Supplemental Table 1. Demographics of the 96 Healthy Subjects from the Brigham and Women's Hospital PhenoGenetic Cohort Involved in the NK Cytometric Profiling.

PARAMETER		VALUE
Age (years, Mean ± SD)		27.7 ± 8.8
Sex (%)		
	Female	57.3
	Male	42.7
Race and Ethnicity (%)		
	Caucasian, Non-Hispanic	71.9
	Caucasian, Hispanic	4.2
	African American, Non-Hispanic	8.3
	East Asian	6.2
	Multi-racial or others	9.3

Supplemental Table 2. Association between the candidate SNP (rs9916629^{C}) and the Frequency of NKG2A expressing NK cells Using Additive, Dominant and Recessive Models.

	UNADJUSTED		MULTIVARIATE*	
VARIABLE	**Direction of Effect**	**P**	**Direction of Effect***	**P***
NKG2A/NK				
Additive	↑	0.00046	↑	0.00020
Dominant	↑	0.00051	↑	0.00022
Recessive	↑	0.096	↑	0.081
NKG2A/CD56^{bright}				
Additive	↓	0.62	↓	0.74
Dominant	↓	0.24	↓	0.31
Recessive	↓	0.29	↓	0.27
NKG2A/CD56^{dim}				
Additive	↑	0.0024	↑	0.0017
Dominant	↑	0.0016	↑	0.0011
Recessive	↑	0.22	↑	0.22

Refer to Table 2 for the median percentage of expression of NKG2A/NK, NKG2A/CD56^{bright}, and NKG2A/CD56^{dim} for the three genotypes of rs9916629. Direction of effect is relative to the C allele and is determined from the beta value. * In the multivariate analysis, association between rs9916629 and the phenotype was adjusted for age and sex as covariates.

Supplemental Table 3. Association between the candidate SNP (rs9916629^{C}) and the RNA expression profile in NK cells in a subset of the healthy cohort (n=20: 2 with CC, 9 with CT, and 9 with TT genotype).

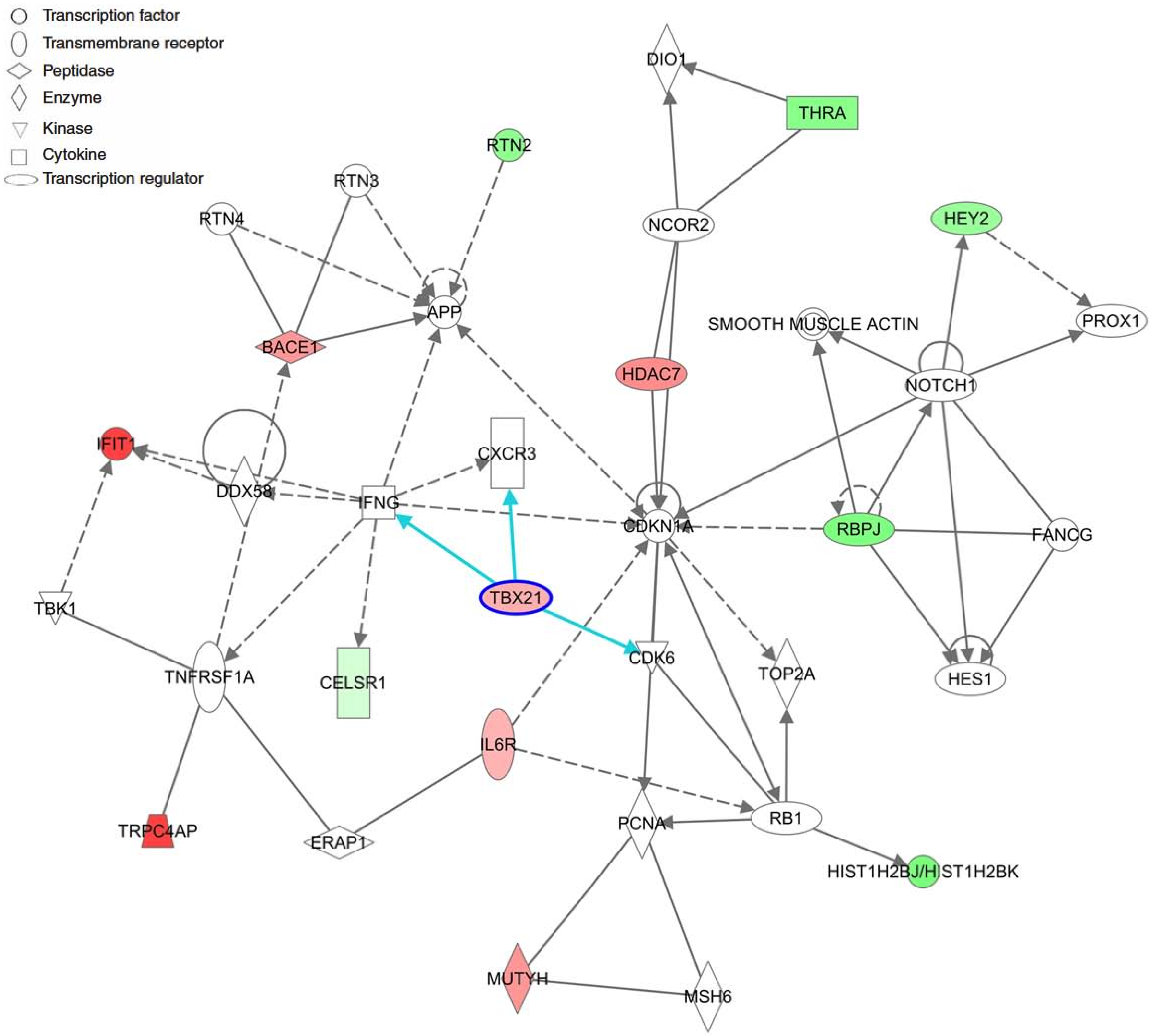
Gene Symbol	Probe ID	Beta values	P-value
TRPC4AP	ILMN_2402805	0.40	0.000027
DNAI2	ILMN_1756921	-0.23	0.000120
AGPAT3	ILMN_1661373	0.18	0.000224
HS.258077	ILMN_1838281	0.19	0.000263
CECR7	ILMN_1773764	-0.16	0.000399
RAD51	ILMN_2363027	-0.12	0.000438
FBXW8	ILMN_2342793	-0.20	0.000471
PKHD1	ILMN_1720034	-0.21	0.000527
LGALS2	ILMN_1687306	0.28	0.000592
MUTYH	ILMN_2277537	0.22	0.000613
S100A13	ILMN_2407168	-0.13	0.000706
COL20A1	ILMN_1753182	-0.11	0.000924
TAGLN	ILMN_2400935	0.22	0.000940
RPS27A	ILMN_1755883	-0.21	0.000963
PGM5	ILMN_1709590	0.23	0.001001
HSPA6	ILMN_1806165	0.41	0.001172
MGAT4A	ILMN_1755643	-0.42	0.001242
THRA	ILMN_1661683	-0.22	0.001555
NPTXR	ILMN_1684143	-0.16	0.001566
ABCC12	ILMN_1762093	-0.17	0.001703
ANTXR2	ILMN_1812926	0.43	0.001789
CALML5	ILMN_1749118	0.17	0.002021
LHFPL1	ILMN_1725031	0.18	0.002125
UPK3B	ILMN_1701565	0.25	0.002259
ZBED5	ILMN_1664424	0.16	0.002354
FOXI2	ILMN_1808388	-0.21	0.002553
PSMG3	ILMN_1802627	-0.13	0.002707
OBFC2A	ILMN_1785852	0.24	0.002711
HDAC7A	ILMN_1728521	0.24	0.002736
RNF141	ILMN_1815010	0.19	0.002798
LSR	ILMN_1749396	0.19	0.002923
COL12A1	ILMN_1741695	0.16	0.003064
C7ORF50	ILMN_1718336	-0.29	0.003110
HS.344169	ILMN_1890120	0.17	0.003168
TOMM7	ILMN_2087060	-0.18	0.003206

DPP7	ILMN_2252309	-0.29	0.003262
HS.576768	ILMN_1845602	0.13	0.003338
GZMM	ILMN_1690561	-0.28	0.003424
RMND1	ILMN_1694533	0.11	0.003441
CASK	ILMN_1654773	0.15	0.003503
MGC5139	ILMN_1660935	0.14	0.003507
GART	ILMN_1793220	0.13	0.003543
DUS1L	ILMN_1653342	-0.16	0.003588
TBX21	ILMN_1692714	0.17	0.003738
COL4A3BP	ILMN_1680109	0.19	0.003789
PKN1	ILMN_1662687	0.22	0.003792
BCAT1	ILMN_1766169	0.29	0.003849
RBPJ	ILMN_1708537	-0.24	0.003925
C12ORF62	ILMN_1804656	-0.24	0.003935
CAND2	ILMN_2073592	-0.11	0.003955
PRDM8	ILMN_1802082	0.24	0.003999
GSTM3	ILMN_1736184	-0.15	0.004167
CHST13	ILMN_1734707	0.37	0.004443
CHN2	ILMN_2403237	0.24	0.004781
ZFAND2A	ILMN_1694671	-0.31	0.004794
RUSC2	ILMN_1810037	0.14	0.004824
HS.578136	ILMN_1902508	0.16	0.004826
RAB13	ILMN_1788180	0.20	0.004858
HIST1H2BJ	ILMN_1658702	-0.25	0.004946
DGCR2	ILMN_1713301	0.15	0.005002
HS.538759	ILMN_1894930	0.15	0.005093
PANK2	ILMN_1708095	0.15	0.005310
PLAC2	ILMN_1725831	-0.12	0.005452
PKP4	ILMN_1749410	0.19	0.005623
RTN2	ILMN_1685357	-0.21	0.005635
ARL6IP4	ILMN_2393144	-0.16	0.005726
CHCHD9	ILMN_1677237	-0.15	0.005905
HCG27	ILMN_1746436	0.21	0.005937
TOP2B	ILMN_1777663	0.24	0.005963
LOC654114	ILMN_1698835	0.16	0.005970
DKFZP667M2411	ILMN_1802518	-0.15	0.005982
ANKRD35	ILMN_1798006	-0.17	0.006060
AP1S1	ILMN_1751345	-0.12	0.006279
RHOT1	ILMN_1731484	0.19	0.006285
RIMS3	ILMN_1742382	-0.17	0.006293
C6ORF25	ILMN_1709799	0.23	0.006352
MBD3	ILMN_1698491	-0.14	0.006380
ANKRD35	ILMN_2145153	0.11	0.006572
CCHCR1	ILMN_1674051	0.13	0.006627
SFRS9	ILMN_1760683	0.18	0.006722
PAFAH2	ILMN_1682919	-0.23	0.006884

MTP18	ILMN_2372040	-0.37	0.006904
MICALCL	ILMN_1743232	0.18	0.006922
TMED1	ILMN_1693045	-0.22	0.006950
DTX2	ILMN_2275098	0.26	0.006986
NR2F6	ILMN_1672080	0.15	0.007105
HS.520750	ILMN_1851677	0.14	0.007256
ZNF655	ILMN_1728528	-0.10	0.007307
LOC654254	ILMN_1734939	-0.16	0.007310
FAM116B	ILMN_1659029	0.25	0.007326
KLC4	ILMN_1687873	0.13	0.007337
CREB5	ILMN_1728677	0.13	0.007602
RGPD1	ILMN_2116827	0.18	0.007613
LOC130773	ILMN_1672009	-0.23	0.007704
C17ORF68	ILMN_1702676	0.18	0.007707
IL6R	ILMN_1696394	0.16	0.007715
HEY2	ILMN_1682034	-0.19	0.007759
PPHLN1	ILMN_1805788	-0.13	0.007790
FEZ1	ILMN_1794106	-0.16	0.008447
SMAD7	ILMN_2203891	-0.26	0.008448
ARID3A	ILMN_1670130	0.24	0.008453
SMYD2	ILMN_1721605	-0.13	0.008488
LHX6	ILMN_1683752	-0.22	0.008493
KIAA0232	ILMN_1795704	0.10	0.008524
HS.560740	ILMN_1887928	0.26	0.008713
SDSL	ILMN_1750674	0.34	0.008811
LOC648605	ILMN_1773819	0.19	0.008827
RAD51L1	ILMN_1727831	0.12	0.009008
PHF5A	ILMN_1775901	-0.22	0.009070
HS.527387	ILMN_1893798	0.18	0.009127
UXS1	ILMN_1776334	0.17	0.009174
LARP5	ILMN_1766222	0.22	0.009205
KIAA1683	ILMN_2158003	0.16	0.009263
CELSR1	ILMN_1694482	-0.08	0.009430
FABP4	ILMN_1773006	0.14	0.009437
RAB3IP	ILMN_1803197	0.14	0.009546
LOC143543	ILMN_1664602	-0.18	0.009555
FLOT2	ILMN_1726222	0.15	0.009589
ZFYVE27	ILMN_1793621	0.15	0.009663
FRAT2	ILMN_1788213	0.23	0.009664
BACE1	ILMN_1797804	0.22	0.009738
HS.542848	ILMN_1873394	0.16	0.009756
PXN	ILMN_1684440	-0.22	0.009789
ATP5B	ILMN_1772132	0.21	0.009815
TARBP2	ILMN_1729767	-0.17	0.009835
IFIT1	ILMN_1707695	0.40	0.009936

Supplemental Figure 1. Pathway analysis of eQTL results of rs9916629 and RNA expression profile from bulk CD3$^-$CD56$^+$ NK cells.

Gene expression relative to the C allele of rs9916629. Using the Ingenuity Pathways Analysis software suite, we illustrate the network of genes whose expression is either upregulated (red) or downregulated (green) relative to the rs9916629^C allele in healthy subjects. The magnitude of each gene's association is reflected by the intensity of the color, with brighter color indicating a stronger association between rs9916629 C allele and RNA expression. When available, arrows point to the downstream genes within the network. A white color denotes a gene found in the associated pathway but which failed to meet a nominal $P<0.05$ threshold for association of its RNA expression with rs9916629. The shapes of each gene symbol denote the class of gene as defined by the Ingenuity Pathways application as denoted in the upper left corner of the figure.


Transcription factor
Transmembrane receptor
Peptidase
Enzyme
Kinase
Cytokine
Transcription regulator
DIO1
THRA
RTN2
RTN3
RTN4
NCOR2
HEY2
APP
BACE1
SMOOTH MUSCLE ACTIN
PROX1
HDAC7
NOTCH1
IFIT1
DDX58
CXCR3
IFNG
CDKN1A
RBPJ
FANCG
TBX21
TBK1
TNFRSF1A
CELSR1
CDK6
TOP2A
HES1
IL6R
TRPC4AP
ERAP1
PCNA
RB1
HIST1H2BJ/HIST1H2BK
MUTYH
MSH6