

SUPPLEMENTARY TABLES

Supplementary Table 1. Top canonical pathways that showed differences in yr⁶⁰⁺ versus yr⁶⁰⁻ patients in the first microarray dataset using T4 filter.

Pathway name	<i>p</i> - value	Overlap
PPAR Signaling	2.65E-04	4.0% (4/101)
Acute phase response signaling	2.20E-03	2.2% (4/178)
Melanocyte development and pigmentation signaling	3.13E-03	3.2% (3/95)
Coagulation system	5.18E-03	5.7% (2/35)
Cholecystokinin/Gastrin-mediated signaling	5.61E-03	2.6% (3/117)

Supplementary Table 2. Differentially expressed genes (DEGs) in the SLN in yr⁶⁰⁺ versus yr⁶⁰⁻ patients in the first microarray dataset using T3 filter.

Gene symbol	Gene Name	<i>P</i> value	Fold change
FOSB	FBJ murine osteosarcoma viral oncogene homolog B	0.0208	1.5961
FOS	FBJ murine osteosarcoma viral oncogene homolog	0.0255	1.5558
DUSP1	dual specificity phosphatase 1	0.0453	1.5349
NR4A2	nuclear receptor subfamily 4, group A, member 2	0.0096	1.4719
IDO1	indoleamine 2,3-dioxygenase 1	0.0155	1.454
CLEC4C	C-type lectin domain family 4, member C	0.0486	1.4497
LIX1	limb and CNS expressed 1	0.0098	1.4118
CD8A	CD8a molecule	0.0003	1.4111
BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	0.003	1.3963
NRCAM	neuronal cell adhesion molecule	0.0008	1.3961
NOG	noggin	0.0027	1.3839
KLRC4-KLRK1 /// KLRK1	KLRC4-KLRK1 read through /// killer cell lectin-like receptor subfamily K, member 1	0.0011	1.3827
MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	0.0434	1.3709
KLF4	Kruppel-like factor 4 (gut)	0.0278	1.3662
SATB1	SATB homeobox 1	0.0322	1.3484
LOC101928963	uncharacterized LOC101928963	0.027	1.2614
GRIK2	glutamate receptor, ionotropic, kainate 2	0.0497	0.8748
MUC15	mucin 15, cell surface associated	0.0495	0.8681
DLK1	delta-like 1 homolog (Drosophila)	0.0339	0.8617
RNF152	ring finger protein 152	0.05	0.8483
ITGBL1	integrin beta like 1	0.03	0.8466
ERGIC3	ERGIC and golgi 3	0.0295	0.8456
INHBA	inhibin beta A	0.0461	0.8347
PRUNE2	prune homolog 2 (Drosophila)	0.0059	0.8323
LINC00354	long intergenic non-protein coding RNA 354	0.0292	0.8312
MKX	mohawk homeobox	0.0053	0.8308
WWC1	WW and C2 domain containing 1	0.0295	0.8228
LOC105373225	uncharacterized LOC105373225	0.029	0.8139
SLC13A5	solute carrier family 13 (sodium-dependent citrate transporter), member 5	0.018	0.7921
GRB14	growth factor receptor bound protein 14	0.0135	0.792
ATP2B2	ATPase, Ca ⁺⁺ transporting, plasma membrane 2	0.0295	0.791
COL28A1	collagen, type XXVIII, alpha 1	0.0092	0.7779
LOC100507516	uncharacterized LOC100507516	0.0223	0.7719
MLANA	melan-A	0.0486	0.7057

Supplementary Table 3. Differentially expressed immune genes in younger patients between the recur^{yes} and the recur^{no} group by NanoString analysis ($p < 0.05$).

Gene symbol	Gene Name	P value	Fold change
C6	complement component 6	0.00745	4.28
IL23R	interleukin 23 receptor	0.00545	3.64
BAGE	B melanoma antigen	0.0136	3.58
CCL16	chemokine (C-C motif) ligand 16	0.0168	3.46
SPINK5	serine peptidase inhibitor, Kazal type 5	0.0161	2.96
MAPK11	mitogen-activated protein kinase 11	0.00968	2.84
MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	0.00947	2.52
F2RL1	coagulation factor II (thrombin) receptor-like 1	0.00399	1.97
DOCK9	dedicator of cytokinesis 9	0.00847	1.61
IGF1R	insulin-like growth factor 1 receptor	0.0141	0.971
TBK1	TANK-binding kinase 1	0.0116	0.616
MAP2K2	mitogen-activated protein kinase kinase 2	0.00105	-0.306
HLA-A	major histocompatibility complex, class I, A	0.00051	-0.386
CCL4	chemokine (C-C motif) ligand 4	0.0165	-0.485
ICAM1	intercellular adhesion molecule 1	0.0143	-0.587
C1QBP	complement component 1, q subcomponent binding protein	0.0131	-0.9
PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	0.0121	-0.939
MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	0.016	-1.09
HLA-G	major histocompatibility complex, class I, G	0.00237	-1.18
S100B	S100 calcium binding protein B	0.00859	-5.64

Supplementary Table 4. Differentially expressed immune genes in older patients between the recur^{yes} and the recur^{no} group by NanoString analysis ($p < 0.05$).

Gene symbol	Gene Name	P value	Fold change
FOS	FBJ murine osteosarcoma viral oncogene homolog	0.0221	1.9
CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	0.00867	1.8
CXCR4	chemokine (C-X-C motif) receptor 4	0.0238	1.07
C3	complement component 3	0.00481	0.832
TLR10	toll-like receptor 10	0.0189	0.787
NOD1	nucleotide-binding oligomerization domain containing 1	0.00347	0.768
PLAU	plasminogen activator, urokinase	0.00371	0.741
CYBB	cytochrome b-245, beta polypeptide	0.00314	0.732
TLR6	toll-like receptor 6	0.013	0.626
HLA-DMA	major histocompatibility complex, class II, DM alpha	0.0192	0.606
TNFRSF13B	tumor necrosis factor receptor superfamily, member 13B	0.0191	0.555
CD84	CD84 molecule	0.014	0.504
ATG7	autophagy related 7	0.00748	0.486
HLA-DMB	major histocompatibility complex, class II, DM beta	0.0199	0.313
MAP2K4	mitogen-activated protein kinase kinase 4	0.00196	0.248
INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	0.0117	0.216
ELK1	ELK1, member of ETS oncogene family	0.00172	-0.491
RELA	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	0.0225	-0.52
IFITM1	interferon induced transmembrane protein 1	0.0176	-0.675
NCAM1	neural cell adhesion molecule 1	0.00896	-0.984

Supplementary Table 5. Differentially expressed immune pathway genes in younger patients between the recur^{yes} and the recur^{no} group by NanoString analysis ($p < 0.05$).

Gene symbol	Gene Name	P value	Fold change
IRAK3	interleukin-1 receptor-associated kinase 3	0.00552	2.15
NKD1	naked cuticle homolog 1 (Drosophila)	0.00565	2.13
ACVR1C	activin A receptor, type IC	0.0111	1.9
SOS1	son of sevenless homolog 1 (Drosophila)	0.00681	1.42
EPOR	erythropoietin receptor	0.00773	1.32
ACVR2A	activin A receptor, type IIA	0.012	1.12
RAD50	RAD50 homolog (S. cerevisiae)	0.0101	0.83
SMAD2	SMAD family member 2	0.00233	0.799
DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	0.0113	0.745
RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	0.00593	0.596
MAP2K2	mitogen-activated protein kinase kinase 2	0.00454	-0.363
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	0.00981	-0.439
FANCL	Fanconi anemia, complementation group L	0.00732	-0.554
PPP2R1A	protein phosphatase 2, regulatory subunit A, alpha	0.00791	-0.679
RB1	retinoblastoma 1	0.0108	-0.84
UBB	ubiquitin B	0.0109	-0.849
CDK4	cyclin-dependent kinase 4	0.00456	-1.22
CASP9	caspase 9, apoptosis-related cysteine peptidase	0.00969	-1.22
HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	0.0106	-1.25
PCNA	proliferating cell nuclear antigen	0.00314	-1.45

Supplementary Table 6. Differentially expressed immune pathway genes in older patients between the recur^{yes} and the recur^{no} group by NanoString analysis ($p < 0.05$).

Gene symbol	Gene Name	P value	Fold change
WNT10B	wingless-type MMTV integration site family, member 10B	0.027	2.27
HSPA1A	heat shock 70kDa protein 1A	0.0283	2.04
FOS	FBJ murine osteosarcoma viral oncogene homolog	0.0219	1.96
DKK2	dickkopf WNT signaling pathway inhibitor 2	0.0247	1.7
IL6	interleukin 6 (interferon, beta 2)	0.00111	1.36
TGFB3	transforming growth factor, beta 3	0.0379	1.19
HHEX	hematopoietically expressed homeobox	0.0263	1.06
DLL4	delta-like 4 (Drosophila)	0.00752	0.883
XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	0.0354	0.787
NR4A1	nuclear receptor subfamily 4, group A, member 1	0.0232	0.766
ALKBH2	alkB, alkylation repair homolog 2 (E. coli)	0.0384	0.752
PLAU	plasminogen activator, urokinase	0.00195	0.659
BID	BH3 interacting domain death agonist	0.0369	0.564
ERCC6	excision repair cross-complementing rodent repair deficiency, complementation group 6	0.0236	0.479
LAMA5	laminin, alpha 5	0.00181	0.467
NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	0.00751	0.418
RUNX1	runt-related transcription factor 1	0.0281	0.417
TFDP1	transcription factor Dp-1	0.0364	0.36
STK11	serine/threonine kinase 11	0.0186	0.312
BCOR	BCL6 corepressor	0.0379	-0.377

Supplementary Table 7. Patients' data on age and outcome in all three datasets.

Outcome	1st microarray dataset		2nd NanoString dataset		3rd dataset qRT-PCR	
	< 60	≥ 60	< 60	≥ 60	< 60	≥ 60
No recurrence (recur ^{no})	51	7	3	3	9	13
Recurrence (recur ^{yes})	28	11	3	3	9	5