467.1678	0.7455	1.00E-04	0
159	10224	METRNL	meteorin, glial cell differentiation regulator-like	284207	XM_941466.2	1470.6115	0.7549	1.00E-04	0
160	6840324	RPL13L	ribosomal protein L13-like	283345	NR_002803.1	1473.3493	1.3141	0	0
161	4760243	NULL	NULL	648210	XR_018923.1	1473.563	1.3236	0	0
162	2690390	HCG4	HLA complex group 4	54435	NR_002139.1	1483.3064	0.7057	1.00E-04	0
163	6130168	GSTM2	glutathione S-transferase mu 2 (muscle)	2946	NM_000848.2	1484.5662	1.1586	1.00E-04	0
164	6650035	LOC338758	-	338758	XM_931359.2	1485.0079	0.786	1.00E-04	0
165	2710575	CD69	CD69 molecule	969	NM_001781.1	1492.1903	1.1581	1.00E-04	0

【表４－１６】

RankProd
表4-16

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
166	1030458	C19orf10	chromosome 19 open reading frame 10	56005	NM_019107.3	1495.2283	0.7531	1.00E-04	0
167	3990703	IL10	interleukin 10	3586	NM_000572.2	1496.2645	1.2881	1.00E-04	0
168	2230563	PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	5473	NM_002704.2	1498.9534	0.8688	1.00E-04	0
169	5490768	GPR56	G protein-coupled receptor 56	9289	NM_201525.1	1502.85	0.9478	1.00E-04	0
170	4040576	IL6	interleukin 6 (interferon, beta 2)	3569	NM_000600.1	1503.702	0.8304	1.00E-04	0
171	1850523	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	3002	NM_004131.3	1505.0467	0.8201	1.00E-04	0
172	1570553	IL8	interleukin 8	3576	NM_000584.2	1513.6436	1.115	1.00E-04	0
173	110332	NULL	NULL	NULL	XM_378421	1518.0403	1.3148	1.00E-04	0
174	4670193	PRF1	perforin 1 (pore forming protein)	5551	NM_005041.4	1519.3926	0.8813	1.00E-04	0
175	5670605	MATK	megakaryocyte-associated tyrosine kinase	4145	NM_139354.2	1520.0412	0.81	1.00E-04	0
176	6650735	NULL	NULL	NULL	BC020840	1525.1509	1.2826	1.00E-04	0

【表４－１７】

RankProd
表4-17

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
177	6510246	NULL	NULL	648210	XR_018923.1	1527.7265	1.3216	1.00E-04	0
178	1510681	NULL	NULL	440673	NM_001039703.1	1530.4662	0.7386	2.00E-04	0
179	6650161	GNA13	guanine nucleotide binding protein (G protein), alpha 13	10672	NM_006572.3	1532.1658	1.3018	1.00E-04	0
180	70162	TDG	thymine-DNA glycosylase	6996	NM_003211.3	1532.3669	0.7618	2.00E-04	0
181	6290114	SDPR	serum deprivation response (phosphatidylserine binding protein)	8436	NM_004657.4	1536.2237	0.7967	2.00E-04	0
182	3830242	NULL	NULL	642093	XM_942754.1	1537.7061	1.2013	1.00E-04	0
183	150609	LOC652493	–	652493	XM_941953.1	1538.659	0.8658	2.00E-04	0
184	1410221	S100A12	S100 calcium binding protein A12	6283	NM_005621.1	1538.9825	1.2033	1.00E-04	0
185	1030333	CCL2	chemokine (C-C motif) ligand 2	6347	NM_002982.3	1539.4369	1.0091	2.00E-04	0
186	7000356	RXRA	retinoid X receptor, alpha	6256	NM_002957.3	1541.9695	0.7849	2.00E-04	0
187	4610129	RETN	resistin	56729	NM_020415.2	1542.2649	0.9579	1.00E-04	0

【表４－１８】

RankProd
表4-18

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
188	290687	LOC653884	–	653884	XM_936240.1	1544.2074	0.7447	2.00E-04	0
189	6280332	CXCL16	chemokine (C-X-C motif) ligand 16	58191	NM_022059.1	1546.842	0.7614	2.00E-04	0
190	6860347	FAM46C	family with sequence similarity 46, member C	54855	NM_017709.3	1546.9813	0.8189	2.00E-04	0
191	3890326	SOD2	superoxide dismutase 2, mitochondrial	6648	NM_001024465.1	1548.2034	0.8086	2.00E-04	0
192	940398	EIF3M	eukaryotic translation initiation factor 3, subunit M	10480	NM_006360.3	1548.6574	1.3154	2.00E-04	0
193	5700070	ALPL	alkaline phosphatase, liver/bone/kidney	249	NM_000478.3	1554.899	0.8918	2.00E-04	0
194	3940438	NCF1	neutrophil cytosolic factor 1	653361	NM_000265.4	1557.7407	0.7547	2.00E-04	0
195	2900328	PTPLAD2	protein tyrosine phosphatase-like A domain containing 2	401494	NM_001010915.1	1561.8011	1.2964	2.00E-04	0
196	3930537	NULL	NULL	NULL	M97723	1563.1544	1.2251	2.00E-04	0
197	3060040	PABPC1	poly(A) binding protein, cytoplasmic 1	26986	NM_002568.3	1573.2119	1.3135	2.00E-04	0
198	3870338	IFI44L	interferon-induced protein 44-like	10964	NM_006820.1	1574.4975	0.7976	2.00E-04	0

【表４－１９】

RankProd
表4-19

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
199	3840564	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	58475	NM_206938.1	1576.6213	0.7676	2.00E-04	0
200	3370201	LOC648343	-	648343	XR_018327.1	1584.6649	1.2593	2.00E-04	0
201	6280504	LOC100008589	-	100008589	NR_003287.1	1584.9019	0.8501	2.00E-04	0
202	7200435	ASCL2	achaete-scute complex homolog 2 (Drosophila)	430	NM_005170.2	1588.1072	0.7612	2.00E-04	0
203	7050326	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	1032	NM_079421.2	1592.7956	0.771	2.00E-04	0
204	7320561	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	4939	NM_016817.2	1592.8459	0.782	2.00E-04	0
205	2640088	ALDOA	aldolase A, fructose-bisphosphate	226	NM_184041.1	1601.3395	0.7836	2.00E-04	0
206	6380079	FAM53B	family with sequence similarity 53, member B	9679	NM_014661.3	1601.8988	0.7927	2.00E-04	0
207	6590446	NULL	NULL	651149	XM_940278.1	1603.0262	1.1689	2.00E-04	0
208	5050541	RPL15P3	ribosomal protein L15 pseudogene 3	653232	XM_944104.2	1610.6217	1.2836	2.00E-04	0
209	6620136	MYH9	myosin, heavy chain 9, non-muscle	4627	NM_002473.3	1611.8118	0.7916	2.00E-04	0

【表４－２０】

RankProd
表4-20

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
210	2340743	CPA3	carboxypeptidase A3 (mast cell)	1359	NM_001870.1	1617.7401	1.2372	2.00E-04	0
211	6400392	GSTM1	glutathione S-transferase mu 1	2944	NM_000561.2	1618.8346	1.1278	2.00E-04	0
212	1030348	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	1027	NM_004064.2	1622.318	1.2788	2.00E-04	0
213	130717	ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	10095	NM_005720.2	1622.3622	0.7728	2.00E-04	0
214	3420373	SOD2	superoxide dismutase 2, mitochondrial	6648	NM_001024466.1	1623.9115	0.8404	2.00E-04	0
215	7320424	HNRPA1L-2	-	664709	NR_002944.2	1627.4854	1.3497	2.00E-04	0
216	830356	SLC4A5	solute carrier family 4, sodium bicarbonate cotransporter, member 5	57835	NM_133478.2	1629.4592	1.2662	3.00E-04	0
217	1240450	CD27	CD27 molecule	939	NM_001242.4	1630.1171	1.2929	3.00E-04	0
218	520408	IFIT3	interferon-induced protein with tetratricopeptide repeats 3	3437	NM_001549.2	1636.6346	0.7611	2.00E-04	0
219	5420095	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	4609	NM_002467.3	1636.6524	1.3042	3.00E-04	0
220	7510253	ACRBP	acrosin binding protein	84519	NM_032489.2	1637.0001	0.7754	2.00E-04	0

【表４－２１】

RankProd
表4-21

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
221	520392	P2RY13	purinergic receptor P2Y, G-protein coupled, 13	53829	NM_023914.2	1637.1533	0.7731	2.00E-04	0
222	70630	RNF144B	ring finger protein 144B	255488	NM_182757.2	1637.3458	0.7382	2.00E-04	0
223	5360273	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	6622	NM_007308.1	1637.8283	0.8495	2.00E-04	0
224	1690706	HIST1H3H	histone cluster 1, H3h	8357	NM_003536.2	1645.7986	0.7667	3.00E-04	0
225	7560593	OSM	oncostatin M	5008	NM_020530.3	1647.1147	0.8196	3.00E-04	0
226	770167	CD79B	CD79b molecule, immunoglobulin-associated beta	974	NM_001039933.1	1648.4831	1.2138	3.00E-04	0
227	1010035	NLRP3	NLR family, pyrin domain containing 3	114548	NM_004895.3	1648.7639	0.8612	3.00E-04	0
228	2710451	NULL	NULL	651894	XM_941155.2	1649.6418	1.2523	3.00E-04	0
229	2260551	RAD21	RAD21 homolog (S. pombe)	5885	NM_006265.1	1653.0804	1.2801	3.00E-04	0
230	5670465	ADM	adrenomedullin	133	NM_001124.1	1655.0659	0.7829	3.00E-04	0
231	6420446	CMPK1	cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	51727	NM_016308.1	1656.035	1.3183	3.00E-04	0

【表４－２２】

RankProd
表4-22

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
232	4260372	GTSCR1	Gilles de la Tourette syndrome chromosome region, candidate 1	220158	XM_496277.2	1659.3612	1.26	3.00E-04	0
233	2490450	hCG_1992539	–	91561	XM_934176.1	1661.3741	1.2023	3.00E-04	0
234	4040170	HBQ1	hemoglobin, theta 1	3049	NM_005331.3	1662.4015	0.8109	3.00E-04	0
235	870202	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	8743	NM_003810.2	1663.4194	0.8562	3.00E-04	0
236	1980594	FTHL8	ferritin, heavy polypeptide-like 8	2501	NR_002203.1	1668.0712	1.1674	3.00E-04	0
237	2370041	LRRN3	leucine rich repeat neuronal 3	54674	NM_018334.3	1672.3412	1.3042	3.00E-04	0
238	4220110	NULL	NULL	647450	XM_936518.1	1672.5458	0.8791	3.00E-04	0
239	1510612	MYL4	myosin, light chain 4, alkali; atrial, embryonic	4635	NM_002476.2	1681.4977	0.7979	4.00E-04	0
240	4010139	BANK1	B-cell scaffold protein with ankyrin repeats 1	55024	NM_001083907.1	1683.3115	1.2158	4.00E-04	0
241	5090215	IFI6	interferon, alpha-inducible protein 6	2537	NM_022873.2	1690.3545	0.818	4.00E-04	0
242	620717	CCL5	chemokine (C-C motif) ligand 5	6352	NM_002985.2	1691.5746	0.812	4.00E-04	0

【表４－２３】

RankProd
表4-23

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
243	4610681	LOC653658	–	653658	XM_939687.2	1693.2132	1.3052	4.00E-04	0
244	4290349	LOC643949	–	643949	XR_018645.1	1695.2143	1.2653	4.00E-04	0
245	450615	MT2A	metallothionein 2A	4502	NM_005953.2	1696.9888	0.7903	4.00E-04	0
246	1110373	C15orf48	chromosome 15 open reading frame 48	84419	NM_032413.2	1702.1009	0.946	4.00E-04	0
247	6400243	ABLIM1	actin binding LIM protein 1	3983	NM_001003407.1	1703.3875	1.2737	4.00E-04	0
248	6560279	VAV3	vav 3 guanine nucleotide exchange factor	10451	NM_006113.4	1704.7097	1.0099	4.00E-04	0
249	3940504	CD79A	CD79a molecule, immunoglobulin-associated alpha	973	NM_021601.3	1705.1684	1.136	4.00E-04	0
250	6510072	ACTG1	actin, gamma 1	71	NM_001614.2	1705.2256	0.8476	4.00E-04	0
251	610524	CCL3L1	chemokine (C-C motif) ligand 3-like 1	6349	NM_021006.4	1713.0407	1.1746	4.00E-04	0
252	6590646	FAM26F	family with sequence similarity 26, member F	441168	NM_001010919.1	1714.9816	1.2875	5.00E-04	0
253	3830136	NACAP1	nascent-polypeptide-associated complex alpha polypeptide pseudogene 1	83955	NR_002182.1	1716.7585	1.3074	5.00E-04	0

【表４－２４】

RankProd
表4-24

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
254	7650220	hCG_1787519	–	643007	XM_938089.2	1718.0255	1.2797	5.00E-04	0
255	1070477	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	216	NM_000689.3	1718.8928	1.2672	5.00E-04	0
256	6510754	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	216	NM_000689.3	1720.5388	1.2203	5.00E-04	0
257	3930008	RPL14	ribosomal protein L14	9045	NM_001034996.1	1720.6296	1.0405	5.00E-04	0
258	840551	CEP27	centrosomal protein 27kDa	55142	NM_018097.1	1724.7797	1.2511	5.00E-04	0
259	5050402	HIST1H2BK	histone cluster 1, H2bk	85236	NM_080593.1	1726.2525	0.7687	5.00E-04	0
260	4920228	FFAR2	free fatty acid receptor 2	2867	NM_005306.1	1726.9269	0.8449	5.00E-04	0
261	3400521	NULL	NULL	653086	XM_930995.1	1728.9741	1.249	5.00E-04	0
262	4890241	GPR56	G protein-coupled receptor 56	9289	NM_201524.1	1730.7855	0.9285	5.00E-04	0
263	6280446	NULL	NULL	642989	XM_926370.1	1731.2064	1.2277	5.00E-04	0
264	2030132	LOC653506	–	653506	XM_927769.1	1732.6509	0.8096	5.00E-04	0

【表４－２５】

RankProd
表4-25

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
265	3310538	CD36	CD36 molecule (thrombospondin receptor)	948	NM_000072.2	1732.7017	1.2213	5.00E-04	0
266	2640025	HP	haptoglobin	3240	NM_005143.2	1733.6315	0.7543	5.00E-04	0
267	1940047	AIF1	allograft inflammatory factor 1	199	NM_001623.3	1734.8998	0.7781	5.00E-04	0
268	5690671	GOLGA8B	golgi autoantigen, golgin subfamily a, 8B	440270	NM_001023567.2	1735.7582	1.2537	5.00E-04	0
269	2470601	IL1RN	interleukin 1 receptor antagonist	3557	NM_173842.1	1736.4413	0.8188	5.00E-04	0
270	4150201	BCL2	B-cell CLL/lymphoma 2	596	NM_000633.2	1737.2395	1.2312	5.00E-04	0
271	6580059	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	7351	NM_003355.2	1738.6131	1.2387	5.00E-04	0
272	3180131	hCG_1984468	-	389672	XM_933893.1	1749.2716	1.3078	5.00E-04	0
273	1770273	ANKRD30B	ankyrin repeat domain 30B	374860	NM_001029862.1	1750.2072	1.2567	5.00E-04	0
274	6450102	NULL	NULL	642113	XM_936253.1	1754.1531	0.9366	6.00E-04	0
275	1340743	IL8	interleukin 8	3576	NM_000584.2	1754.2793	1.148	5.00E-04	0

【表４－２６】

RankProd
表4-26

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
276	6620292	C10orf54	chromosome 10 open reading frame 54	64115	NM_022153.1	1755.4366	0.7563	6.00E-04	0
277	2570358	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	9987	NM_031372.1	1756.6323	1.304	6.00E-04	0
278	510209	LOC643310	-	643310	XM_926656.1	1756.8922	1.3155	6.00E-04	0
279	1770603	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	6947	NM_001062.3	1757.6057	1.1103	6.00E-04	0
280	1440121	tcag7.1261	-	645968	XM_928934.1	1759.0714	1.2841	6.00E-04	0
281	160242	C13orf15	chromosome 13 open reading frame 15	28984	NM_014059.2	1764.5447	1.1056	6.00E-04	0
282	4200541	FAM113B	family with sequence similarity 113, member B	91523	NM_138371.1	1768.2475	1.2217	6.00E-04	0
283	990500	AVPI1	arginine vasopressin-induced 1	60370	NM_021732.1	1770.8805	0.8357	7.00E-04	0
284	1440605	ZNF101	zinc finger protein 101	94039	NM_033204.2	1771.8967	1.2622	6.00E-04	0
285	2230167	LOC653773	-	653773	XM_938755.2	1772.9624	1.2915	6.00E-04	0
286	10358	SPN	sialophorin	6693	NM_001030288.1	1772.9705	0.7869	7.00E-04	0

【表４－２７】

RankProd
表4-27

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
287	7150711	ZNF223	zinc finger protein 223	7766	NM_013361.3	1775.2142	1.2356	6.00E-04	0
288	3420154	NLRP3	NLR family, pyrin domain containing 3	114548	NM_001079821.1	1778.0983	0.8935	7.00E-04	0
289	1710630	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	6480	NM_003032.2	1778.5828	1.224	6.00E-04	0
290	5360064	GNLY	granulysin	10578	NM_012483.1	1786.0213	0.8506	7.00E-04	0
291	1500201	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	3183	NM_031314.1	1788.8391	1.3177	7.00E-04	0
292	6020523	PPP2R2B	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	5521	NM_181676.1	1795.9286	0.8076	8.00E-04	0
293	6280008	HSD17B11	hydroxysteroid (17-beta) dehydrogenase 11	51170	NM_016245.3	1796.2197	1.2755	7.00E-04	0
294	3780193	FCRLA	Fc receptor-like A	84824	NM_032738.3	1801.0361	1.1008	7.00E-04	0
295	580706	CCR2	chemokine (C-C motif) receptor 2	1231	NM_000647.4	1810.4502	1.0875	8.00E-04	0
296	7510386	IL1RN	interleukin 1 receptor antagonist	3557	NM_173843.1	1813.3956	0.9866	8.00E-04	0
297	1230767	IFITM2	interferon induced transmembrane protein 2 (1-8D)	10581	NM_006435.2	1814.7255	0.7643	8.00E-04	0

【表４－２８】

RankProd
表4-28

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	RP_Rsum	RP_FC	RP_pfp	RP_pval
298	460164	FTHL11	ferritin, heavy polypeptide-like 11	2503	NR_002204.1	1816.8226	1.1796	8.00E-04	0
299	4150100	PASK	PAS domain containing serine/threonine kinase	23178	NM_015148.2	1817.7821	1.1603	8.00E-04	0
300	4050491	TCEA3	transcription elongation factor A (SII), 3	6920	NM_003196.1	1817.9245	1.2597	8.00E-04	0

【００４６】

表５　Spearmanの順位和係数で選択された上位３００の遺伝子のリスト

【表５－１】

Spearman
表5-1

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
1	1300687	NULL	NULL	731950	XR_016039.1	−0.061135983	0.700750469	0.700750469	1.25E−06	0.0212
2	2710653	FBXO38	F−box protein 38	81545	NM_030793.3	−0.149047116	0.660225141	0.660225141	6.35E−06	0.037
3	5860465	USP9Y	"ubiquitin specific peptidase 9, Y−linked (fat facets−like, Drosophila)"	8287	NM_004654.3	−0.094524102	0.654409006	0.654409006	8.00E−06	0.037
4	3390368	PDP2	−	57546	NM_020786.1	0.068777448	−0.652345216	0.652345216	8.72E−06	0.037
5	3130477	C7orf28A	chromosome 7 open reading frame 28A	51622	XM_001133729.1	−0.383441629	0.634521576	0.634521576	1.73E−05	0.0392
6	1780719	PTGES3	prostaglandin E synthase 3 (cytosolic)	10728	NM_006601.4	−0.528677962	0.633395872	0.633395872	1.80E−05	0.0392
7	6760017	YY1	YY1 transcription factor	7528	NM_003403.3	−0.328869705	0.630393996	0.630393996	2.02E−05	0.0392
8	270544	NR2C1	"nuclear receptor subfamily 2, group C, member 1"	7181	NM_003297.1	−0.155303368	0.626641651	0.626641651	2.32E−05	0.0392
9	5960072	NULL	NULL	NULL	BY797688	−0.097047292	0.626266417	0.626266417	2.35E−05	0.0392
10	2650601	GPBP1L1	GC−rich promoter binding protein 1−like 1	60313	NM_021639.3	−0.185092124	0.623827392	0.623827392	2.58E−05	0.0392
11	6420446	CMPK1	"cytidine monophosphate (UMP−CMP) kinase 1, cytosolic"	51727	NM_016308.1	−0.398631213	0.622514071	0.622514071	2.70E−05	0.0392
12	7510379	SACS	spastic ataxia of Charlevoix−Saguenay (sacsin)	26278	NM_014363.3	−0.121241812	0.621388368	0.621388368	2.82E−05	0.0392
13	3130296	AMY2A	"amylase, alpha 2A (pancreatic)"	279	NM_000699.2	−0.282794372	0.616510319	0.616510319	3.36E−05	0.0392
14	520706	UBE4A	"ubiquitination factor E4A (UFD2 homolog, yeast)"	9354	NM_004788.2	−0.230502672	0.614258912	0.614258912	3.64E−05	0.0392

【表５－２】

Spearman
表5-2

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
15	1230593	SP3	Sp3 transcription factor	6670	NM_001017371.3	−0.175703429	0.613883677	0.613883677	3.69E−05	0.0392
16	2120017	NOL8	nucleolar protein 8	55035	NM_017948.4	−0.189491166	0.612945591	0.612945591	3.82E−05	0.0392
17	990315	TCP1	t−complex 1	6950	NM_030752.2	−0.256767834	0.612195122	0.612195122	3.92E−05	0.0392
18	730288	COG3	component of oligomeric golgi complex 3	83548	NM_031431.2	−0.128112796	0.606941839	0.606941839	4.72E−05	0.0408
19	150672	KLHL7	kelch−like 7 (Drosophila)	55975	NM_001031710.1	−0.155913324	0.605816135	0.605816135	4.91E−05	0.0408
20	6590484	NAP1L1	nucleosome assembly protein 1−like 1	4673	NM_139207.1	−0.357418466	0.605253283	0.605253283	5.01E−05	0.0408
21	770441	DOPEY1	dopey family member 1	23033	NM_015018.2	−0.10084509	0.604878049	0.604878049	5.07E−05	0.0408
22	990044	KIAA1147	KIAA1147	57189	XM_001130020.1	−0.162506963	0.601125704	0.601125704	5.78E−05	0.0408
23	3120075	TIA1	TIA1 cytotoxic granule−associated RNA binding protein	7072	NM_022173.1	−0.154497679	0.600375235	0.600375235	5.93E−05	0.0408
24	4830255	DPP4	dipeptidyl−peptidase 4	1803	NM_001935.3	−0.307400655	0.599249531	0.599249531	6.16E−05	0.0408
25	4880521	CDC16	cell division cycle 16 homolog (S. cerevisiae)	8881	NM_003903.3	−0.34380491	0.598499062	0.598499062	6.32E−05	0.0408
26	150706	UGP2	UDP−glucose pyrophosphorylase 2	7360	NM_006759.3	−0.347146055	0.597560976	0.597560976	6.53E−05	0.0408
27	1780709	DDX17	DEAD (Asp−Glu−Ala−Asp) box polypeptide 17	10521	NM_030881.2	−0.443292451	0.596998124	0.596998124	6.66E−05	0.0408
28	1400240	LDHB	lactate dehydrogenase B	3945	NM_002300.4	−0.605485777	0.596622889	0.596622889	6.74E−05	0.0408

【表５－３】

Spearman
表5-3

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
29	6180497	GOLGA8C	"golgi autoantigen, golgin subfamily a, 8C"	400304	XM_375152.3	−0.242008817	0.594559099	0.594559099	7.23E−05	0.0423
30	5900129	CROP	−	51747	NM_006107.2	−0.443849065	0.593433396	0.593433396	7.51E−05	0.0425
31	4570170	KIAA0947	−	23379	NM_015325.1	−0.180354486	0.590243902	0.590243902	8.35E−05	0.0446
32	5720300	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	10146	NM_005754.2	−0.241645343	0.590056285	0.590056285	8.41E−05	0.0446
33	1110102	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	9653	NM_012262.2	−0.075582168	0.587992495	0.587992495	9.00E−05	0.0463
34	2640025	HP	haptoglobin	3240	NM_005143.2	0.40681683	−0.585553471	0.585553471	9.79E−05	0.0476
35	6020575	NNT	nicotinamide nucleotide transhydrogenase	23530	NM_012343.3	−0.191702435	0.584803002	0.584803002	0.000100019	0.0476
36	7400376	RABL2A	"RAB, member of RAS oncogene family-like 2A"	11159	NM_013412.1	−0.178370764	0.58424015	0.58424015	0.000101881	0.0476
37	4220731	P4HA1	"prolyl 4-hydroxylase, alpha polypeptide I"	5033	NM_000917.2	−0.307837835	0.583677298	0.583677298	0.000103774	0.0476
38	1110091	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	7073	NM_001033925.1	−0.233908998	0.581425891	0.581425891	0.000111672	0.0486
39	670209	ZNF700	zinc finger protein 700	90592	NM_144566.1	−0.134476397	0.581425891	0.581425891	0.000111672	0.0486
40	3930561	PRKCI	"protein kinase C, iota"	5584	NM_002740.5	−0.105841727	0.577298311	0.577298311	0.000127583	0.0538
41	4880463	SEC24A	"SEC24 family, member A (S. cerevisiae)"	10802	NM_021982.1	−0.069649892	0.57673546	0.57673546	0.000129906	0.0538
42	450195	Sept7	septin 7	989	NM_001788.4	−0.31815245	0.573921201	0.573921201	0.000142102	0.0538

【表５－４】

Spearman
表5-4

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
43	7000521	PRPS2	phosphoribosyl pyrophosphate synthetase 2	5634	NM_001039091.1	−0.203904286	0.573733583	0.573733583	0.000142951	0.0538
44	3130370	ZNF83	zinc finger protein 83	55769	NM_018300.2	−0.30567958	0.573170732	0.573170732	0.000145525	0.0538
45	6650056	ZNF566	zinc finger protein 566	84924	NM_032838.2	−0.051770571	0.573170732	0.573170732	0.000145525	0.0538
46	240463	RNF216L	ring finger protein 216−like	441191	XR_001271.1	0.162378967	−0.572795497	0.572795497	0.000147702	0.0538
47	5900731	SFRS12	"splicing factor, arginine/serine−rich 12"	140890	NM_001077199.1	−0.290167988	0.572420263	0.572420263	0.000149023	0.0538
48	1740136	SLC38A2	"solute carrier family 38, member 2"	54407	NM_018976.3	−0.214673013	0.568105066	0.568105066	0.000170654	0.0603
49	6280521	NULL	NULL	648399	XM_937448.1	−0.092941768	0.567354597	0.567354597	0.000174694	0.0605
50	840358	EXOSC10	exosome component 10	5394	NM_002685.2	−0.226165883	0.565853659	0.565853659	0.000183034	0.0609
51	5360719	MAPK9	mitogen−activated protein kinase 9	5601	NM_002752.3	−0.123212945	0.565853659	0.565853659	0.000183034	0.0609
52	1090692	GPBP1	GC−rich promoter binding protein 1	65056	NM_022913.1	−0.264875927	0.564165103	0.564165103	0.000192846	0.0623
53	6380673	TUBE1	"tubulin, epsilon 1"	51175	NM_016262.3	−0.138726153	0.563602251	0.563602251	0.00019622	0.0623
54	2570132	CLEC2D	"C−type lectin domain family 2, member D"	29121	NM_001004419.2	−0.163087579	0.563227017	0.563227017	0.0001985	0.0623
55	3990608	MAN2A1	"mannosidase, alpha, class 2A, member 1"	4124	NM_002372.2	−0.327379686	0.562288931	0.562288931	0.000204303	0.0623
56	4670605	MGC40489	−	146880	XR_016048.1	−0.029223716	0.562101313	0.562101313	0.000205482	0.0623

【表５－５】

Spearman
表5-5

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
57	4830605	NULL	NULL	NULL	AV735490	−0.046858933	0.560037523	0.560037523	0.000218863	0.0652
58	6940176	ACTR3	ARP3 actin−related protein 3 homolog (yeast)	10096	NM_005721.3	−0.459963089	0.556097561	0.556097561	0.000246612	0.0721
59	5560465	NOP56	NOP56 ribonucleoprotein homolog (yeast)	10528	NM_006392.2	−0.266935568	0.553095685	0.553095685	0.000269844	0.0768
60	7000474	GARNL1	GTPase activating Rap/RanGAP domain−like 1	253959	NM_194301.2	−0.175348366	0.55272045	0.55272045	0.000272883	0.0768
61	4850735	TAF4B	″TAF4b RNA polymerase II, TATA box binding protein (TBP)−associated factor, 105kDa″	6875	NM_005640.1	−0.058542324	0.552345216	0.552345216	0.000275952	0.0768
62	3800707	XPO4	exportin 4	64328	NM_022459.3	−0.217365077	0.551594747	0.551594747	0.000282185	0.077
63	3290669	SFRS12	″splicing factor, arginine/serine−rich 12″	140890	NM_139168.2	−0.132873689	0.551031895	0.551031895	0.000286942	0.077
64	6110630	HIST1H2BK	″histone cluster 1, H2bk″	85236	NM_080593.1	0.379122401	−0.550469043	0.550469043	0.000292583	0.077
65	5810619	TADA1L	″transcriptional adaptor 1 (HFI1 homolog, yeast)−like″	117143	NM_053053.2	−0.16203449	0.550093809	0.550093809	0.000295032	0.077
66	510209	LOC643310	−	643310	XM_926656.1	−0.395581648	0.549530957	0.549530957	0.000299984	0.0771
67	6450437	NULL	NULL	NULL	BF445990	0.102742584	−0.545028143	0.545028143	0.000343313	0.0859
68	4050195	FAM10A4	″family with sequence similarity 10, member A4 pseudogene″	145165	NR_002183.1	−0.370567771	0.544840525	0.544840525	0.000344253	0.0859
69	7380707	ZFAND1	″zinc finger, AN1−type domain 1″	79752	NM_024699.1	−0.254784176	0.544090056	0.544090056	0.000351858	0.0865
70	70128	NULL	NULL	NULL	AK123745	−0.051335734	0.543339587	0.543339587	0.000359613	0.0869

【表５－６】

Spearman
表5-6

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
71	2030332	PTPN18	″protein tyrosine phosphatase, non-receptor type 18 (brain-derived)″	26469	NM_014369.2	0.083763446	−0.541838649	0.541838649	0.000376607	0.0869
72	6650594	ATP11B	″ATPase, class VI, type 11B″	23200	NM_014616.1	−0.252853775	0.541838649	0.541838649	0.000375587	0.0869
73	2120537	SPOCD1	SPOC domain containing 1	90853	NM_144569.4	0.09473433	−0.541838649	0.541838649	0.000376607	0.0869
74	6380768	EIF4E	eukaryotic translation initiation factor 4E	1977	NM_001968.2	−0.084050702	0.540900563	0.540900563	0.000385893	0.0869
75	6980253	PTPLB	″protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b″	201562	NM_198402.2	−0.336175973	0.540337711	0.540337711	0.000392197	0.0869
76	6060553	RBP5	″retinol binding protein 5, cellular″	83758	NM_031491.1	0.051243739	−0.540337711	0.540337711	0.000393257	0.0869
77	60553	NDFIP1	Nedd4 family interacting protein 1	80762	NM_030571.2	−0.171766084	0.540150094	0.540150094	0.000394319	0.0869
78	4210129	ELOVL5	″ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like,	60481	NM_021814.3	−0.284710319	0.538836773	0.538836773	0.000409464	0.0891
79	6760326	ZNF658	zinc finger protein 658	26149	NM_033160.4	−0.078993442	0.537898687	0.537898687	0.0004206	0.0903
80	3060040	PABPC1	″poly(A) binding protein, cytoplasmic 1″	26986	NM_002568.3	−0.393451244	0.537148218	0.537148218	0.000429704	0.0905
81	460386	PTMA	″prothymosin, alpha″	5757	NM_001099285.1	−0.590989351	0.5369606	0.5369606	0.000432007	0.0905
82	290128	NULL	NULL	643985	XM_927235.1	−0.048540479	0.536022514	0.536022514	0.000443691	0.0918
83	3310309	CCDC135	coiled-coil domain containing 135	84229	NM_032269.4	0.099558313	−0.535272045	0.535272045	0.000454449	0.0929
84	7400047	LOC388344	-	388344	XM_371023.4	−0.327727336	0.534521576	0.534521576	0.000462978	0.0935

【表５－７】

Spearman
表5-7

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
85	6550750	ARMC8	armadillo repeat containing 8	25852	NM_014154.2	−0.087200394	0.533020638	0.533020638	0.000483014	0.095
86	2600204	SACM1L	SAC1 suppressor of actin mutations 1-like (yeast)	22908	NM_014016.2	−0.262966982	0.532457786	0.532457786	0.000490726	0.095
87	6620356	ARPP-19	–	10776	NM_006628.4	−0.261668585	0.532457786	0.532457786	0.000490726	0.095
88	3710465	C6orf211	chromosome 6 open reading frame 211	79624	NM_024573.1	−0.114858487	0.532270169	0.532270169	0.000493321	0.095
89	6020048	LOC646103	–	646103	XM_377879.3	−0.029867018	0.531894934	0.531894934	0.000498548	0.095
90	4010632	LQK1	–	642946	XM_927142.1	0.072739876	−0.531332083	0.531332083	0.000507815	0.0957
91	2320577	SSR2	"signal sequence receptor, beta (translocon-associated protein beta)"	6746	XM_945427.1	0.064320484	−0.530956848	0.530956848	0.00051318	0.0957
92	1780639	LOC645355	–	645355	XM_932842.1	0.036028447	−0.530206379	0.530206379	0.000524062	0.0967
93	1850612	PARP2	poly (ADP-ribose) polymerase 2	10038	NM_005484.2	−0.097585163	0.528893058	0.528893058	0.000542187	0.0989
94	4220673	NULL	NULL	NULL	AA971450	0.072927449	−0.528517824	0.528517824	0.000549307	0.0992
95	2970196	DEFB125	"defensin, beta 125"	245938	NM_153325.2	0.07618092	−0.527204503	0.527204503	0.00056969	0.1018
96	2640274	ALDH5A1	"aldehyde dehydrogenase 5 family, member A1"	7915	NM_001080.3	−0.078301425	0.526266417	0.526266417	0.000583149	0.1031
97	4780767	FLJ40473	–	285226	XR_001031.1	−0.068012051	0.525891182	0.525891182	0.000589222	0.1031
98	4760243	NULL	NULL	648210	XR_018923.1	−0.404442095	0.52532833	0.52532833	0.000598437	0.1031

【表５－８】

Spearman
表5-8

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
99	4540356	UFM1	ubiquitin-fold modifier 1	51569	NM_016617.1	-0.290998607	0.525140713	0.525140713	0.000601537	0.1031
100	2680440	NULL	NULL	NULL	BF338665	0.061724508	-0.523639775	0.523639775	0.000628477	0.1066
101	770021	PRKRA	"protein kinase, interferon-inducible double stranded RNA dependent activator"	8575	NM_003690.3	-0.229357783	0.522138837	0.522138837	0.000653139	0.1081
102	840064	LOC645489	-	645489	XM_928514.1	-0.199041088	0.52195122	0.52195122	0.000656492	0.1081
103	6650646	C4orf39	chromosome 4 open reading frame 39	152756	NM_153027.1	-0.056865183	0.52195122	0.52195122	0.000656492	0.1081
104	7000754	AMY2B	"amylase, alpha 2B (pancreatic)"	280	NM_020978.3	-0.131806513	0.520825516	0.520825516	0.000676935	0.1095
105	6860148	SLC9A6	"solute carrier family 9 (sodium/hydrogen exchanger), member 6"	10479	NM_001042537.1	-0.17456976	0.520637899	0.520637899	0.000680398	0.1095
106	7400343	STX2	syntaxin 2	2054	NM_001980.2	-0.258793675	0.520450281	0.520450281	0.000683875	0.1095
107	5420053	CCT6P1	"chaperonin containing TCP1, subunit 6 (zeta) pseudogene 1"	643253	NR_003110.2	-0.281922881	0.519324578	0.519324578	0.000705079	0.1118
108	6560162	TMED7	transmembrane emp24 protein transport domain containing 7	51014	NM_181836.3	-0.243305775	0.518949343	0.518949343	0.000712276	0.1119
109	1850300	TC2N	"tandem C2 domains, nuclear"	123036	NM_152332.3	-0.236871126	0.518198874	0.518198874	0.000726869	0.113
110	4150168	ARSA	arylsulfatase A	410	NM_000487.3	0.091560891	-0.51782364	0.51782364	0.000736124	0.113
111	6560161	NULL	NULL	NULL	BX111675	0.054993081	-0.517448405	0.517448405	0.000743605	0.113
112	1500465	AASS	aminoadipate-semialdehyde synthase	10157	NM_005763.2	-0.034373234	0.516697936	0.516697936	0.000756858	0.113

【表５－９】

Spearman
表5-9

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
113	4250154	NULL	NULL	648749	XM_937834.2	−0.061658345	0.516510319	0.516510319	0.000760684	0.113
114	2750411	RGAG4	retrotransposon gag domain containing 4	340526	NM_001024455.2	0.0613934	−0.516135084	0.516135084	0.000770323	0.113
115	6420730	RPL9	ribosomal protein L9	6133	NM_001024921.2	−0.56653985	0.515947467	0.515947467	0.000772264	0.113
116	4180356	RBBP6	retinoblastoma binding protein 6	5930	NM_032626.5	−0.053093332	0.51575985	0.51575985	0.000776159	0.113
117	4150553	TAF13	"TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa"	6884	NM_005645.3	0.061312413	−0.515572233	0.515572233	0.000782035	0.113
118	3610521	PCDHGB6	"protocadherin gamma subfamily B, 6"	56100	NM_018926.2	0.176789549	−0.515384615	0.515384615	0.000785974	0.113
119	4180142	KIAA1370	KIAA1370	56204	NM_019600.1	−0.224539294	0.514634146	0.514634146	0.0007999	0.1139
120	6450538	TCERG1	transcription elongation regulator 1	10915	NM_006706.3	−0.153163323	0.514258912	0.514258912	0.000807957	0.1139
121	5310736	FAM162A	"family with sequence similarity 162, member A"	26355	NM_014367.3	−0.324511803	0.514071295	0.514071295	0.000812012	0.1139
122	290687	LOC653884	−	653884	XM_936240.1	0.425268736	−0.513320826	0.513320826	0.000830488	0.1155
123	3710681	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	10565	NM_006421.3	−0.094839399	0.512757974	0.512757974	0.000840913	0.116
124	2000035	NULL	NULL	NULL	AL042883	0.08373784	−0.512382739	0.512382739	0.000851456	0.1165
125	7160767	RBBP4	retinoblastoma binding protein 4	5928	NM_005610.1	−0.101719082	0.510881801	0.510881801	0.000883795	0.12
126	2570358	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	9987	NM_031372.1	−0.382998221	0.509943715	0.509943715	0.000905959	0.122

【表５－１０】

Spearman
表5-10

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
127	4390576	DFFA	"DNA fragmentation factor, 45kDa, alpha polypeptide"	1676	NM_213566.1	0.121909434	−0.50956848	0.50956848	0.000917226	0.1225
128	1820528	PAPSS1	3'−phosphoadenosine 5'−phosphosulfate synthase 1	9061	NM_005443.4	−0.222706769	0.509005629	0.509005629	0.000928618	0.1231
129	6040379	ZBTB11	zinc finger and BTB domain containing 11	27107	NM_014415.2	−0.043557823	0.508067542	0.508067542	0.000951782	0.1235
130	160440	NULL	NULL	643389	XM_926721.1	−0.052401185	0.507879925	0.507879925	0.000956476	0.1235
131	1710646	C11orf63	chromosome 11 open reading frame 63	79864	NM_024806.2	−0.036113925	0.507692308	0.507692308	0.000961191	0.1235
132	3120537	GAB2	GRB2−associated binding protein 2	9846	NM_080491.1	0.113527825	−0.507317073	0.507317073	0.000973069	0.1235
133	4540138	NGB	neuroglobin	58157	NM_021257.3	0.062540263	−0.506941839	0.506941839	0.000982665	0.1235
134	5910131	PDE6H	"phosphodiesterase 6H, cGMP−specific, cone, gamma"	5149	NM_006205.1	0.060610886	−0.506754221	0.506754221	0.000987495	0.1235
135	6980286	RNF219	ring finger protein 219	79596	NM_024546.2	−0.105227382	0.506754221	0.506754221	0.000985077	0.1235
136	6650161	GNA13	"guanine nucleotide binding protein (G protein), alpha 13"	10672	NM_006572.3	−0.380533537	0.506566604	0.506566604	0.000989917	0.1235
137	6380747	ANKRD32	ankyrin repeat domain 32	84250	NM_032290.2	−0.104537188	0.505253283	0.505253283	0.001024398	0.1251
138	580014	C12orf43	chromosome 12 open reading frame 43	64897	NM_022895.1	−0.20852646	0.505065666	0.505065666	0.00102941	0.1251
139	3850180	CHCHD7	coiled−coil−helix−coiled−coil−helix domain containing 7	79145	NM_001011670.1	−0.119451503	0.505065666	0.505065666	0.00102941	0.1251
140	610367	HECA	headcase homolog (Drosophila)	51696	NM_016217.2	−0.312188665	0.504878049	0.504878049	0.001034444	0.1251

【表５－１１】

Spearman
表5-11

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
141	780402	RTN4	reticulon 4	57142	NM_020532.4	−0.274156562	0.504690432	0.504690432	0.0010395	0.1251
142	770128	L3MBTL3	l(3)mbt-like 3 (Drosophila)	84456	NM_032438.1	−0.161561418	0.503939962	0.503939962	0.001059945	0.1251
143	3780465	SMARCA5	"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	8467	NM_003601.2	−0.115124978	0.503752345	0.503752345	0.001065112	0.1251
144	5490603	hCG_1783417	-	401019	NM_001080831.1	−0.173305696	0.503752345	0.503752345	0.001065112	0.1251
145	4610138	CAPZA1	"capping protein (actin filament) muscle Z-line, alpha 1"	829	NM_006135.1	−0.36644329	0.503377111	0.503377111	0.001075513	0.1251
146	2450326	NULL	NULL	642047	XM_936157.1	0.047996723	−0.503377111	0.503377111	0.001078127	0.1251
147	6580064	C14orf19	chromosome 14 open reading frame 19	280655	NR_002937.1	−0.152106349	0.503001876	0.503001876	0.001086005	0.1251
148	7040524	FAM76A	"family with sequence similarity 76, member A"	199870	NM_152660.1	−0.052516764	0.502814259	0.502814259	0.001091285	0.1251
149	6770634	USP8	ubiquitin specific peptidase 8	9101	NM_005154.2	−0.15261273	0.50206379	0.50206379	0.001112634	0.1253
150	2120468	C10orf58	chromosome 10 open reading frame 58	84293	NM_032333.2	−0.327354271	0.501876173	0.501876173	0.001118029	0.1253
151	2070019	UBA6	ubiquitin-like modifier activating enzyme 6	55236	NM_018227.5	−0.194843638	0.501688555	0.501688555	0.001123447	0.1253
152	5390433	DICER1	"dicer 1, ribonuclease type III"	23405	NM_030621.2	−0.111116126	0.501688555	0.501688555	0.001123447	0.1253
153	6450129	ITM2A	integral membrane protein 2A	9452	NM_004867.3	−0.126988076	0.501125704	0.501125704	0.001139843	0.1253
154	20288	Sept11	septin 11	55752	NM_018243.2	−0.136166131	0.500938086	0.500938086	0.001145356	0.1253

【表５－１２】

Spearman
表5-12

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
155	6370736	EIF1AX	"eukaryotic translation initiation factor 1A, X-linked"	1964	NM_001412.3	−0.117614043	0.500375235	0.500375235	0.001162036	0.1253
156	730379	LOC388621	−	388621	XM_941195.2	−0.448108038	0.500187617	0.500187617	0.001167644	0.1253
157	1500047	RIN1	Ras and Rab interactor 1	9610	NM_004292.2	0.132155916	−0.5	0.5	0.001176101	0.1253
158	5960594	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	5378	NM_000534.3	−0.077033315	0.5	0.5	0.001173276	0.1253
159	4220114	NULL	NULL	NULL	DA160411	0.070349309	−0.499624765	0.499624765	0.001187461	0.1253
160	5910463	PKIA	"protein kinase (cAMP-dependent, catalytic) inhibitor alpha"	5569	NM_006823.2	−0.254561014	0.499437148	0.499437148	0.001190317	0.1253
161	1410170	GOPC	golgi associated PDZ and coiled-coil motif containing	57120	NM_020399.2	−0.088182858	0.498686679	0.498686679	0.001213381	0.1253
162	4780768	FAM8A1	"family with sequence similarity 8, member A1"	51439	NM_016255.1	−0.099801523	0.498499062	0.498499062	0.001219209	0.1253
163	1580286	SEH1L	SEH1-like (S. cerevisiae)	81929	NM_031216.3	−0.083010039	0.498311445	0.498311445	0.001225062	0.1253
164	4570403	NULL	NULL	NULL	BX106581	0.112837902	−0.497748593	0.497748593	0.001245745	0.1253
165	5310747	PSIP1	PC4 and SFRS1 interacting protein 1	11168	NM_033222.2	−0.298779917	0.497748593	0.497748593	0.001242771	0.1253
166	460682	CCDC132	coiled-coil domain containing 132	55610	NM_017667.2	−0.123015026	0.497748593	0.497748593	0.001242771	0.1253
167	7550221	NULL	NULL	NULL	BG207842	0.067923939	−0.497748593	0.497748593	0.001245745	0.1253
168	3520601	MPO	myeloperoxidase	4353	NM_000250.1	0.96554979	−0.497373358	0.497373358	0.001257702	0.1253

【表５－１３】

Spearman
表5-13

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
169	2570725	PPCS	phosphopantothenoylcysteine synthetase	79717	NM_001077447.1	−0.310167811	0.497373358	0.497373358	0.001254703	0.1253
170	6200747	LOC220433	–	220433	XM_941684.2	−0.448374765	0.497185741	0.497185741	0.001260707	0.1253
171	3710682	NULL	NULL	642033	XM_936103.1	0.143366073	−0.496998124	0.496998124	0.001269761	0.1253
172	2100594	BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)	9184	NM_004725.2	−0.303162523	0.496247655	0.496247655	0.001291113	0.1253
173	2760605	MTMR1	myotubularin related protein 1	8776	NM_176789.1	−0.027175642	0.496247655	0.496247655	0.001291113	0.1253
174	6900768	NULL	NULL	NULL	DA572426	−0.08577853	0.49587242	0.49587242	0.001303457	0.1253
175	7150685	CBX5	"chromobox homolog 5 (HP1 alpha homolog, Drosophila)"	23468	NM_012117.1	0.077258047	−0.495121951	0.495121951	0.001331616	0.1253
176	160047	LOC389787	–	389787	XM_497072.2	−0.49206406	0.495121951	0.495121951	0.00132846	0.1253
177	3830598	CARTPT	CART prepropeptide	9607	NM_004291.2	0.027959175	−0.495121951	0.495121951	0.001331616	0.1253
178	870040	ASCC3	activating signal cointegrator 1 complex subunit 3	10973	NM_006828.2	−0.10465835	0.494934334	0.494934334	0.001334777	0.1253
179	2100292	RBBP7	retinoblastoma binding protein 7	5931	NM_002893.2	−0.173081269	0.494746717	0.494746717	0.001341121	0.1253
180	5860327	PRPF18	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	8559	NM_003675.3	−0.26670234	0.494371482	0.494371482	0.001353889	0.1253
181	7560300	TCTEX1D1	Tctex1 domain containing 1	200132	NM_152665.1	0.124259481	−0.494183865	0.494183865	0.001363536	0.1253
182	5360619	CDC16	cell division cycle 16 homolog (S. cerevisiae)	8881	NM_001078645.1	−0.262987116	0.494183865	0.494183865	0.001360314	0.1253

【表５－１４】

Spearman
表5-14

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
183	3440189	ZBTB20	zinc finger and BTB domain containing 20	26137	NM_015642.3	−0.287117754	0.493996248	0.493996248	0.001366765	0.1253
184	940168	GTPBP8	GTP-binding protein 8 (putative)	29083	NM_014170.2	0.193620887	−0.493996248	0.493996248	0.001370001	0.1253
185	10142	CD164	″CD164 molecule, sialomucin″	8763	NM_006016.3	−0.14302977	0.493996248	0.493996248	0.001366765	0.1253
186	6020273	RPS4Y2	″ribosomal protein S4, Y-linked 2″	140032	NM_001039567.2	−0.29587893	0.49380863	0.49380863	0.001373244	0.1253
187	3990112	CAST	calpastatin	831	NM_001042445.1	−0.280052769	0.493058161	0.493058161	0.001399433	0.127
188	3120762	MSH5	mutS homolog 5 (E. coli)	4439	NM_002441.3	0.058093161	−0.492682927	0.492682927	0.001416025	0.1278
189	160537	KDSR	3-ketodihydrosphingosine reductase	2531	NM_002035.1	−0.165230376	0.491932458	0.491932458	0.001439548	0.1292
190	5290358	CPT1A	carnitine palmitoyltransferase 1A (liver)	1374	NM_001031847.1	0.165571989	−0.490994371	0.490994371	0.001477215	0.131
191	3440670	NULL	NULL	402251	XM_377933.3	−0.279019599	0.490994371	0.490994371	0.001473755	0.131
192	3370673	GUSBL2	″glucuronidase, beta-like 2″	375513	NM_206910.1	0.128073825	−0.490806754	0.490806754	0.001484157	0.131
193	4260767	GP1BA	″glycoprotein Ib (platelet), alpha polypeptide″	2811	NM_000173.4	0.13089936	−0.490243902	0.490243902	0.001505156	0.131
194	6550600	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	4609	NM_002467.3	−0.337363684	0.489493433	0.489493433	0.001529989	0.131
195	1740154	TMEM106B	transmembrane protein 106B	54664	NM_018374.2	−0.106689074	0.489493433	0.489493433	0.001529989	0.131
196	7160332	NULL	NULL	NULL	CF552427	0.054930882	−0.489305816	0.489305816	0.001540742	0.131

【表５－１５】

Spearman
表5-15

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
197	4010452	SLC38A6	"solute carrier family 38, member 6"	145389	NM_153811.1	−0.136358094	0.489305816	0.489305816	0.00153715	0.131
198	510050	LOC652837	-	652837	XM_942529.1	−0.036184103	0.489305816	0.489305816	0.00153715	0.131
199	5720703	AKTIP	AKT interacting protein	64400	NM_022476.2	−0.132110131	0.489118199	0.489118199	0.001544342	0.131
200	380575	RPL23	ribosomal protein L23	9349	NM_000978.3	−0.338815803	0.489118199	0.489118199	0.001544342	0.131
201	1980626	SMARCA5	"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	8467	NM_003601.2	−0.146115776	0.488742964	0.488742964	0.001558814	0.1316
202	6110747	GIMAP2	"GTPase, IMAP family member 2"	26157	NM_015660.2	−0.45531031	0.488555347	0.488555347	0.001566095	0.1316
203	7380382	RNF115	ring finger protein 115	27246	NM_014455.1	0.278371033	−0.48836773	0.48836773	0.001577073	0.1318
204	6510619	NAE1	NEDD8 activating enzyme E1 subunit 1	8883	NM_001018160.1	−0.29276015	0.487992495	0.487992495	0.00158812	0.1321
205	6110091	WSB1	WD repeat and SOCS box-containing 1	26118	NM_134265.2	−0.29256262	0.485928705	0.485928705	0.001671249	0.1376
206	2970296	ALG8	"asparagine-linked glycosylation 8, alpha-1,3-glucosyltransferase homolog (S. cerevisiae)"	79053	NM_001007027.2	−0.171596568	0.485928705	0.485928705	0.001671249	0.1376
207	7150554	LCOR	ligand dependent nuclear receptor corepressor	84458	NM_032440.1	−0.293176479	0.485741088	0.485741088	0.001678994	0.1376
208	6560609	CNOT8	"CCR4-NOT transcription complex, subunit 8"	9337	NM_004779.4	−0.206326635	0.484990619	0.484990619	0.001710294	0.1395
209	20091	GABARAPL2	GABA(A) receptor-associated protein-like 2	11345	NM_007285.6	−0.164409469	0.484615385	0.484615385	0.001726137	0.1395
210	2900112	PPIB	peptidylprolyl isomerase B (cyclophilin B)	5479	NM_000942.4	−0.126826389	0.484615385	0.484615385	0.001726137	0.1395

【表５－１６】

Spearman
表5-16

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
211	4730458	CLTC	"clathrin, heavy chain (Hc)"	1213	NM_004859.3	-0.126167554	0.483864916	0.483864916	0.001758214	0.1407
212	3140553	SAR1A	SAR1 homolog A (S. cerevisiae)	56681	NM_020150.3	-0.181453186	0.483677298	0.483677298	0.001766316	0.1407
213	5960561	DBR1	debranching enzyme homolog 1 (S. cerevisiae)	51163	NM_016216.2	-0.051928612	0.483677298	0.483677298	0.001766316	0.1407
214	4050609	DNAJA2	"DnaJ (Hsp40) homolog, subfamily A, member 2"	10294	NM_005880.2	-0.266568167	0.483489681	0.483489681	0.00177445	0.1407
215	990543	SFRS11	"splicing factor, arginine/serine-rich 11"	9295	NM_004768.2	-0.164426621	0.482926829	0.482926829	0.001799054	0.1408
216	7570189	GAGE6	G antigen 6	2578	NM_001476.1	0.084017945	-0.482363977	0.482363977	0.001828139	0.1408
217	1500201	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	3183	NM_031314.1	-0.397999182	0.48217636	0.48217636	0.001832328	0.1408
218	2760400	WDSOF1	WD repeats and SOF1 domain containing	25879	NM_015420.5	-0.059823595	0.481613508	0.481613508	0.00185764	0.1408
219	5820544	CTGLF1	"centaurin, gamma-like family, member 1"	119016	NM_133446.1	-0.040059562	0.481613508	0.481613508	0.00185764	0.1408
220	2680433	MOSPD1	motile sperm domain containing 1	56180	NM_019556.1	-0.042888816	0.481613508	0.481613508	0.00185764	0.1408
221	4260504	SNX14	sorting nexin 14	57231	NM_020468.2	-0.218109366	0.481425891	0.481425891	0.001866146	0.1408
222	5910543	GLOD4	glyoxalase domain containing 4	51031	NM_016080.2	-0.177207323	0.481238274	0.481238274	0.001874687	0.1408
223	840673	ZNF383	zinc finger protein 383	163087	NM_152604.1	-0.129968709	0.481238274	0.481238274	0.001874687	0.1408
224	5550711	SYNE1	"spectrin repeat containing, nuclear envelope 1"	23345	NM_182961.2	0.075512374	-0.481050657	0.481050657	0.001887563	0.1408

【表５－１７】

Spearman
表5-17

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
225	4760037	NULL	NULL	651648	XM_940853.1	−0.018758212	0.481050657	0.481050657	0.001883262	0.1408
226	5820202	LOC644131	-	644131	XR_018325.1	−0.244724622	0.480863039	0.480863039	0.001891872	0.1408
227	4730408	ANAPC5	anaphase promoting complex subunit 5	51433	NM_016237.3	−0.212087146	0.480863039	0.480863039	0.001891872	0.1408
228	3850008	NULL	NULL	654189	XM_942687.1	−0.093486403	0.480675422	0.480675422	0.001900517	0.1408
229	460333	SPAST	spastin	6683	NM_199436.1	−0.064545186	0.480675422	0.480675422	0.001900517	0.1408
230	1110192	PPM2C	"protein phosphatase 2C, magnesium-dependent, catalytic subunit"	54704	NM_018444.2	−0.100238781	0.48011257	0.48011257	0.001926661	0.1421
231	3520470	RBMXP3	"RNA binding motif protein, X-linked pseudogene 3"	143543	NR_002197.1	−0.129523594	0.479924953	0.479924953	0.001935447	0.1422
232	5900482	HMGB2	high-mobility group box 2	3148	NM_002129.2	−0.440289057	0.479174484	0.479174484	0.001970944	0.1442
233	2230300	ZNF561	zinc finger protein 561	93134	NM_152289.1	−0.059435926	0.47879925	0.47879925	0.001988907	0.1448
234	6280524	CCNL1	cyclin L1	57018	NM_020307.2	−0.186663803	0.476923077	0.476923077	0.002080918	0.1503
235	6650133	LSM5	"LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)"	23658	NM_012322.1	−0.157326463	0.476923077	0.476923077	0.002080918	0.1503
236	1170288	PRMT1	protein arginine methyltransferase 1	3276	NM_198319.2	0.067974089	−0.476172608	0.476172608	0.002123537	0.1518
237	7320424	HNRPA1L-2	-	664709	NR_002944.2	−0.432630765	0.475797373	0.475797373	0.002137913	0.1518
238	2070025	SAV1	salvador homolog 1 (Drosophila)	60485	NM_021818.2	−0.083084103	0.475797373	0.475797373	0.002137913	0.1518

【表５－１８】

Spearman
表5-18

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
239	3940333	ZNF266	zinc finger protein 266	10781	NM_006631.2	−0.108968593	0.475797373	0.475797373	0.002137913	0.1518
240	4810072	TUSC2	tumor suppressor candidate 2	11334	NM_007275.1	0.162628207	−0.475234522	0.475234522	0.002171795	0.1533
241	7610608	RP11-122C9.1	–	653702	NM_001093763.1	−0.316189323	0.475046904	0.475046904	0.002176674	0.1533
242	840601	MEGF10	multiple EGF-like-domains 10	84466	NM_032446.1	0.047723662	−0.474859287	0.474859287	0.002191368	0.1536
243	3870209	RTEL1	regulator of telomere elongation helicase 1	51750	NM_032957.3	0.061308622	−0.474484053	0.474484053	0.002211097	0.1544
244	4900343	MORF4L1	mortality factor 4 like 1	10933	NM_206839.1	−0.24904666	0.473921201	0.473921201	0.002235979	0.1552
245	6270433	hCG_1646420	–	644672	XM_938396.1	0.038585438	−0.473921201	0.473921201	0.002240985	0.1552
246	3780482	NULL	NULL	NULL	BQ011293	0.031282267	−0.473545966	0.473545966	0.002261108	0.1557
247	3190059	IMMT	"inner membrane protein, mitochondrial (mitofilin)"	10989	NM_001100169.1	−0.221779779	0.473358349	0.473358349	0.002266164	0.1557
248	5560703	C6orf120	chromosome 6 open reading frame 120	387263	NM_001029863.1	−0.109371386	0.472232645	0.472232645	0.002327616	0.1586
249	7000672	AGL	"amylo-1, 6-glucosidase, 4-alpha-glucanotransferase"	178	NM_000642.2	−0.081394333	0.472232645	0.472232645	0.002327616	0.1586
250	6980328	ANP32C	"acidic (leucine-rich) nuclear phosphoprotein 32 family, member C"	23520	NM_012403.1	−0.074417224	0.471669794	0.471669794	0.00235889	0.1589
251	2640255	NULL	NULL	641848	XM_935588.1	−0.645965338	0.471482176	0.471482176	0.002369397	0.1589
252	2190390	NCOA1	nuclear receptor coactivator 1	8648	NM_147223.2	−0.208822548	0.471482176	0.471482176	0.002369397	0.1589

【表５－１９】

Spearman
表5-19

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
253	5360204	NMD3	NMD3 homolog (S. cerevisiae)	51068	NM_015938.3	−0.201253758	0.471482176	0.471482176	0.002369397	0.1589
254	4040242	FAM89A	"family with sequence similarity 89, member A"	375061	NM_198552.1	0.108042121	−0.471294559	0.471294559	0.002385235	0.1591
255	2690561	RPLP1	"ribosomal protein, large, P1"	6176	NM_001003.2	−0.685558024	0.471106942	0.471106942	0.002390536	0.1591
256	3390286	ADRA2B	"adrenergic, alpha−2B−, receptor"	151	NM_000682.5	0.054174105	−0.470731707	0.470731707	0.002417192	0.1602
257	5960332	SLC39A10	"solute carrier family 39 (zinc transporter), member 10"	57181	NM_020342.1	−0.147299889	0.470168856	0.470168856	0.002444111	0.1608
258	7380068	CNBP	"CCHC−type zinc finger, nucleic acid binding protein"	7555	NM_003418.1	−0.327720874	0.469981238	0.469981238	0.002454952	0.1608
259	1820300	CTSO	cathepsin O	1519	NM_001334.2	−0.231977107	0.469981238	0.469981238	0.002454952	0.1608
260	6100170	NULL	NULL	NULL	AI004472	0.074355718	−0.469606004	0.469606004	0.002482242	0.1612
261	7610079	HSF2BP	heat shock transcription factor 2 binding protein	11077	NM_007031.1	−0.038423478	0.469606004	0.469606004	0.002476763	0.1612
262	6480600	THUMPD1	THUMP domain containing 1	55623	NM_017736.3	−0.123219301	0.469230769	0.469230769	0.002498744	0.1612
263	990528	DNAJC10	"DnaJ (Hsp40) homolog, subfamily C, member 10"	54431	NM_018981.1	−0.085780126	0.469230769	0.469230769	0.002498744	0.1612
264	4860066	NULL	NULL	647346	XM_936495.2	−0.209955699	0.468667917	0.468667917	0.002532038	0.1624
265	5050402	HIST1H2BK	"histone cluster 1, H2bk"	85236	NM_080593.1	0.379454337	−0.4684803	0.4684803	0.002548832	0.1624
266	7040482	LOC642934	−	642934	XM_942991.2	−0.452151346	0.4684803	0.4684803	0.002543223	0.1624

【表５－２０】

Spearman
表5-20

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
267	2060050	NULL	NULL	NULL	BM932227	−0.116682268	0.467917448	0.467917448	0.00257704	0.1624
268	6590278	CBX2	"chromobox homolog 2 (Pc class homolog, Drosophila)"	84733	NM_005189.1	0.077041967	−0.467542214	0.467542214	0.002605523	0.1624
269	60053	RPL11	ribosomal protein L11	6135	NM_000975.2	−0.156372832	0.467542214	0.467542214	0.002599804	0.1624
270	1820068	AMY1C	"amylase, alpha 1C (salivary)"	278	NM_001008219.1	−0.195378515	0.467542214	0.467542214	0.002599804	0.1624
271	430100	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	2547	NM_001469.3	−0.202101353	0.467354597	0.467354597	0.002611253	0.1624
272	520133	SUMO2	SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)	6613	NM_001005849.1	−0.316672366	0.467354597	0.467354597	0.002611253	0.1624
273	3060379	SEC14L1	SEC14-like 1 (S. cerevisiae)	6397	NM_003003.1	0.211393155	−0.467354597	0.467354597	0.002616994	0.1624
274	2760553	UBA3	ubiquitin-like modifier activating enzyme 3	9039	NM_198197.1	−0.187898967	0.467166979	0.467166979	0.002622746	0.1624
275	4540689	ANKRD10	ankyrin repeat domain 10	55608	NM_017664.2	−0.170575575	0.466791745	0.466791745	0.002645865	0.1624
276	7100519	CEP57	centrosomal protein 57kDa	9702	NM_014679.3	−0.122048981	0.466604128	0.466604128	0.002657493	0.1624
277	4860431	NBPF14	"neuroblastoma breakpoint family, member 14"	25832	NM_015383.1	−0.189228519	0.46641651	0.46641651	0.002669165	0.1624
278	6110014	FUSIP1	FUS interacting protein (serine/arginine-rich) 1	10772	NM_054016.1	0.343795227	−0.46641651	0.46641651	0.002675018	0.1624
279	6250609	KPNA2	"karyopherin alpha 2 (RAG cohort 1, importin alpha 1)"	3838	NM_002266.2	−0.04951944	0.46641651	0.46641651	0.002669165	0.1624
280	2360630	FDFT1	farnesyl-diphosphate farnesyltransferase 1	2222	NM_004462.3	−0.242595956	0.466041276	0.466041276	0.002692645	0.1624

【表５－２１】

Spearman
表5-21

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
281	6860673	NUS1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	116150	NM_138459.3	−0.049044618	0.466041276	0.466041276	0.002692645	0.1624
282	6270674	RECQL	RecQ protein−like (DNA helicase Q1−like)	5965	NM_032941.1	−0.04289978	0.465853659	0.465853659	0.002704453	0.1624
283	6370435	ETS1	v−ets erythroblastosis virus E26 oncogene homolog 1 (avian)	2113	NM_005238.2	−0.467750348	0.465666041	0.465666041	0.002716307	0.1624
284	270091	C19orf68	chromosome 19 open reading frame 68	374920	NM_199341.1	0.052642885	−0.465478424	0.465478424	0.002734174	0.1624
285	1050148	LOC653264	−	653264	XM_932721.2	−0.102751263	0.465478424	0.465478424	0.002728207	0.1624
286	3990563	IFNA10	″interferon, alpha 10″	3446	NM_002171.1	0.151388979	−0.465290807	0.465290807	0.002746142	0.1624
287	2690370	ZNF92	zinc finger protein 92	168374	NM_007139.2	−0.058140458	0.465290807	0.465290807	0.002740152	0.1624
288	2640551	CMPK1	″cytidine monophosphate (UMP−CMP) kinase 1, cytosolic″	51727	NM_016308.1	−0.272595837	0.464915572	0.464915572	0.002764182	0.1624
289	3830470	PLB1	phospholipase B1	151056	NM_153021.3	0.102166339	−0.464915572	0.464915572	0.002770218	0.1624
290	1940008	LOC644330	−	644330	XR_017492.1	−0.238139626	0.464727955	0.464727955	0.002776266	0.1624
291	3610348	FAM10A4	″family with sequence similarity 10, member A4 pseudogene″	145165	NR_002183.1	−0.192448279	0.464540338	0.464540338	0.002788397	0.1626
292	6650672	ZNF439	zinc finger protein 439	90594	NM_152262.2	−0.168089512	0.464165103	0.464165103	0.002812798	0.1635
293	6590441	TRIP12	thyroid hormone receptor interactor 12	9320	NM_004238.1	−0.196624966	0.463789869	0.463789869	0.002837388	0.1643
294	3310372	NULL	NULL	NULL	AI066603	0.060736288	−0.463414634	0.463414634	0.002868392	0.1651

【表５－２２】

Spearman
表5-22

No.	プローブID	遺伝子名	遺伝子の説明	EntrezID	Acc	limma_logFC	Cor_Spearman_R	Cor_Spearman_absR	Cor_Spearman_Pval	Cor_Spearman_adPval
295	1740647	FAM180B	"family with sequence similarity 180, member B"	399888	XM_941808.2	0.083819707	-0.4630394	0.4630394	0.002893409	0.1651
296	3870670	MED7	mediator complex subunit 7	9443	NM_004270.3	-0.059699888	0.4630394	0.4630394	0.002887137	0.1651
297	6940102	TNC	tenascin C	3371	NM_002160.1	0.032850087	-0.4630394	0.4630394	0.002893409	0.1651
298	3940653	PREPL	prolyl endopeptidase-like	9581	NM_006036.2	-0.129916608	0.462664165	0.462664165	0.002912298	0.1651
299	1570292	NULL	NULL	NULL	AI807878	-0.087151047	0.462476548	0.462476548	0.002924951	0.1651
300	5890477	SNORA32	"small nucleolar RNA, H/ACA box 32"	692063	NR_003032.1	-0.085303112	0.462288931	0.462288931	0.002937652	0.1651

【００４７】

表６　Pearsonの積率相関係数、潜在変数３、上位５０遺伝子の遺伝子セットによる各患者の生存日数予測に使用した係数

【表６－１】

表6-1

ProbeID	S2_pre	S3_pre	S4_pre	S6_pre	S7_pre	S8_pre	L3_pre	L4_pre	L1_pre	S10_pre
3390368	-185	-188	-199	-198	-173	-185	-184	-184	-190	-187
1300687	127	134	118	138	138	130	130	131	135	128
5860465	38	35	45	33	32	37	34	31	35	32
4390576	-348	-362	-360	-383	-349	-346	-354	-350	-366	-362
4830255	185	201	184	208	174	206	186	177	186	202
4570403	-406	-422	-427	-449	-416	-423	-415	-410	-422	-433
1780719	33	69	-21	74	32	27	59	64	70	33
3130477	-34	-41	-45	-49	-84	-62	-53	-31	-51	-79
6110630	-478	-476	-513	-525	-493	-476	-469	-473	-446	-508
3310309	-344	-350	-340	-366	-352	-335	-342	-337	-363	-351
4220731	137	146	224	170	140	157	153	167	149	151
520706	46	47	71	53	63	72	46	42	56	38
6420446	-57	-80	-87	-74	-62	-73	-77	-86	-68	-116
1400240	350	368	295	432	401	364	376	381	347	439
7510379	17	14	36	12	31	34	15	4	6	1
2640025	-89	-80	-56	-49	-58	-43	-66	-63	-62	-78
3130296	-98	-113	-83	-115	-108	-99	-96	-94	-55	-79
3520601	-160	-166	-163	-149	-177	-173	-168	-165	-153	-224
1110091	271	264	228	263	251	281	259	262	284	255
3130370	427	415	396	457	395	389	425	431	432	450
2030332	-173	-171	-165	-189	-178	-165	-178	-173	-186	-178
670209	246	244	261	263	256	256	247	253	252	264
6560161	-235	-240	-235	-260	-241	-245	-240	-238	-244	-250
1740647	-300	-310	-305	-321	-296	-303	-300	-297	-305	-322
4880463	68	68	86	70	70	83	69	66	79	61
990315	-32	-37	-47	-43	-16	-71	-36	-34	-47	-61
240463	-72	-69	-65	-61	-63	-63	-56	-67	-32	-22
2000035	-298	-304	-289	-326	-309	-297	-298	-293	-308	-309
1780709	-58	-53	-115	-60	-65	-27	-61	-70	-50	-95
2680440	-184	-187	-191	-203	-184	-183	-188	-189	-186	-198
150672	131	132	148	147	121	126	134	145	135	125
6940176	-76	-88	7	-89	-36	-74	-89	-84	-68	-121
6180497	121	118	116	123	123	111	122	121	135	116
150706	-20	-22	17	-8	-33	-45	-23	-26	-29	-22
5900129	-181	-167	-165	-166	-144	-156	-151	-169	-119	-187
6450437	-363	-368	-359	-396	-368	-369	-365	-360	-379	-369
3990608	293	286	317	336	239	291	287	288	280	298
3120075	-57	-65	8	-67	-61	-74	-67	-68	-68	-84
1500047	-193	-196	-222	-209	-206	-186	-198	-190	-208	-204
840358	-52	-46	-57	-44	-78	-21	-52	-45	-52	-41
6590484	-70	-74	-67	-82	-82	-82	-77	-73	-66	-112
2100594	-84	-103	-61	-117	-112	-98	-101	-114	-124	-126
6650056	166	176	186	187	180	166	174	172	191	166
2120017	69	67	74	77	87	76	74	78	84	61
1780639	-65	-64	-52	-64	-70	-60	-62	-63	-67	-66
6650594	-285	-322	-247	-342	-298	-272	-310	-320	-339	-356
3420136	-139	-144	-126	-153	-149	-131	-141	-139	-139	-144
6760017	-138	-123	-130	-136	-162	-124	-134	-119	-136	-163
510209	-66	-60	-126	-63	-44	-70	-56	-66	-80	-14
4220673	-191	-199	-199	-210	-175	-195	-188	-185	-191	-198
Intercept	19978	20602	19656	20443	20673	19330	19853	19517	19384	23046

【表６－２】

表6-2

ProbeID	S12_pre	S13_pre	S14_pre	S15_pre	S16_pre	S17_pre	S18_pre	S20_pre	S21_pre
3390368	−183	−189	−191	−180	−184	−184	−183	−184	−197
1300687	130	134	140	127	134	133	131	133	175
5860465	32	28	33	28	29	33	33	33	29
4390576	−354	−365	−365	−359	−370	−356	−351	−354	−396
4830255	190	182	193	177	190	187	182	188	247
4570403	−410	−432	−429	−392	−415	−418	−405	−416	−481
1780719	65	65	95	77	65	64	54	68	129
3130477	−45	−55	−35	−39	−46	−44	−45	−42	−166
6110630	−460	−454	−487	−492	−446	−480	−464	−482	−432
3310309	−334	−346	−352	−346	−347	−342	−336	−340	−408
4220731	158	173	182	175	157	164	168	164	236
520706	45	55	33	47	51	49	42	47	57
6420446	−78	−71	−78	−89	−66	−78	−89	−75	17
1400240	383	347	373	367	370	368	366	360	296
7510379	10	3	10	8	7	12	13	10	67
2640025	−38	−54	−64	−12	−48	−63	−68	−66	−94
3130296	−104	−110	−124	−116	−107	−100	−84	−103	−185
3520601	−176	−182	−165	−202	−176	−176	−165	−169	−231
1110091	260	263	252	245	243	261	251	258	172
3130370	444	436	415	411	418	427	408	421	352
2030332	−177	−178	−186	−185	−182	−180	−168	−181	−200
670209	243	253	267	240	250	250	252	252	368
6560161	−239	−242	−251	−242	−240	−242	−239	−241	−275
1740647	−298	−309	−309	−287	−304	−299	−295	−299	−342
4880463	68	69	72	58	64	69	61	68	147
990315	−29	−32	−25	−39	−32	−34	−43	−29	4
240463	−43	−49	−59	−39	−61	−57	−55	−53	−101
2000035	−293	−311	−309	−297	−313	−300	−297	−300	−349
1780709	−75	−48	−73	−89	−47	−67	−55	−63	−36
2680440	−185	−186	−193	−191	−195	−188	−186	−188	−208
150672	136	141	150	142	144	137	134	140	213
6940176	−81	−104	−81	−80	−92	−86	−97	−90	−141
6180497	118	111	120	78	124	122	129	118	93
150706	−19	−24	−21	1	−18	−22	−29	−20	−31
5900129	−161	−135	−199	−141	−158	−161	−139	−162	−225
6450437	−363	−369	−380	−358	−379	−367	−358	−364	−448
3990608	287	292	272	289	310	296	315	290	90
3120075	−60	−66	−66	−60	−70	−65	−66	−66	−21
1500047	−195	−213	−195	−203	−203	−195	−193	−197	−241
840358	−51	−36	−52	−61	−30	−45	−37	−47	−50
6590484	−81	−92	−84	−91	−70	−79	−93	−80	−218
2100594	−112	−114	−114	−137	−118	−109	−130	−101	−141
6650056	173	181	184	171	177	175	176	174	234
2120017	79	79	73	102	78	72	80	76	117
1780639	−62	−65	−67	−60	−61	−62	−63	−62	−78
6650594	−312	−331	−332	−311	−330	−310	−300	−319	−270
3420136	−140	−146	−146	−145	−147	−142	−139	−140	−185
6760017	−128	−108	−113	−114	−137	−122	−113	−126	−20
510209	−67	−61	−78	−68	−79	−67	−48	−65	−85
4220673	−188	−200	−196	−189	−203	−190	−186	−190	−240
Intercept	19209	20247	20979	20488	20162	19945	19272	19998	24896

【表６－３】

表6-3

ProbeID	S22_pre	S23_pre	S25_pre	S26_pre	L5_pre	L6_pre	L7_pre	L8_pre	L9_pre	L10_pre
3390368	-184	-172	-180	-185	-180	-198	-100	-179	-160	-170
1300687	134	128	144	137	128	149	84	109	126	124
5860465	33	21	31	21	32	15	34	19	26	41
4390576	-352	-337	-359	-374	-362	-374	-211	-318	-314	-308
4830255	187	170	162	144	215	209	97	258	187	212
4570403	-418	-412	-427	-443	-421	-436	-237	-359	-373	-377
1780719	98	102	66	98	61	83	-7	163	66	11
3130477	-21	14	0	-51	-48	-60	57	-55	-43	-53
6110630	-481	-446	-453	-429	-493	-435	-515	-399	-472	-444
3310309	-337	-322	-356	-362	-341	-372	-193	-292	-285	-297
4220731	147	142	202	159	161	230	-48	186	147	180
520706	36	9	79	92	28	43	78	22	69	36
6420446	-66	-82	-36	-72	-99	-68	-68	-62	-54	-119
1400240	361	404	280	323	402	443	157	363	363	399
7510379	8	6	16	0	17	8	-1	-57	15	32
2640025	-47	-25	-46	-60	-67	-27	-283	87	-62	-124
3130296	-93	-77	-104	-139	-128	-170	95	-187	-92	-83
3520601	-180	-194	-167	-170	-178	-198	-99	-230	-184	-148
1110091	271	232	273	254	248	283	242	157	254	241
3130370	396	425	412	493	406	410	477	346	425	373
2030332	-175	-170	-184	-177	-174	-184	-146	-177	-166	-176
670209	244	232	243	261	273	256	109	198	239	213
6560161	-235	-228	-253	-251	-246	-260	-133	-227	-220	-214
1740647	-287	-279	-314	-325	-312	-325	-157	-273	-255	-266
4880463	66	75	75	76	63	83	36	79	67	50
990315	-32	-17	-54	-19	-66	-14	-32	-4	-3	-44
240463	-59	-33	-75	-78	-77	-52	-59	-30	-75	-73
2000035	-287	-293	-306	-324	-299	-326	-175	-252	-266	-264
1780709	-87	-94	-63	-40	-32	-126	25	-84	-63	-83
2680440	-190	-166	-178	-208	-194	-173	-125	-177	-180	-164
150672	115	151	158	152	138	151	66	150	122	143
6940176	-109	-143	-106	-79	-54	-62	-106	-33	-131	-126
6180497	139	141	101	116	139	47	183	18	119	145
150706	-20	-14	-31	-26	11	-24	-73	51	-13	-77
5900129	-159	-154	-168	-158	-173	-190	47	-266	-164	-123
6450437	-367	-333	-376	-399	-373	-404	-231	-313	-333	-314
3990608	286	249	360	292	275	286	214	334	316	334
3120075	-65	-66	-42	-74	-61	-52	-73	-87	-62	-82
1500047	-173	-196	-189	-177	-196	-195	-39	-222	-153	-194
840358	-57	-50	-40	-30	-70	-52	19	-144	-20	-34
6590484	-80	-92	-65	-63	-98	-88	-96	5	-100	-39
2100594	-142	-90	-95	-152	-126	-133	-12	-178	-97	-64
6650056	179	161	176	183	171	210	95	142	155	165
2120017	78	65	74	76	64	70	102	1	74	20
1780639	-73	-46	-55	-65	-65	-67	-30	-66	-50	-54
6650594	-308	-325	-300	-345	-336	-376	-227	-257	-292	-259
3420136	-134	-140	-136	-139	-148	-172	-90	-99	-134	-126
6760017	-81	-100	-115	-73	-138	-128	-92	-118	-129	-107
510209	-81	-61	-84	-99	-86	-27	-121	49	-63	-37
4220673	-188	-175	-180	-202	-194	-213	-97	-165	-171	-169
Intercept	19939	18424	19115	20488	21351	20804	13062	17736	17185	17648

【表６－４】

表6-4

ProbeID	L11_pre	L12_pre	L13_pre	L14_pre	L15_pre	L16_pre	L17_pre	L18_pre	L20_pre	L21_pre
3390368	−192	−186	−187	−182	−185	−183	−179	−185	−193	−191
1300687	139	133	130	121	133	138	136	135	135	153
5860465	28	34	40	47	34	41	39	40	44	33
4390576	−362	−360	−378	−376	−355	−356	−335	−359	−349	−375
4830255	180	185	154	231	185	163	203	189	201	202
4570403	−417	−420	−419	−425	−419	−422	−401	−419	−426	−428
1780719	37	67	85	54	62	43	63	68	79	82
3130477	−24	−50	−57	−39	−37	−50	−11	−42	−55	−44
6110630	−502	−469	−441	−463	−482	−458	−469	−483	−447	−450
3310309	−355	−344	−362	−353	−342	−348	−334	−341	−341	−356
4220731	183	157	146	170	160	157	161	160	158	174
520706	18	55	74	41	52	28	43	51	32	56
6420446	−62	−78	−89	−47	−78	−75	−83	−82	−100	−96
1400240	336	368	368	332	366	369	383	375	385	367
7510379	20	15	31	17	14	20	21	9	11	20
2640025	−10	−70	−109	25	−58	−51	−55	−70	−25	−54
3130296	−108	−100	−102	−102	−100	−85	−97	−111	−99	−134
3520601	−169	−169	−153	−165	−176	−170	−148	−170	−177	−133
1110091	275	260	299	273	260	264	254	254	271	268
3130370	454	421	398	377	425	430	433	426	441	411
2030332	−172	−178	−175	−184	−180	−170	−181	−183	−180	−178
670209	241	247	271	272	249	252	253	237	261	255
6560161	−229	−242	−260	−242	−241	−241	−235	−243	−239	−253
1740647	−301	−303	−308	−324	−302	−302	−295	−307	−311	−314
4880463	63	70	61	71	70	64	57	72	75	84
990315	−37	−31	−26	−31	−31	−24	−28	−40	−45	−8
240463	−68	−56	−45	−28	−59	−46	−58	−52	−58	−53
2000035	−297	−301	−308	−302	−302	−301	−295	−302	−306	−316
1780709	−121	−65	−27	−77	−65	−79	−85	−73	−10	−55
2680440	−195	−189	−201	−191	−189	−184	−182	−193	−188	−195
150672	123	137	135	107	137	140	144	151	150	168
6940176	−62	−91	−94	−80	−85	−96	−71	−77	−63	−54
6180497	92	121	119	145	121	138	138	77	170	134
150706	−5	−23	−4	−45	−25	−27	−16	−32	−32	−11
5900129	−187	−168	−153	−186	−159	−126	−148	−184	−153	−170
6450437	−362	−367	−367	−376	−368	−360	−336	−363	−381	−388
3990608	263	295	283	336	290	260	284	285	284	320
3120075	−55	−65	−52	−54	−65	−67	−66	−62	−76	−59
1500047	−194	−194	−217	−238	−198	−199	−195	−203	−203	−204
840358	−51	−48	−22	−74	−44	−39	−57	−37	−53	−65
6590484	−38	−79	−136	−38	−82	−75	−53	−67	−100	−42
2100594	−68	−106	−120	−76	−109	−119	−113	−114	−121	−103
6650056	173	176	170	170	174	174	177	185	180	179
2120017	97	78	85	77	74	84	66	77	54	92
1780639	−62	−63	−65	−66	−63	−62	−64	−64	−70	−63
6650594	−277	−309	−307	−266	−309	−291	−302	−320	−317	−321
3420136	−141	−141	−148	−129	−142	−142	−139	−143	−151	−155
6760017	−146	−117	−118	−123	−122	−120	−125	−111	−112	−134
510209	−24	−61	−92	−46	−68	−46	−48	−46	−106	−80
4220673	−201	−192	−194	−184	−190	−187	−175	−193	−204	−197
Intercept	19780	19946	20285	18703	20057	19357	17800	20390	19420	18749

【表６－５】

表6-5

ProbeID	L19_pre
3390368	-195
1300687	125
5860465	21
4390576	-385
4830255	161
4570403	-435
1780719	83
3130477	-14
6110630	-519
3310309	-348
4220731	206
520706	59
6420446	-86
1400240	381
7510379	-6
2640025	-69
3130296	-112
3520601	-159
1110091	331
3130370	406
2030332	-189
670209	255
6560161	-250
1740647	-311
4880463	57
990315	-13
240463	-97
2000035	-291
1780709	-68
2680440	-193
150672	102
6940176	-74
6180497	115
150706	-24
5900129	-195
6450437	-390
3990608	312
3120075	-80
1500047	-193
840358	-30
6590484	-104
2100594	-124
6650056	164
2120017	63
1780639	-68
6650594	-327
3420136	-139
6760017	-98
510209	-81
4220673	-195
Intercept	21296

【００４８】

表７　ランダム選択による３０の遺伝子セット

【表７】

表7

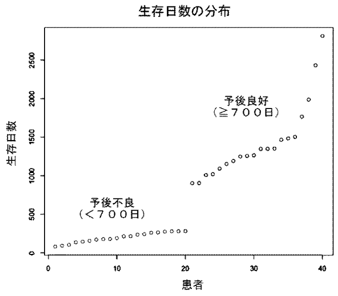
遺伝子セット	Gene ID1	Gene ID2	Gene ID3	Gene ID4	Gene ID5	Gene ID6	Gene ID7	Gene ID8	Gene ID9	Gene ID10	Gene ID11	Gene ID12	Gene ID13	Gene ID14	Gene ID15	Gene ID16	Gene ID17	Gene ID18	Gene ID19	Gene ID20	Gene ID21	Gene ID22	Gene ID23	Gene ID24	Gene ID25	Gene ID26	Gene ID27	Gene ID28	Gene ID29	Gene ID30
1	97	281	275	300	4	239	55	146	240	140	218	53	126	210	205	31	221	136	132	3	30	182	201	166	142	107	212	264	162	
2	243	211	99	113	49	291	205	259	276	127	48	218	112	18																
3	144	4	76	103	157	115	245	278	7	274	225	151	291	273	54	83	91													
4	103	255	188	275	109	11	78	74	257	167	296	119	278	126	138	64	116	36												
5	96	93	211	85	76	184	216	153	252	54	87	13	209	11	210	83	109	253	107											
6	8	298	185	253	254	135	62	69	291	178	256	26	188	272	275	165	182	289	167	20	6	204								
7	59	84	261	273	155	251	175	49	86	112	205	198	266	81	162	71	126	246	44	128	156	22	85	177	80	74				
8	67	4	80	14	297	86	271	171	12	135	226	239	3	69	264	46	184	160	84	186	45	285	230	203	278	25	292			
9	47	163	141	113	295	233	137	150	94	97	276	100	182	79	293	267	247	70	1	272	203	38	84	180	39	211	82	178		
10	206	119	201	93	239	222	19	237	14	245	41	184	299	210	85	231	177	208	150	175	23									
11	233	227	106	19	171	282	118	295	146	266	122	174	108	254	175	123	128	66	79											
12	266	257	245	197	165	182	137	21	88	228	167	231	206	242	123	155	293	290	102	258	240	16	162	144	221	38				
13	108	69	194	63	10	35	101	242	186	61	278	107	106	11	168	246	277	68	78	139	218									
14	244	98	67	260	278	287	144	65	201	108	58	247																		
15	103	58	257	83	108	159	280	284	132	63	123	264	206	24	72	208	93	65	52	203	17	81	117	142	299	47	131	288	98	177
16	24	189	154	33	64	273	62	9	178	199	149	278	34	88	272	299	168	206	203	263										
17	178	179	248	66	37	218	103	167	183	264	242	41	300	100	47	245	9	175	57	287	106	196	150							
18	48	63	102	235	169	141	41	264	151	175																				
19	191	130	89	77	196	247	134	7	259	232	64	56	224	128	11	273	276	69	243	291	155	254	266	63	92	219	136	185	299	132
20	77	169	248	257	225	158	253	281	282	80	128	299	254	148	260	291	298	74	5											
21	40	207	229	67	256	63	298	254	102	79	82	112	211	290	89	133														
22	67	161	110	236	90	283	164	10	45	134	36	132	52	23	9	203	230	299	202	28	255	125	296	103	62	47	72	178	162	238
23	21	84	260	224	111	249	172	92	203	209	274																			
24	11	265	268	4	191	154	274	292	199	142	224	139	185	239	257	113	267	120	150	247	27	201	91	112	178	13	125			
25	162	296	183	85	33	41	286	93	251	224	48	221	40	7	73	184	67	174	298	173	234	269	102	3	43					
26	222	101	181	186	145	6	135	120	157	291	295	235	53	102	160	155	273	83	297	298	191	243	249	70	27	230				
27	238	30	279	275	135	97	200	44	232	237	35	173	207	27	234	202	298	158	194	136	118	28	268	210	299	188	262			
28	87	40	175	138	72	43	300	65	187	90	80	50	282	263	124	297	213	294	242	104	201	214								
29	48	117	157	57	244	13	289	276	218	49	251	283	140	181	145	267	287	246												
30	49	168	121	271	47	232	238	95	233	264	71	297	246	27	160	150	262	129	98	251	69	237	294	156						

＊数字は表１における順位を示す。

【図１】

患者データ

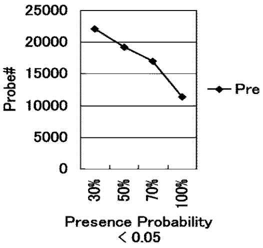
	投与前
予後良好	20 例
予後不良	20 例



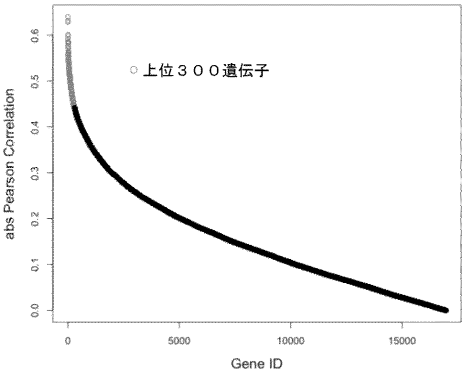
【図２】

マイクロアレイデータの前処理

- 正規化
  - VST(variance-stabilizing transformation)
  - RNS(Robust spline normalization)
- Presence Call
  - 解析対象データ内で70%以上のpresence probability<0.05を満たすプローブ



【図３】



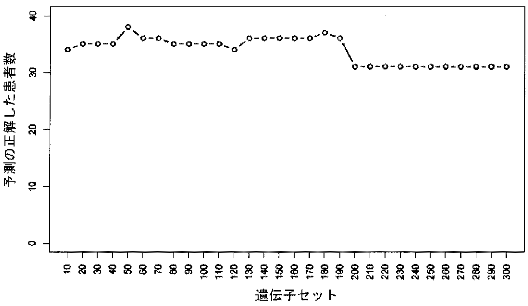
【図４】

予測精度の比較

遺伝子選択方法	正解数(正解率)	遺伝子セット-潜在変数(LV)
Limma	36 (90%)	10-LV1, 30-LV2
SAM	35 (87.5%)	10-LV1
Rank Prod	32 (80%)	70-LV3, 60-LV4, 90-LV5, 100-LV5
Pearson	38 (95%)	50-LV3
Spearman	35 (87.5%)	40-LV8, 40-LV9, 40-LV10, 50-LV8, 50-LV9, 270-LV7, 270-LV8

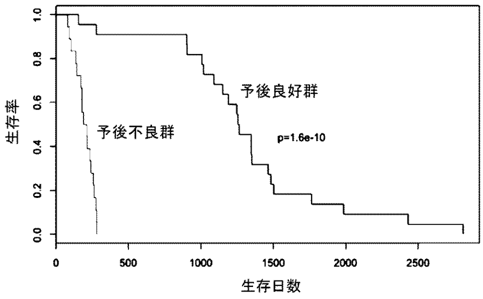
【図５】

予測精度（ascent：1→300）



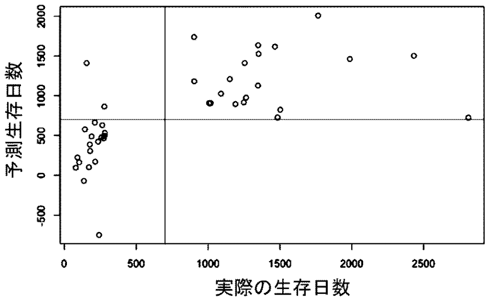
【図７】

Kaplan-Meier 曲線（Pearson、LV=3、50 遺伝子）



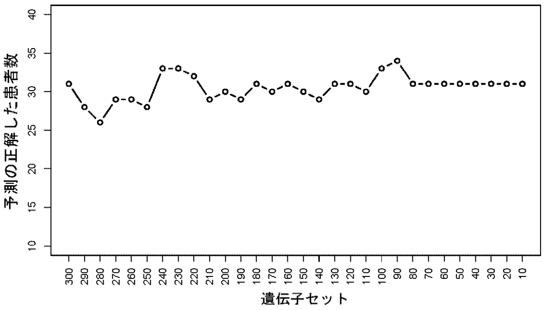
【図６】

Pearson、LV=3、50 遺伝子

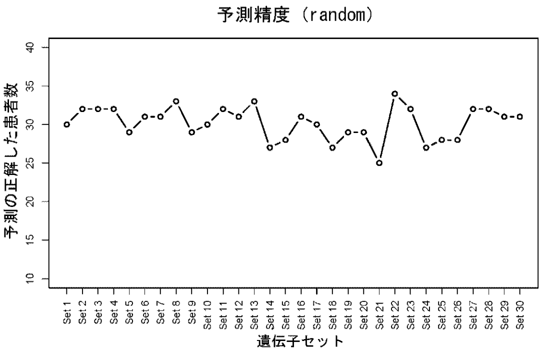


【図８】

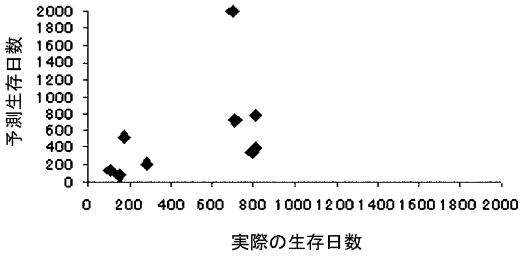
予測精度（descent：300→1）



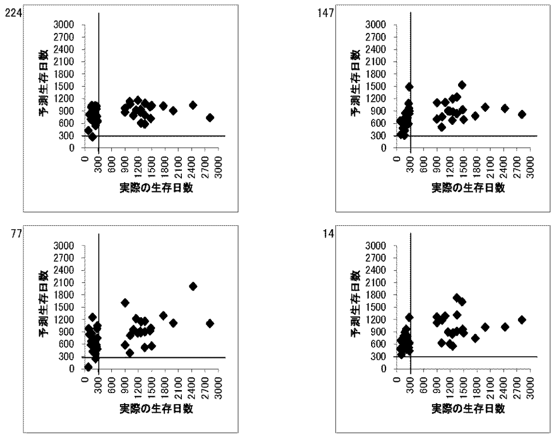
【図９】



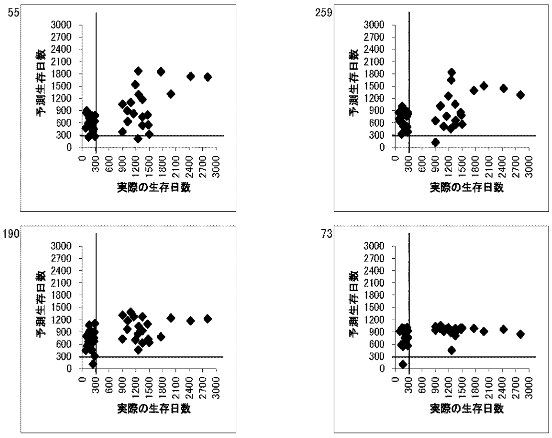
【図１０】



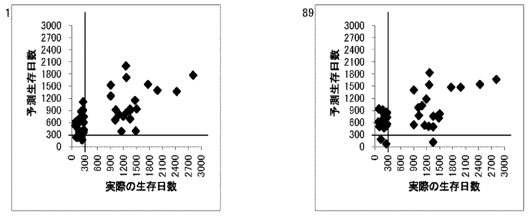
【図１１－１】



【図１１－２】



【図１１－３】



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(72)発明者　野口　正典
福岡県久留米市旭町６７番地　久留米大学内
(72)発明者　山田　亮
福岡県久留米市旭町６７番地　久留米大学内
(72)発明者　七條　茂樹
福岡県久留米市旭町６７番地　久留米大学内
(72)発明者　小松　誠和
福岡県久留米市旭町６７番地　久留米大学内

審査官　柴原　直司

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ＪＳＴＰｌｕｓ／ＪＭＥＤＰｌｕｓ／ＪＳＴ７５８０（ＪＤｒｅａｍＩＩＩ）
ＰｕｂＭｅｄ
ＢＩＯＳＩＳ／ＭＥＤＬＩＮＥ／ＷＰＩＤＳ（ＳＴＮ）

专利名称(译)	用于预测癌症患者和/或免疫疗法的免疫疗法后的预后的方法，基因组和用于所述方法的试剂盒		
公开(公告)号	JP5892794B2	公开(公告)日	2016-03-23
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申请(专利权)人(译)	学校法人 久留米大学		
当前申请(专利权)人(译)	学校法人 久留米大学		
[标]发明人	伊東恭悟 野口正典 山田亮 七條茂樹 小松誠和		
发明人	伊東 恭悟 野口 正典 山田 亮 七條 茂樹 小松 誠和		
IPC分类号	C12N15/09 C12Q1/68 C12M1/00 G01N33/53 G01N37/00		
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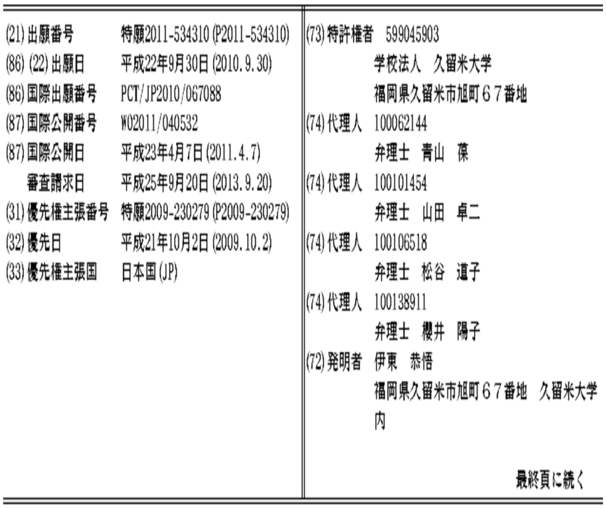
代理人(译)	山田卓司 櫻井洋子		
优先权	2009230279 2009-10-02 JP		
其他公开文献	JPWO2011040532A1		
外部链接	Espacenet		

摘要(译)

技术领域本发明涉及用于预测癌症患者和/或免疫疗法的免疫疗法后的预后的方法，以及用于该方法的基因组和试剂盒。



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(73) 特許権者	599045903 学校法人　久留米大学 福岡県久留米市旭町６７番地
(74) 代理人	100062144 弁理士　青山　葆
(74) 代理人	100101454 弁理士　山田　卓二
(74) 代理人	100106518 弁理士　松谷　道子
(74) 代理人	100138911 弁理士　櫻井　陽子
(72) 発明者	伊東　恭悟 福岡県久留米市旭町６７番地　久留米大学内

最終頁に続く