

Identifikasi Differentially Expressed Genes (DEG) pada Patogenesis Psoriasis Menggunakan GEO2R

1. PENDAHULUAN

1.1 Latar Belakang

Psoriasis merupakan penyakit autoimun inflamasi kronis yang diderita oleh sekitar 7,4 juta orang dewasa di Amerika Serikat. Prevalensi tertinggi ditemukan pada varian psoriasis plak, yang mencakup 80% hingga 90% dari keseluruhan kasus (Mutmainna et al., 2020). Psoriasis bersifat multifaktoral yang dipengaruhi oleh predisposisi genetik, paparan lingkungan, dan proses inflamasi termediasi imunologis. Selain itu, kondisi ini berkaitan dengan faktor penyerta seperti obesitas, trauma fisik, infeksi, serta defisiensi bentuk aktif vitamin D3. Pemahaman mengenai psoriasis sangat penting karena penanganannya tidak hanya terfokus pada masalah kulit saja. Meskipun banyak penelitian dalam beberapa tahun terakhir telah mencoba menjelaskan mekanisme molekulernya, penyebab utama penyakit ini masih belum diketahui secara pasti (Yuliastuti, 2015).

Salah satu pendekatan untuk memahami mekanisme tersebut adalah melalui teknologi *microarray*, yang memungkinkan pemantauan ribuan ekspresi gen sekaligus. Kemampuannya dalam menangani data besar menjadikan analisis ini krusial di bidang biostatistika dan penelitian medis lainnya (Rusamsi et al., 2018). Melalui perbandingan antara jaringan kulit sehat (non-lesional) dan kulit yang terdampak (lesional), dapat diidentifikasi gen yang mengalami perubahan ekspresi atau *Differentially Expressed Genes* (DEG). Identifikasi DEG ini sangat krusial dalam menemukan biomarker diagnostik baru serta menentukan target terapi yang lebih presisi bagi penderita psoriasis.

1.2 Tujuan Analisis

Analisis ini bertujuan untuk:

1. Menganalisis data ekspresi gen dari dataset publik GSE41662 menggunakan tools web-based GEO2R.

2. Mengidentifikasi daftar gen yang mengalami peningkatan ekspresi (up-regulated) dan penurunan ekspresi (down-regulated) secara signifikan pada lesi psoriasis.

2. METODE

2.1 Dataset dan Sumber Data

Analisis ini menggunakan dataset transkriptomik dengan nomor akses **GSE41662** yang diperoleh dari database Gene Expression Omnibus (GEO) NCBI. Data tersebut dihasilkan menggunakan platform **Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)** (Bigler et al., 2013). Pemilihan dataset ini didasarkan pada desain studinya yang representatif, yakni membandingkan sampel berpasangan (*paired samples*) dari 24 orang pasien psoriasis dengan metode *paired biopsies*, yakni mengambil satu sampel dari lesi psoriasis dan satu sampel dari kulit non-lesional (sehat) pada area tubuh yang sama dari pasien yang sama. Prosedur ini bertujuan meminimalkan variasi genetik antar individu.

2.2 Pengelompokan Sampel

Sampel dibagi menjadi dua kelompok utama, yaitu:

- **Kelompok Uji (Group 1 - Psoriasis/Lesional):** Terdiri dari sampel kulit yang diambil langsung dari area lesi psoriasis.

GSM1021248	GSM1021272	GSM1021260	GSM1021284
GSM1021250	GSM1021274	GSM1021262	GSM1021286
GSM1021252	GSM1021276	GSM1021264	GSM1021288
GSM1021254	GSM1021278	GSM1021266	GSM1021290
GSM1021256	GSM1021280	GSM1021268	GSM1021292
GSM1021258	GSM1021282	GSM1021270	GSM1021294

- **Kelompok Kontrol (Group 2 - Normal/Non-Lesional):** Terdiri dari sampel kulit sehat dari pasien yang sama.

GSM1021281	GSM1021293	GSM1021271	GSM1021259
GSM1021283	GSM1021295	GSM1021269	GSM1021257
GSM1021285	GSM1021279	GSM1021267	GSM1021255
GSM1021287	GSM1021277	GSM1021265	GSM1021253
GSM1021289	GSM1021275	GSM1021263	GSM1021251
GSM1021291	GSM1021273	GSM1021261	GSM1021249

2.3 Parameter Statistik

Analisis *Differentially expressed genes* (DEG) dilakukan menggunakan instrumen GEO2R dengan parameter statistik sebagai berikut:

- **Koreksi P-value:** Menggunakan metode Benjamini & Hochberg (*False Discovery Rate*) untuk meminimalisasi temuan positif palsu (*false positive*) akibat pengujian ribuan gen secara simultan.
- **Ambang Batas Signifikansi:** Gen diklasifikasikan sebagai DEG apabila memiliki nilai P-value yang disesuaikan (*Adjusted P-value*) $< 0,05$ dan nilai absolut \log_2 Fold Change > 1 .
- **Transformasi Data:** Data dideteksi secara otomatis untuk aplikasi transformasi logaritma (\log_2) guna menormalisasi distribusi nilai ekspresi gen.

2.4 Skema Replikasi dan Validasi

Sesuai dengan prinsip *reproducibility*, seluruh tahapan analisis, mulai dari pengelompokan sampel hingga perhitungan statistik diulang sebanyak tiga kali secara mandiri. Konsistensi hasil dipastikan dengan mengecek urutan gen pada daftar Top 250 serta melihat apakah nilai \log_2 FC tetap stabil di setiap pengulangan.

3. HASIL DAN INTERPRETASI

3.1 Ringkasan Output Statistik DEG

Berdasarkan hasil analisis terhadap 48 sampel (24 pasien dengan metode *paired-samples*), ditemukan profil ekspresi gen yang sangat signifikan antara kulit lesi psoriasis dan kulit normal. Hasil pengolahan data menggunakan GEO2R menunjukkan adanya perubahan transkriptomik masif, yang dibuktikan dengan banyaknya jumlah gen yang melewati ambang batas signifikansi.

Nilai Signifikansi statistik yang sangat tinggi ditemukan pada dataset ini, di mana gen-gen teratas memiliki nilai *Adjusted P-value* pada orde 10^{-25} (seperti terlihat pada gen KYNU). Hal ini menunjukkan bahwa data ekspresi gen antara kulit psoriasis dan normal memiliki perbedaan yang sangat nyata. Sesuai dengan kategori grup pada metode penelitian, di mana Group 1 didefinisikan sebagai Psoriasis (Lesional), maka arah perubahan ekspresi gen ditentukan oleh nilai \log_2 Fold Change. Nilai positif (+) pada kolom tersebut merepresentasikan gen yang mengalami peningkatan ekspresi (Up-regulated) pada kondisi patologis, sedangkan nilai negatif (-) menunjukkan penurunan ekspresi gen (Down-regulated) dibandingkan dengan kondisi normal.

Tabel 1. 10 Gen Berdasarkan Nilai Signifikansi Statistik (GSE41662)

No.	ID	Gene Symbol	Adj.P.Val	logFC	Status
1	217388_s_at	KYNU	6.67e-25	+3.46	Up-regulated
2	204385_at	KYNU	8.85e-24	+4.26	Up-regulated
3	210663_s_at	KYNU	4.09e-21	+4.05	Up-regulated
4	213523_at	CCNE1	2.25e-19	+1.93	Up-regulated
5	220664_at	SPRR2C	2.25e-19	+6.21	Up-regulated
6	204032_at	BCAR3	1.19e-14	-1.32	Down-regulated
7	227172_at	TMEM116	1.35e-14	-1.37	Down-regulated
8	213050_at	COBL	2.01e-14	-1.18	Down-regulated
9	230197_s_at	TPPP	7.84e-14	-2.19	Down-regulated
10	218517_at	JADE1	7.84e-14	-1.07	Down-regulated

3.2 Interpretasi Arah Perubahan Ekspresi

Analisis data menunjukkan dinamika ekspresi gen yang cukup signifikan pada kondisi psoriasis. Lima urutan teratas didominasi oleh gen **up-regulated** dengan nilai logFC positif, di mana gen **SPRR2C** menunjukkan peningkatan tertinggi sebesar **+6.21**. Sebaliknya, lima urutan berikutnya menunjukkan status **down-regulated** dengan nilai logFC negatif. Penurunan paling signifikan terlihat pada gen **TPPP** dengan nilai **-2.19**, yang mengindikasikan bahwa ekspresi gen tersebut berkurang cukup tinggi dibandingkan kulit normal.

3.3 Kaitan Biologis dan Patofisiologi

Gen-gen yang teridentifikasi dalam Tabel 1 memiliki peran krusial dalam mekanisme terjadinya psoriasis, beberapa gen yang melibatkan gangguan pada jalur metabolisme, respon imun, dan stabilitas struktur epidermis:

- **Pemicu Peradangan Kulit melalui Jalur Metabolisme (KYNU):** Dominasi gen **KYNU** (*Kynureninase*) pada peringkat teratas menunjukkan adanya gangguan pengolahan protein di kulit. Aktivasi gen ini dipicu oleh sinyal peradangan (**IFN γ**) yang merusak keseimbangan asam amino triptofan. Hal ini membuat kondisi kulit terus-menerus meradang dan menjadi pemicu utama mengapa luka psoriasis sulit sembuh (Harden et al., 2016).
- **Gangguan Struktur dan Respon Pertahanan Kulit (S100A7A):** Kondisi fisik kulit yang bersisik pada psoriasis berkaitan erat dengan aktivitas gen S100A7A (atau dikenal

sebagai Psoriasin) yang meningkat sangat tajam. Menurut penelitian Liang et al. (2023), gen ini bekerja seperti "alarm" yang memanggil sel-sel imun untuk berkumpul di kulit dan mengeluarkan zat-zat peradangan baru. Selain membuat kulit makin merah, gen ini juga merusak lapisan lemak pelindung kulit. Akibatnya, pertahanan kulit jadi hancur dan sel-sel kulit mati tidak bisa lepas dengan normal, melainkan menumpuk menjadi sisik tebal berwarna perak yang khas pada pasien psoriasis.

4. KESIMPULAN



Analisis pada dataset GSE41662 menyimpulkan bahwa terdapat perbedaan ekspresi gen yang sangat signifikan antara kulit lesi psoriasis dan kulit normal, yang menunjukkan adanya perubahan sistem biologis yang signifikan. Hasil identifikasi menunjukkan bahwa peningkatan gen **KYNU** dan **S100A7A** (Psoriasin) menjadi salah satu kunci utama dalam perkembangan penyakit ini. Gen **KYNU** berperan dalam memperparah kondisi peradangan kronis melalui gangguan metabolisme protein, sementara **S100A7A** bertindak sebagai pemicu penumpukan sel imun dan kerusakan lapisan pelindung kulit yang menyebabkan munculnya gejala khas berupa sisik tebal berwarna perak. Secara keseluruhan, gen-gen tersebut merupakan biomarker krusial yang menggambarkan bagaimana gangguan imunologi dan struktur kulit saling berkaitan dalam patofisiologi psoriasis.

DAFTAR PUSTAKA

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LAMPIRAN

- **Lampiran 1:** Informasi Dataset (NCBI GEO)


Gene Expression Omnibus

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Scope: **Self** Format: **HTML** Amount: **Quick** GEO accession: **GSE41662** **GO**

Series GSE41662 [Query DataSets for GSE41662](#)

Status

Public on Jan 28, 2013

Title

Gene expression profiling in psoriatic lesional and non-lesional skin [Set 2]

Organism

[Homo sapiens](#)

Experiment type

Expression profiling by array

Summary

To explore the psoriasis phenotype and pathways involved in psoriasis, we characterized gene expression in lesional and non-lesional skin from psoriasis patients.

Overall design

From each of the 24 psoriasis patients, we obtained two biopsies, one from a lesion and the other from non-lesional skin in the same general body geography. Total RNA was extracted from 6mm punch biopsies that were split in half. A total of 48 samples were run on Affymetrix HU133 Plus 2.0 microarrays.

Contributor(s)

[Bigler J](#), [Timour M](#), [Kerkof K](#), [Russell CB](#)

Citation(s)

[Bigler J](#), [Rand HA](#), [Kerkof K](#), [Timour M](#) et al. Cross-study homogeneity of psoriasis gene expression in skin across a large expression range. *PLoS One* 2013;8(1):e52242. PMID: [23308107](#)

Analyze with GEO2R

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Platforms (1)

[GPL570](#) [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array

Samples (48)

[GSM1021248](#) 1134 lesional

[More...](#)

[GSM1021249](#) 1134 non-lesional

[GSM1021250](#) 1135 lesional

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[GSE41664](#) Comparison of Gene Expression in Psoriatic Skin from Different Sources

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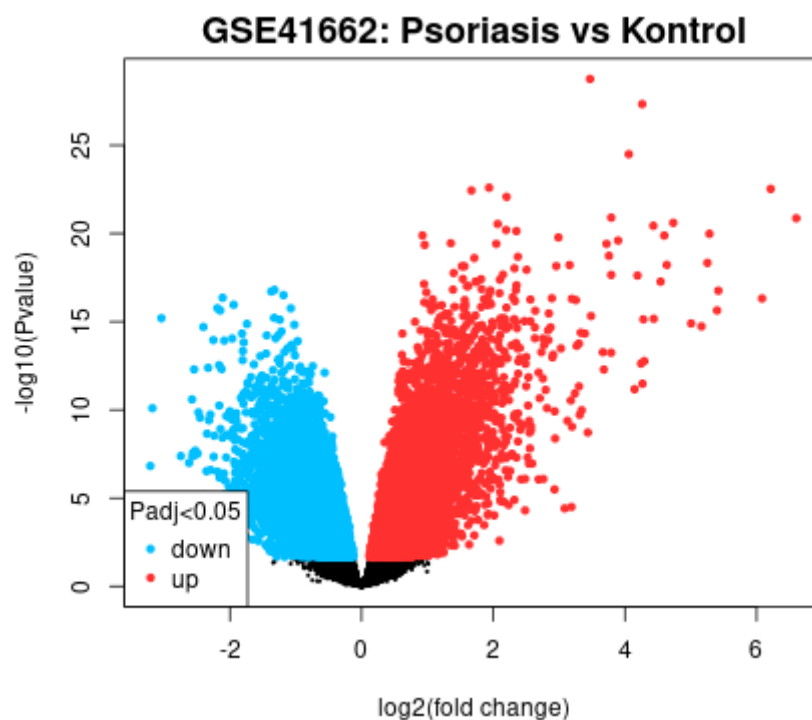
Supplementary file	Size	Download	File type/resource
GSE41662_RAW.tar	258.9 Mb	(http)(custom)	TAR (of CEL)

Processed data included within Sample table

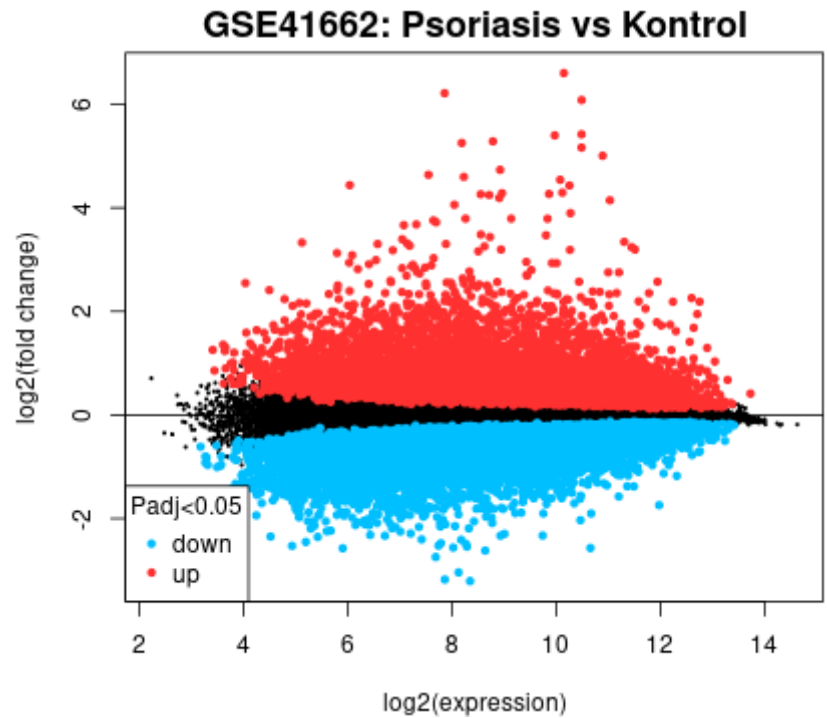
- **Lampiran 2:** Dokumentasi Pengelompokan Sampel pada GEO2R

Sample Groups	Kontrol:
Psoriasis: GSM1021248, GSM1021250, GSM1021252, GSM1021254, GSM1021256, GSM1021258, GSM1021260, GSM1021262, GSM1021264, GSM1021266, GSM1021268, GSM1021270, GSM1021272, GSM1021274, GSM1021276, GSM1021278, GSM1021280, GSM1021282, GSM1021284, GSM1021286, GSM1021288, GSM1021290, GSM1021292, GSM1021294	GSM1021281, GSM1021283, GSM1021285, GSM1021287, GSM1021289, GSM1021291, GSM1021293, GSM1021295, GSM1021279, GSM1021277, GSM1021275, GSM1021273, GSM1021271, GSM1021269, GSM1021267, GSM1021265, GSM1021263, GSM1021261, GSM1021259, GSM1021257, GSM1021255, GSM1021253, GSM1021251, GSM1021249

- **Lampiran 3:** Visualisasi Data (*Volcano Plot*)



- Lampiran 4: Visualisasi Data (*Mean-Difference Plot*)



- Lampiran 5: Hasil Output GSE41662

Top differentially expressed genes [®]							
Download full table		Select columns					
ID	adj.P.Val	P.Value	t	B	logFC	Gene.symbol	Gene.title
† 217388_s_at	6.67e-25	1.75e-29	24.8	55.9	3.469	KYNU	kynureninase
† 204385_at	8.85e-24	4.66e-28	23	52.9	4.263	KYNU	kynureninase
† 210663_s_at	4.09e-21	3.22e-25	19.9	46.7	4.059	KYNU	kynureninase
† 213523_at	2.25e-19	2.55e-23	18	42.6	1.937	CCNE1	cyclin E1
† 220664_at	2.25e-19	2.96e-23	17.9	42.4	6.214	SPRR2C	small proline rich protein 2...
† 220011_at	2.33e-19	3.67e-23	17.8	42.2	1.669	AUNIP	aurora kinase A and ninein...
† 218384_at	4.58e-19	8.43e-23	17.5	41.4	2.202	CARHSP1	calcium regulated heat sta...
† 205783_at	5.79e-18	1.26e-21	16.4	38.8	3.792	KLK13	kallikrein related peptidas...
† 232170_at	5.79e-18	1.37e-21	16.4	38.8	6.602	S100A7A	S100 calcium binding prot...
† 232220_at	9.49e-18	2.49e-21	16.1	38.2	4.734	S100A7A	S100 calcium binding prot...
† 203127_s_at	9.92e-18	2.87e-21	16.1	38.1	2.067	SPTLC2	serine palmitoyltransferas...
† 212531_at	1.16e-17	3.68e-21	16	37.8	4.432	LOC2	lipocalin 2
† 208650_s_at	1.87e-17	6.40e-21	15.8	37.3	2.194	CD24	CD24 molecule
† 209800_at	1.98e-17	7.28e-21	15.7	37.2	2.352	KRT16	keratin 16
† 206513_at	2.66e-17	1.05e-20	15.6	36.8	5.284	TCN1	transcobalamin 1
† 203740_at	2.94e-17	1.30e-20	15.5	36.6	0.925	MPHOSPH6	M-phase phosphoprotein 6
† 238430_at	2.94e-17	1.32e-20	15.5	36.6	4.587	IGF1	IGF like family member 1
† 236198_at	3.55e-17	1.68e-20	15.4	36.3	2.99	LINC01215	long intergenic non-protei...
† 206561_s_at	5.06e-17	2.53e-20	15.3	35.9	3.897	AKR1B10	aldo-keto reductase family...
† 211762_s_at	6.71e-17	3.57e-20	15.1	35.6	1.356	KPNA2	karyopherin subunit alpha 2
† 210652_s_at	6.71e-17	3.87e-20	15.1	35.5	2.046	TTC38A	tetratricopeptide repeat do...
† 232074_at	6.71e-17	3.88e-20	15.1	35.5	3.721	PRSS27	protease, serine 27
† 212460_at	7.37e-17	4.46e-20	15.1	35.4	0.958	SPTSSA	serine palmitoyltransferas...
† 216250_s_at	2.92e-16	1.85e-19	14.5	34	3.757	SERPINE13	serpin family B member 13
† 210951_x_at	3.21e-16	2.11e-19	14.5	33.9	2.374	RAB27A	RAB27A, member RAS on...
† 206364_at	3.63e-16	2.48e-19	14.4	33.7	1.712	KIF14	kinesin family member 14
† 202859_x_at	6.56e-16	4.65e-19	14.2	33.1	5.252	CXCL8	C-X-C motif chemokine lig...
† 1569555_s_at	8.16e-16	6.06e-19	14.1	32.9	4.637	GDA	guanine deaminase
† 215808_at	8.16e-16	6.22e-19	14.1	32.8	3.16	KLK10	kallikrein related peptidas...
† 209773_s_at	8.63e-16	7.14e-19	14.1	32.7	2.957	RRM2	ribonucleotide reductase r...
† 202805_s_at	8.63e-16	7.20e-19	14	32.7	1.524	ABCC1	ATP binding cassette subf...
† 223570_at	8.63e-16	7.26e-19	14	32.7	1.562	MCM10	minichromosome mainten...
† 209514_s_at	1.09e-15	9.43e-19	14	32.4	2.321	RAB27A	RAB27A, member RAS on...
† 207008_at	1.28e-15	1.14e-18	13.9	32.2	2.506	CXCR2	C-X-C motif chemokine re...
† 217834_s_at	1.88e-15	1.73e-18	13.7	31.8	1.399	SYNCRIP	synaptotagmin binding cyt...
† 220651_s_at	2.28e-15	2.15e-18	13.7	31.6	2.148	MCM10	minichromosome mainten...
† 214490_at	2.30e-15	2.24e-18	13.6	31.6	3.792	ARSF	arylsulfatase F
† 224239_at	2.40e-15	2.39e-18	13.6	31.5	4.191	DEFB103A/DEFB103B	defensin beta 103A//defe...
† 218454_at	3.71e-15	3.80e-18	13.5	31.1	1.538	PLBD1	phospholipase B domain c...
† 204825_at	3.74e-15	3.93e-18	13.5	31	1.815	MELK	maternal embryonic leucin...
† 214710_s_at	3.89e-15	4.20e-18	13.4	31	2.1	CCNB1	cyclin B1
† 204995_at	4.76e-15	5.37e-18	13.3	30.7	1.733	CDKSR1	cyclin dependent kinase 5 ...
† 220322_at	4.76e-15	5.42e-18	13.3	30.7	4.542	IL36G	interleukin 36, gamma
† 218542_at	4.76e-15	5.50e-18	13.3	30.7	1.743	CEP55	centrosomal protein 55
† 202352_s_at	6.29e-15	7.44e-18	13.2	30.4	0.95	PSMD12	proteasome 26S subunit, ...
† 211361_s_at	7.16e-15	8.69e-18	13.2	30.3	2.354	SERPINE13	serpin family B member 13
† 222690_s_at	7.69e-15	9.49e-18	13.2	30.2	1.621	DTL	denticleless E3 ubiquitin p...
† 206653_at	7.69e-15	9.71e-18	13.1	30.2	1.599	POLR3G	RNA polymerase III subun...
† 204092_s_at	1.10e-14	1.41e-17	13	29.8	1.823	AURKA	aurora kinase A
† 201196_s_at	1.15e-14	1.52e-17	13	29.7	1.388	AMD1	adenosylmethionine decar...

* 204032_at	1.19e-14	1.59e-17	-13	29.7	-1.324	BCAR3	breast cancer anti-estrogen...
* 242271_at	1.19e-14	1.62e-17	13	29.7	2.343	SLC26A9	solute carrier family 26 me...
* 212022_s_at	1.23e-14	1.71e-17	13	29.6	1.955	MKI67	marker of proliferation Ki-67
* 209719_x_at	1.24e-14	1.76e-17	12.9	29.6	5.42	SERPINE3	serpin family B member 3
* 227172_at	1.35e-14	1.95e-17	-12.9	29.5	-1.372	TMEM116	transmembrane protein 116
* 221987_s_at	1.49e-14	2.19e-17	12.9	29.4	0.985	TSR1	TSR1, ribosome maturatio...
* 212021_s_at	1.63e-14	2.44e-17	12.8	29.3	2.095	MKI67	marker of proliferation Ki-67
* 226696_at	1.83e-14	2.80e-17	12.8	29.1	1.935	FCHSD1	FCH and double SH3 dom...
* 213050_at	2.01e-14	3.11e-17	-12.8	29	-1.187	COBL	cordon-bleu WH2 repeat p...
* 228729_at	2.64e-14	4.16e-17	12.7	28.7	2.296	CCNE1	cyclin B1
* 239906_at	2.74e-14	4.40e-17	-12.6	28.7	-2.111		
* 214088_s_at	2.88e-14	4.69e-17	12.6	28.6	2.89	FUT3	fucosyltransferase 3 (Lewi...
* 207356_at	2.93e-14	4.85e-17	12.6	28.6	6.083	DEFB4B//DEFB4A	defensin beta 4B//defensi...
* 206008_at	3.04e-14	5.11e-17	12.6	28.5	3.195	TGM1	transglutaminase 1
* 219358_s_at	3.04e-14	5.19e-17	12.6	28.5	1.858	ADAP2	ArfGAP with dual PH dom...
* 203476_at	3.10e-14	5.38e-17	12.6	28.5	1.08	TPBG	trophoblast glycoprotein
* 209921_at	3.16e-14	5.56e-17	12.6	28.4	2.565	SLC7A11	solute carrier family 7 me...
* 209231_s_at	3.30e-14	5.92e-17	12.5	28.4	1.566	DCTN5	dynactin subunit 5
* 233687_s_at	3.30e-14	5.98e-17	12.5	28.4	3.254	KLK3//KLK8	kallikrein related peptidas...
* 205822_at	3.71e-14	6.82e-17	12.5	28.2	2.33	LRP8	LDL receptor related prote...
* 205990_s_at	3.81e-14	7.10e-17	12.5	28.2	1.936	WNT5A	Wnt family member 5A
* 201912_s_at	4.27e-14	8.08e-17	12.4	28.1	0.954	GSP1T	G1 to S phase transition 1
* 229610_at	5.45e-14	1.05e-16	12.3	27.8	1.967	CKAP2L	cytoskeleton associated pr...
* 1563271_at	5.59e-14	1.10e-16	-12.3	27.8	-1.942		
* 222038_at	5.59e-14	1.11e-16	12.3	27.8	1.578	KIF18B	kinesin family member 18B
* 225655_at	5.59e-14	1.12e-16	12.3	27.8	1.031	UHRF1	ubiquitin like with PH an...
* 207593_at	5.61e-14	1.13e-16	12.3	27.7	1.91	ABCO4	ATP binding cassette subf...
* 222981_s_at	5.63e-14	1.15e-16	12.3	27.7	1.217	RAB10	RAB10, member RAS onc...
* 231948_s_at	6.42e-14	1.33e-16	12.3	27.6	1.13	UBE2F	ubiquitin conjugating ency...
* 223278_at	6.81e-14	1.43e-16	12.2	27.5	1.411	GJ22	gap junction protein beta 2
* 228323_at	6.84e-14	1.46e-16	12.2	27.5	1.538	KNL1	kinetochore scaffold 1
* 209642_at	6.84e-14	1.47e-16	12.2	27.5	1.816	BUB1	BUB1 mitotic checkpoint s...
* 1554406_s_at	7.46e-14	1.63e-16	12.2	27.4	2.201	CLEC7A	C-type lectin domain fami...
* 230197_s_at	7.84e-14	1.73e-16	-12.2	27.3	-2.191	TPPP	tubulin polymerization pro...
* 218517_at	7.84e-14	1.75e-16	-12.2	27.3	-1.075	JADE1	jade family PHD finger 1
* 202575_at	8.07e-14	1.83e-16	12.2	27.3	1.565	CRABP2	cellular retinoic acid bindi...
* 218719_s_at	9.85e-14	2.25e-16	12.1	27.1	1.057	GIN3	GIN3 complex subunit 3
* 209720_s_at	9.87e-14	2.31e-16	12.1	27	5.399	SERPINE3	serpin family B member 3
* 230104_s_at	9.87e-14	2.31e-16	-12.1	27	-2.147	TPPP	tubulin polymerization pro...
* 203779_s_at	1.02e-13	2.40e-16	12.1	27	2.638	MPZL2	myelin protein zero like 2
* 209588_at	1.42e-13	3.42e-16	12	26.7	2.845	EPHB2	EPH receptor B2
* 209853_s_at	1.42e-13	3.43e-16	12	26.7	1.327	PSME3	proteasome activator subu...
* 1553132_s_at	1.47e-13	3.59e-16	11.9	26.6	1.267	TC2N	tandem C2 domains, nuclear
* 208079_s_at	1.72e-13	4.26e-16	11.9	26.4	1.597	AURKA	aurora kinase A
* 217272_s_at	1.77e-13	4.41e-16	11.9	26.4	1.728	SERPINE13	serpin family B member 13
* 217739_s_at	1.86e-13	4.74e-16	11.9	26.3	1.267	NAMPT	nicotinamide phosphorbo...
* 205660_at	1.86e-13	4.75e-16	11.9	26.3	3.485	OASL	Z'-5'-oligoadenylate synth...
* 222962_s_at	1.86e-13	4.78e-16	11.9	26.3	1.544	MCM10	minichromosome mainten...
* 225686_at	2.00e-13	5.19e-16	11.8	26.3	1.195	SKA2	spindle and kinetochore a...
* 228727_at	2.30e-13	6.05e-16	-11.8	26.1	-1.329	ANXA11	annexin A11
* 203764_at	2.36e-13	6.28e-16	11.8	26.1	2.159	DLGAP5	DLG associated protein 5
* 204033_at	2.36e-13	6.36e-16	11.8	26.1	1.626	TRIP13	thyroid hormone receptor i...
* 228806_at	2.36e-13	6.39e-16	-11.8	26.1	-3.041	RORC	RAR related orphan recep...
* 232001_at	2.36e-13	6.46e-16	11.8	26	2.111	PRKCO-AS1	PRKCO antisense RNA 1
* 205242_at	2.49e-13	6.89e-16	11.7	26	4.438	CXCL13	C-X-C motif chemokine lig...
* 203234_at	2.56e-13	7.14e-16	11.7	25.9	2.32	UPP1	uridine phosphorylase 1
* 219403_s_at	2.63e-13	7.41e-16	11.7	25.9	4.281	HPSE	heparanase
* 226890_at	2.69e-13	7.64e-16	11.7	25.9	2.183	DEPDC1B	DEP domain containing 1B
* 232481_s_at	2.73e-13	7.81e-16	-11.7	25.9	-1.242	SLITR6	SLIT and NTRK like family...
* 201420_s_at	2.87e-13	8.30e-16	11.7	25.8	1.166	WDR77	WD repeat domain 77
* 206166_s_at	2.96e-13	8.65e-16	11.7	25.8	1.662	CLCA2	chloride channel accessor...
* 209792_s_at	3.00e-13	8.82e-16	11.7	25.7	2.109	KLK10	kallikrein related peptidas...
* 209897_x_at	3.05e-13	9.07e-16	11.6	25.7	1.363	PSME3	proteasome activator subu...
* 227458_at	3.08e-13	9.23e-16	11.6	25.7	2.474	CD274	CD274 molecule
* 209237_s_at	3.11e-13	9.39e-16	11.6	25.7	2.565	SLC23A2	solute carrier family 23 me...
* 209100_at	3.34e-13	1.02e-15	11.6	25.6	0.812	IFRD2	interferon related develop...
* 226226_at	3.36e-13	1.03e-15	11.6	25.6	2.343	TMEM45B	transmembrane protein 45B
* 205046_at	3.37e-13	1.04e-15	11.6	25.6	1.986	CENPE	centromere protein E
* 203691_at	4.04e-13	1.26e-15	11.5	25.4	5.006	PI3	peptidase inhibitor 3
* 237120_at	4.26e-13	1.34e-15	-11.5	25.3	-1.741	KRT77	keratin 77
* 218532_s_at	4.71e-13	1.50e-15	-11.5	25.2	-1.022	FAM134B	family with sequence simil...
* 235117_at	4.73e-13	1.52e-15	11.5	25.2	1.594	CHAC2	ChaC cation transport reg...
* 230323_s_at	4.74e-13	1.54e-15	11.5	25.2	1.826	TMEM45B	transmembrane protein 45B
* 219905_at	4.74e-13	1.55e-15	11.5	25.2	2.172	HS3ST3A1	heparan sulfate-glucosami...
* 223225_s_at	5.16e-13	1.70e-15	11.4	25.1	1.142	SEH1L	SEH1 like nucleoporin
* 222774_s_at	5.17e-13	1.71e-15	11.4	25.1	2.112	NETO2	neuropilin and tolloid like 2
* 201890_at	5.31e-13	1.77e-15	11.4	25	1.76	RRM2	ribonucleotide reductase r...
* 220727_at	5.33e-13	1.79e-15	11.4	25	2.241	KCNK10	potassium two pore domai...
* 203214_x_at	5.39e-13	1.83e-15	11.4	25	1.811	CDK1	cyclin dependent kinase 1
* 41469_at	5.40e-13	1.85e-15	11.4	25	5.163	PI3	peptidase inhibitor 3
* 228066_at	5.60e-13	1.93e-15	11.4	25	1.982	C17orf96	chromosome 17 open rea...
* 209025_s_at	5.61e-13	1.95e-15	11.4	25	1.221	SYNCRIP	synaptotagmin binding cyt...

‡ 241412_at	5.69e-13	1.99e-15	-11.4	24.9	-2.404	BTC	betacellulin
‡ 224204_x_at	5.92e-13	2.09e-15	11.4	24.9	2.632	ARNTL2	aryl hydrocarbon receptor ...
‡ 219225_at	5.92e-13	2.10e-15	11.4	24.9	2.871	PGBD5	piggyBac transposable ele...
‡ 236641_at	6.41e-13	2.29e-15	11.4	24.8	1.773	KIF14	kinesin family member 14
‡ 243296_at	6.45e-13	2.32e-15	11.3	24.8	1.301	NAMPT	nicotinamide phosphorbo...
‡ 233504_at	6.47e-13	2.35e-15	11.3	24.8	2.361	CtbrB4	chromosome 9 open read...
‡ 205554_s_at	6.94e-13	2.54e-15	11.3	24.7	1.542	DNASE1L3	deoxyribonuclease 1 like 3
‡ 232112_at	6.95e-13	2.56e-15	11.3	24.7	2.197	RALGPS2	Ral GEF with PH domain ...
‡ 1557136_at	7.67e-13	2.89e-15	11.3	24.6	1.406	ATP13A4	ATPase 13A4
‡ 219316_s_at	7.67e-13	2.89e-15	11.3	24.6	1.263	FLVCR2	feline leukemia virus subg...
‡ 209408_at	7.82e-13	2.94e-15	11.3	24.6	1.947	KIF2C	kinesin family member 2C
‡ 226936_at	7.98e-13	3.02e-15	11.3	24.5	1.39	CENPW	centromere protein W
‡ 202918_s_at	8.03e-13	3.06e-15	11.3	24.5	0.897	HSPE1-MOB4//MOB4	HSPE1-MOB4 readthrough...
‡ 204465_s_at	8.09e-13	3.12e-15	11.3	24.5	2.833	INA	interneurin neuronal interm...
‡ 235678_at	8.09e-13	3.13e-15	11.3	24.5	1.405	GM2A	GM2 ganglioside activator
‡ 204822_at	8.47e-13	3.31e-15	11.2	24.4	1.898	TTK	TTK protein kinase
‡ 32069_at	8.47e-13	3.32e-15	11.2	24.4	0.982	NBDP1	NEDD4 binding protein 1
‡ 212268_at	8.75e-13	3.45e-15	11.2	24.4	1.722	SERPINF1	serpin family B member 1
‡ 218510_x_at	8.89e-13	3.56e-15	-11.2	24.4	-1.217	FAM134B	family with sequence simil...
‡ 209891_at	8.89e-13	3.56e-15	11.2	24.4	1.933	SPC25	SPC25, NDC80 kinetoch...
‡ 226863_at	8.89e-13	3.57e-15	11.2	24.4	1.327	FAM110C	family with sequence simil...
‡ 209093_s_at	1.01e-12	4.10e-15	11.2	24.2	1.522	GBAP1//GBA	glucosylceramidase beta ...
‡ 222753_s_at	1.01e-12	4.12e-15	11.2	24.2	1.026	SPC33	signal peptidase complex ...
‡ 224414_s_at	1.02e-12	4.22e-15	11.2	24.2	1.377	CARD6	caspase recruitment doma...
‡ 206367_at	1.02e-12	4.22e-15	11.2	24.2	3.329	REN	renin
‡ 214435_x_at	1.05e-12	4.38e-15	11.1	24.2	1.07	RALA	RALA Ras like proto-onco...
‡ 225787_at	1.06e-12	4.42e-15	11.1	24.2	1.276	UBE2F	ubiquitin conjugating enzy...
‡ 206134_at	1.11e-12	4.72e-15	11.1	24.1	3.392	ADAMDEC1	ADAM like decysin 1
‡ 203755_at	1.11e-12	4.73e-15	11.1	24.1	1.365	BUB1B	BUB1 mitotic checkpoint s...
‡ 239017_at	1.11e-12	4.75e-15	-11.1	24.1	-1.815		
‡ 203105_s_at	1.12e-12	4.78e-15	11.1	24.1	0.62	DNM1L	dynamin 1 like
‡ 231697_s_at	1.24e-12	5.34e-15	11.1	24	1.347	MIR21//VMP1	microRNA 21//vacuole m...
‡ 207381_at	1.24e-12	5.40e-15	11.1	24	2.105	ALOX12B	arachidonate 12-lipoxygen...
‡ 212695_at	1.35e-12	5.90e-15	-11.1	23.9	-1.263	CRY2	cryptochrome circadian cl...
‡ 210606_s_at	1.35e-12	5.91e-15	11.1	23.9	1.704	FUT2	fucosyltransferase 2
‡ 238512_at	1.36e-12	6.02e-15	-11	23.8	-1.442	WNT2B	Wnt family member 2B
‡ 225367_at	1.43e-12	6.37e-15	11	23.8	1.139	PGM2	phosphoglucosutase 2
‡ 230242_at	1.45e-12	6.48e-15	11	23.8	1.008	NFASC	neurofascin
‡ 221608_s_at	1.53e-12	6.89e-15	11	23.7	1.436	CLEC7A	C-type lectin domain fami...
‡ 219722_s_at	1.65e-12	7.46e-15	11	23.6	1.53	GDPD3	glycerophosphodiester ph...
‡ 218663_at	1.80e-12	8.18e-15	11	23.5	1.588	NCAPG	non-SMC condensin I com...
‡ 205085_at	1.88e-12	8.62e-15	10.9	23.5	1.619	ORC1	origin recognition complex...
‡ 1555756_s_at	1.89e-12	8.69e-15	10.9	23.5	2.632	CLEC7A	C-type lectin domain fami...
‡ 226435_at	1.91e-12	8.86e-15	-10.9	23.5	-1.306	PAPLN	papilin, proteoglycan like s...
‡ 222223_s_at	1.91e-12	8.92e-15	10.9	23.5	2.755	IL36RN	interleukin 36 receptor ant...
‡ 218312_s_at	1.91e-12	8.97e-15	-10.9	23.5	-1.965	ZSCAN18	zinc finger and SCAN dom...
‡ 217755_at	1.91e-12	9.02e-15	10.9	23.4	1.536	HN1	hematological and neurolo...
‡ 202503_s_at	1.91e-12	9.06e-15	10.9	23.4	1.959	KIAA0101	KIAA0101
‡ 208080_at	2.06e-12	9.79e-15	10.9	23.4	1.835	AURKA	aurora kinase A
‡ 205909_at	2.24e-12	1.08e-14	10.9	23.3	1.135	POLE2	DNA polymerase epsilon 2...
‡ 231227_at	2.24e-12	1.08e-14	10.9	23.3	2.082		
‡ 206068_s_at	2.30e-12	1.11e-14	-10.9	23.2	-2.252	ACADL	acyl-CoA dehydrogenase, ...
‡ 209774_x_at	2.32e-12	1.13e-14	10.9	23.2	2.838	CXCL2	C-X-C motif chemokine lig...
‡ 228281_at	2.41e-12	1.18e-14	10.8	23.2	2.049	DDIAS	DNA damage induced apo...
‡ 204709_s_at	2.41e-12	1.19e-14	10.8	23.2	1.656	KIF23	kinesin family member 23
‡ 213661_at	2.41e-12	1.19e-14	-10.8	23.2	-2.087	PAWR1	peptidase domain containi...
‡ 212677_s_at	2.52e-12	1.25e-14	-10.8	23.1	-0.97	CEP68	centrosomal protein 68
‡ 203432_at	2.93e-12	1.46e-14	10.8	23	1.147	TMPO	thymopoietin
‡ 235278_at	2.98e-12	1.50e-14	-10.8	23	-1.792	MACROD2	MACRO domain containin...
‡ 203780_at	3.03e-12	1.53e-14	10.8	22.9	1.027	MPZL2	myelin protein zero like 2
‡ 230748_at	3.13e-12	1.59e-14	10.7	22.9	1.333	SLC16A6	solute carrier family 16 me...
‡ 215465_at	3.19e-12	1.63e-14	10.7	22.9	2.347	ABCA12	ATP binding cassette subf...
‡ 201695_s_at	3.35e-12	1.72e-14	10.7	22.8	1.284	PNP	purine nucleoside phosph...
‡ 210164_at	3.38e-12	1.74e-14	10.7	22.8	3.302	GZMB	granzyme B
‡ 201487_at	3.42e-12	1.78e-14	10.7	22.8	1.165	CTSC	cathepsin C
‡ 208023_at	3.42e-12	1.78e-14	10.7	22.8	0.989	TNFRSF4	TNF receptor superfamily ...
‡ 212769_at	3.48e-12	1.82e-14	10.7	22.8	1.558	TLE3	transducin like enhancer o...
‡ 211075_s_at	3.48e-12	1.83e-14	10.7	22.8	1.104	CD47	CD47 molecule
‡ 220865_s_at	3.73e-12	1.97e-14	10.7	22.7	1.003	PDSS1	prenyl (decaprenyl) diphos...
‡ 205383_s_at	3.86e-12	2.05e-14	-10.7	22.6	-1.063	ZBTB20	zinc finger and BTB domai...
‡ 202924_s_at	3.89e-12	2.08e-14	10.7	22.6	1.133	FLAGL2	FLAG1 like zinc finger 2
‡ 205844_at	3.95e-12	2.12e-14	10.7	22.6	2.771	VNN1	vanin 1
‡ 213425_at	4.00e-12	2.16e-14	10.7	22.6	1.6	WNT5A	Wnt family member 5A
‡ 203967_at	4.03e-12	2.18e-14	10.7	22.6	1.892	CDC6	cell division cycle 6
‡ 228846_at	4.05e-12	2.20e-14	10.6	22.6	2.275	MXD1	MAX dimerization protein 1
‡ 228096_at	4.14e-12	2.26e-14	-10.6	22.5	-1.056	MINOS1	mitochondrial inner memb...
‡ 222442_s_at	4.15e-12	2.28e-14	10.6	22.5	1.466	ARL8B	ADP ribosylation factor lik...
‡ 204170_s_at	4.15e-12	2.29e-14	10.6	22.5	1.583	CKS2	CDC28 protein kinase reg...
‡ 243244_at	4.17e-12	2.31e-14	10.6	22.5	1.79	CACNB4	calcium voltage-gated cha...
‡ 216257_at	4.18e-12	2.33e-14	10.6	22.5	3.267	SERPINF13	serpin family B member 13
‡ 219402_s_at	4.18e-12	2.34e-14	10.6	22.5	1.12	DERL1	derlin 1
‡ 223518_at	4.18e-12	2.35e-14	10.6	22.5	1.328	DFFA	DNA fragmentation factor ...

‡ 205393_s_at	4.67e-12	2.64e-14	10.6	22.4	1.772	CHEK1	checkpoint kinase 1
‡ 213427_at	4.69e-12	2.66e-14	10.6	22.4	1.06	RPP40	ribonuclease P/MRP subu...
‡ 241985_at	4.73e-12	2.70e-14	10.6	22.4	1.576	JMY	junction mediating and reg...
‡ 208934_s_at	4.85e-12	2.78e-14	10.6	22.3	0.851	LGALS8	galectin 8
‡ 243840_at	4.94e-12	2.84e-14	10.6	22.3	2.09	CLSPN	claspin
‡ 212365_at	5.20e-12	3.01e-14	10.6	22.3	1.324	MYO1B	myosin IB
‡ 209772_s_at	5.31e-12	3.08e-14	10.5	22.2	2.404	CD24	CD24 molecule
‡ 238805_at	5.45e-12	3.18e-14	-10.5	22.2	-1.121	HSPB2-C11orf52//C11orf...	HSPB2-C11orf52 readthro...
‡ 204751_x_at	5.54e-12	3.25e-14	10.5	22.2	2.367	DSC2	desmocollin 2
‡ 231033_at	5.57e-12	3.28e-14	10.5	22.2	3.028	DSC2	desmocollin 2
‡ 204715_at	5.71e-12	3.38e-14	10.5	22.1	1.008	PANX1	pannexin 1
‡ 235024_at	5.81e-12	3.45e-14	-10.5	22.1	-1.044	JADE1	jade family FHD finger 1
‡ 204641_at	5.90e-12	3.52e-14	10.5	22.1	1.821	NEK2	NIMA related kinase 2
‡ 223307_at	6.73e-12	4.04e-14	10.5	22	1.758	CDC43	cell division cycle associat...
‡ 225601_at	6.95e-12	4.19e-14	10.5	21.9	1.45	HMGB3	high mobility group box 3
‡ 204146_at	6.95e-12	4.20e-14	10.5	21.9	1.291	RAD51AP1	RAD51 associated protein 1
‡ 202134_s_at	7.01e-12	4.26e-14	10.4	21.9	1.921	WWTR1	WW domain containing tra...
‡ 202625_at	7.12e-12	4.34e-14	10.4	21.9	0.994	LYN	LYN proto-oncogene, Src f...
‡ 224164_at	7.20e-12	4.41e-14	10.4	21.9	1.528	TPM3	tropomyosin 3
‡ 201202_at	7.58e-12	4.67e-14	10.4	21.8	0.872	PCNA	proliferating cell nuclear a...
‡ 236963_at	7.58e-12	4.68e-14	-10.4	21.8	-1.802		
‡ 228852_at	7.80e-12	4.84e-14	10.4	21.8	1.526	ENSA	endosulfine alpha
‡ 220944_at	7.84e-12	4.90e-14	10.4	21.8	1.715	PGLYRP4	peptidoglycan recognition ...
‡ 228273_at	7.84e-12	4.91e-14	10.4	21.8	1.533	PRR11	proline rich 11
‡ 238973_s_at	7.89e-12	4.98e-14	10.4	21.8	1.929		
‡ 240770_at	7.89e-12	4.98e-14	10.4	21.8	2.171	TMEM171	transmembrane protein 171
‡ 205339_at	8.16e-12	5.17e-14	10.4	21.7	1.381	STIL	SCL/TAL1 interrupting locus
‡ 214070_s_at	8.25e-12	5.26e-14	10.4	21.7	1.944	ATP10B	ATPase phospholipid tran...
‡ 212390_at	8.25e-12	5.27e-14	-10.4	21.7	-1.172	LOC101930416//LOC101...	myomegalin-like//lunchara...
‡ 210038_at	8.28e-12	5.34e-14	10.4	21.7	2.731	PRKCQ	protein kinase C theta
‡ 225783_at	8.28e-12	5.34e-14	10.4	21.7	1.113	UBE2F	ubiquitin conjugating enzy...
‡ 216670_at	8.28e-12	5.38e-14	10.4	21.7	3.665	KLK13	kalikrein related peptidas...
‡ 227735_s_at	8.88e-12	5.77e-14	10.4	21.6	3.79	C10orf99	chromosome 10 open rea...
‡ 1555758_a_at	9.24e-12	6.03e-14	10.3	21.6	1.885	CDKN3	cyclin dependent kinase in...
‡ 204026_s_at	9.62e-12	6.30e-14	10.3	21.5	1.152	ZWINT	ZW10 interacting kinetoch...
‡ 238483_at	9.88e-12	6.50e-14	-10.3	21.5	-1.449	SSBP2	single stranded DNA bindi...