ImmGen Report:
Molecular definition of NK cell identity and activation
Supplementary Note 1

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Microarray hybridization

All RNA isolation, amplification, microarray hybridization, and data filtering and normalization were performed as previously described[1], and are described in extensive detail in the ImmGen Data Generation and Quality Control Documentation available at http://www.immgen.org/Protocols/ImmGenDataGenerationAndQCDocumentation.pdf. Specific details of individual analyses are provided below.

Microarray analysis: Differential Gene Expression by DeltaScore calculation

The DeltaScore module for GenePattern[2] was specifically developed for the analysis of ImmGen microarray data (Scott Davis and Christophe Benoist) and is available at http://cbdm.hms.harvard.edu/LabMembersPges/SD.html. As previously described[3], the delta score is defined as:

$$\delta(a,b) = log_2\left(\frac{\mu_a}{\mu_b}\right) - (\sigma_a + \sigma_b)^2$$

where μ and σ are the geometric mean and geometric standard deviation of populations *a* and *b*, respectively. The first term represents the log fold change between the two class means, and the second term is the total two-class variance. Thus, the delta score represents a variance-adjusted fold change, or a measure of fold change that is increasingly penalized for noise.

Microarray analysis: Leukocyte lineage analysis

A subset of the full ImmGen dataset representing all major splenic leukocyte populations (78 samples across 23 populations; hereafter referred to as the "core" dataset) was selected for lineage analysis. Prior to analysis, genes not expressed at a normalized intensity value of 120 across all replicates within at least one population were categorized as not being expressed and excluded from further analysis. Principal components analysis was performed using the PopulationDistances module of GenePattern[2] with the 15% most variable genes across the core dataset being used to identify the most significant vectors. Signature genes of the NK/T complex were identified by conducting pairwise comparisons of every NK/T population with every non-NK/T population using the DeltaScore module of GenePattern, followed by identification of the intersection of all pairwise comparisons at each delta threshold in order to rank predictions by statistical significance. Heatmaps were generated with Java Treeview[4], with data represented as $\log_2$ relative expression values zero-transformed to the median expression value of non-NK/T complex populations.

A novel algorithm termed Ontogenet was developed for regulatory network prediction on the ImmGen dataset[4]. Ontogenet finds a regulatory program for each module of co-expressed genes, based on regulators expression and the structure of the lineage tree. The regulatory program uses a form of regularized linear regression, in which each cell type can have its own regulatory program, but regulatory programs of related cells are encouraged to be similar. This allows switching in the regulatory program but still allows robust fitting given the available data.

Microarray analysis: NK/T complex lineage analysis

Splenic subsets of the NK/T complex (28 datasets representing 9 populations) were filtered for expression intensity and analyzed by PCA on the 15% most variable genes within this subset, as described above. Hierarchical clustering was performed with a Euclidean distance similarity metric on the full intensity-filtered filtered dataset with average linkage in xCluster[5]. Intersection analysis of the innate-like lymphocyte subsets was performed in two steps. First, significantly differentially expressed genes were identified using the DeltaScore module between each innate-like population and naïve $\alpha\beta$ T cells. Next, intersection analysis was used to identify genes significantly upregulated in more than one innate-like lymphocyte population relative to $\alpha\beta$ T cells and represented as a Venn diagram to demonstrate shared expression. Heatmaps were generated using Java Treeview, with data represented as $\log_2$ expression values median centered across all samples.

Microarray analysis: Resting NK cell signature analysis

The core dataset was subjected to pairwise comparisons of NK cells versus every other population using the DeltaScore module of GenePattern. The intersection of these analyses was identified at each delta threshold in order to rank predictions by statistical significance. Heatmap data represent $\log_2$ expression values median centered across all populations. Putative regulators of the signature were identified as previously described and rank ordered based on the proportion of the NK cell signature with which each regulator is associated.

Microarray analysis: NK cell pre-priming analysis

A sub-dataset containing naïve NK cells, naïve $CD8^+$ T cells, and $CD8^+$ T cells responding to VSV or *Lm* on days 5 and 6 post-infection was generated (18 datasets representing 6 populations) and filtered for expression as described above. Genes significantly upregulated in naïve splenic NK cells or $CD8^+$ T cells responding to VSV or *Lm* infection were identified by comparison to naïve splenic T cells using the DeltaScore module of GenePattern. Genes meeting a delta of 2.0 and above are depicted for clarity (Fig. 4a), but all genes meeting a delta of 0.5 and above are available as a supplementary table. Genes were ordered by manually curated functional groups. Regression analysis of $\log_2$ expression intensities was performed in GraphPad Prism and plotted with 95% confidence bands.

Microarray analysis: NK cell response to MCMV infection

A sub-dataset containing NK cell responses to MCMV infection was generated (11 datasets representing 4 populations) and filtered for expression as described above. Significantly induced genes were identified using the DeltaScore module for each time point post-infection with MCMV (day 1.5, day 7, and day 27). The genes were grouped according to expression pattern and depicted as a heatmap representing $\log_2$ expression values zero-transformed to median expression in naïve NK cells. Hierarchical clustering relationships between the populations were calculated using Euclidean distance in xCluster. Response patterns and representative genes were manually selected and depicted as median $\log_2$ expression values in overlapping line plots.

Microarray analysis: Common effector response of NK cells and CD8$^+$ T cells

A sub-dataset containing NK cell response to MCMV infection and CD8$^+$ T cell responses to VSV or *Lm* infection was generated (40 datasets representing 14 populations) and filtered for expression as described above. Pairwise correlation coefficients were calculated for the mean $\log^2$ expression value for each dataset representing the CD8$^+$ T cell response to VSV or *Lm* infection and the day 1.5 and day 7 NK cell datasets representing the response to MCMV infection. The datasets with the three highest correlations for each CD8$^+$ T cell infection with the NK cell response to MCMV were selected for subsequent analysis, as these data points represent the most similar overall responses. Fold induction was calculated as the difference between median $\log_2$ expression intensity in activated and corresponding naïve population for NK cells and CD8$^+$ T cells. Expression intensities were calculated as $\log_2$ raw expression values. Linear regression with 95% confidence bands was calculated in GraphPad Prism.

Microarray analysis: Common memory response of NK cells and CD8$^+$ T cells

A sub-dataset of naïve and memory NK cell and CD8$^+$ T cell populations (18 datasets representing 7 populations) was generated and filtered for intensity as described above. Both days 45 and 106 were included as memory populations in the CD8$^+$ response to VSV, and days 45 and 100 for *Lm*. Data transforms and fold induction calculations for NK cells and CD8$^+$ T cells were performed as described above for common effector responses.

References

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3. Malhotra, D. *et al.* Transcriptional profiling of stroma from inflamed and resting lymph nodes defines immunological hallmarks. *Nature Immunology* **13**, 499–510 (2012).
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Supplementary Table 1. NK cell signature genes

Delta score	Significant Genes
5.0	_Klra8, Ncr1_
4.5	_Gzma_
4.0	_Adamts14_
3.5	_Klra9, Klra10, Klrb1a, LOC640965_
3.0	_Gzmb, Klra3, Klrb1b_
2.5	_Itga2, Klra9, Klre1, Serpinb9b, Styk1_
2.0	_Car5b, Dapk2, Klra1, Klrc3, Klri2, Mcam, Prf1, S1pr5*, St5_
1.5	_Cma1, Gem, I830127L07Rik*, Khdc1a, Klrk1, Nrarp, Osbpl3, Plscr4, Spry2_
1.0	_A930038C07Rik, Angpt1, Cdc20b, Cuedc1, Cym, Cyp17a1, Eomes, Gm10522, Il18rap*, Itgam, Kcnj8*, Klf12, Klhl4, Klra6, Klrb1c, Klrc2, Klrd1, Ptpn12, Slc25a24*, Sytl3_
0.5	_4831426I19Rik, Abcg2, Agpat2, Aoah, Arsb, Arsb, B4galt5*, Camk2n1, Car2, Ccl5*, Cdc42ep3*, Chrne, Chsy1*, Cldnd2*, Ctsw, Fbxl2, Fzd5, Garnl4*, Gm11435, Igsf5, Il12rb2, Klhl30, Klrg1*, Lpin1, Nelf, Nfil3, Nkg7, Oxr1, Pam, Pogk*, Rap2a*, Rasl12, Rbpms, Samd3, Sept5, Serpinb9, Sos2, Spn, Xdh_

__*__ These 14 genes are significantly expressed in effector $CD8^+$ T cells responding to *L. monocytogenes* infection.

Supplementary Table 2. NK cell pre-priming genes (common to naïve NK cells and effector $CD8^+$ T cells)

Delta score	Significant Genes
5.0	_Klrc1, Plek_
4.5	_Ccr5, Itgax_
4.0	_Gzmb_
3.5	_Car5b, Ccl5, Ccr2, Itgam_
3.0	_Anxa2, Gzma, Osbpl3, S100a6, Slamf7, Tbx21_
2.5	_Anxa1, Il18rap, Itgb1, Klrc2_
2.0	_Id2, Klrg1, Klrk1, Lgals1, Myo1f, Prdm1_
1.5	_Ahnak, Csda, Dock5, Fam129a, Garnl4, Gem, Gm11435, Hmgb2, Hmgb2, Hmgb2, Hmgb2, Itga4, Klrc3, Mapre2, Pglyrp1, Pik3ap1, Ptprj, Slc25a24_
1.0	_1700025G04Rik, Adap1, Aplp2, Arsb, Atp2b4, B4galt5, Bhlhe40, Ccl3, Cd44, Chsy1, Cobll1, Ctla2a, Cx3cr1, Dapk2, Eea1, Efhd2, Entpd1, Fasl, Il10ra, Kcnk5, Lrrk1, Nqo2, Plscr1, Pogk, Prr5l, Ptms, Ptprj, Raph1, Rnf216, Runx2, S100a11, S100a11, Serpinb6b, Slc9a7, Soat2, Stard10, Stk39, Stx11, Tigit, Tmem163, Ttc39c, Unc119, Whsc1_
0.5	_2210412E05Rik, 4831426I19Rik, Acot7, Adora2a, Ak3, Ap3s1, Arhgap18, Arsb, Atf6, Atp2b1, Bspry, Capg, Capn2, Carhsp1, Casp1, Casp3, Casp7, Ccdc50, Ccnd2, Chst11, Cited2, Cmklr1, Ctsd, Cxcr3, Cyfip1, Dennd4a, Dennd5a, Dusp5, Ehbp1l1, Endod1, Eomes, Errfi1, F2rl2, Fam129b, Fbxl2, Fbxw8, Ggh, Gnptab, Gpr160, Gramd1b, Hip1r, Hopx, Ifng, Il18r1, Il2rb, Itga2, Itgal, Itgb3bp, Katnb1, Kif13b, Klf10, Ksr1, L1cam, Lpin2, Mdfic, Myadm, Myo1c, N4bp1, Nbeal2, Nelf, Nkg7, Nptn, Nrarp, Nsmaf, Plp2, Plp2, Plscr1, Ppm1j, Ppp1r12a, Prex1, Prr13, Prr5, Rad21, Reep5, S100a10, Sept11, Smad3, St3gal6, Stk32c, Stmn1, Stmn1, Syne2, Sytl2, Tnfrsf1b, Ttc39b, Ttc39b, Vcl, Vim, Wee1, Zcchc18, Zeb2_

Supplementary Table 3. NK cell response to MCMV infection

Category	Significant Genes
Early effector	*1300018I05Rik, 2410002F23Rik, 2610318N02Rik, 2810417H13Rik, 2810417H13Rik, 4930412M03Rik, 4930422G04Rik, 4930579G18Rik, 4930588K23Rik, 4932442E05Rik, 4933407C03Rik, 4933437N03Rik, 5930422O12Rik, 6430526N21Rik, 9230105E10Rik, 9330175E14Rik, A230050P20Rik, Aars, Abcb1a, Abcb1b, Abtb2, Actn4, Adap1, Adar, Agfg1, Agpat1, Ahctf1, Ahdc1, Ahr, AI451617, AI848100, Airn, Aldh18a1, Alg8, Alms1, Amfr, Amica1, Amigo3, Ankrd28, Ankrd52, Anp32b, Ap1s3, Apex1, Apobec3, Arf6, Arid1a, Arl5a, Art2b, Asf1b, Asna1, Atad2, Atad5, Atf6, Atf7, Athl1, Atn1, Atp11a, Atp13a1, Atp2a2, Atp2b4, Atr, Atxn2l, Atxn7l1, AU017193, B4galt5, Bak1, Banf1, Bat2, Baz1a, BC016423, BC057170, Bcl2, Bhlhe40, Brca1, Bspry, Bst2, Bysl, C1qtnf6, C530030P08Rik, C530030P08Rik, Calr, Camta2, Canx, Car5b, Carm1, Cars, Casp3, Casp4, Cblb, Cbx5, Ccl3, Ccl4, Ccnd3, Ccne1, Ccnyl1, Ccr5, Cct2, Cd22, Cd38, Cd69, Cdc25a, Cdc2a, Cdc45l, Cdca3, Cdca7, Cdh24, Cdk6, Cdkn1a, Cenpm, Cenpn, Chaf1a, Chaf1b, Chd3, Chd7, Chd7, Chd7, Chd7, Chek1, Cherp, Chsy1, Chtf18, Cirh1a, Cish, Cit, Ckb, Cks1b, Cldnd2, Clic4, Clpb, Cmpk2, Coro1c, Coro2a, Cpsf7, Csda, Csrnp1, Cxcl10, Cyfip2, Cysltr2, D17Wsu92e, D4Ertd22e, D8Ertd82e, Dazap1, Dcakd, Dctd, Ddx18, Ddx54, Dek, Dennd4a, Dennd4a, Dennd4a, Dennd4a, Dennd4a, Dennd4a, Dennd4a, Dennd4a, Dennd4a, Dennd4b, Dgat1, Dgkh, Dhfr, Dhx58, Dis3, Dkc1, Dnajb11, Dnajc13, Dnajc13, Dot1l, Dot1l, Dusp16, Dusp5, E030037K03Rik, E2f1, E2f4, Eftud2, Egr1, Egr2, Ehd4, Eif2ak2, Eif2c2, Eif2s2, Eif3a, Eif3b, Eif4a1, Eif4a1, Eif4enif1, Eif4g1, Eif5a, Eif5a, Elavl1, Elmo2, Entpd1, Eprs, Ern1, Errfi1, Etnk1, Etv6, Ezh2, F2r, F2rl2, F730047E07Rik, Fam120a, Fam188a, Fanca, Fbl, Fen1, Fgr, Fignl1, Fnbp4, Fndc3a, Fosl2, Foxk2, Fubp1, Gadd45g, Gapdh, Gapdh, Gapdh, Gapdh, Gapdh, Gapdh, Gapdh, Gapdh, Gapdh, Gapdh, Gapdh, Gapdh, Gapdh, Gapdh, Gapdh, Gapdh, Gbp4, Gdf11, Gfpt1, Gins2, Glcci1, Gm10521, Gm10537, Gm12070, Gm12070, Gm12070, Gm12070, Gm12250, Gm15470, Gm2173, Gm4955, Gm5069, Gm5145, Gm5523, Gm5785, Gm614, Gm6560, Gm6742, Gm6907, Gm6981, Gm8587, Gm9034, Gnaq, Gnb5, Gns, Got2, Gpd2, Gpr171, Gpr52, Gramd4, Gsk3a, Gsk3a, Gspt1, Gsta3, H2-T24, Hdlbp, Hectd1, Hells, Herc5, Hic1, Hif1a, Hist1h3a, Hist1h3f, Hist1h3f, Hist1h3f, Hist1h3g, Hist1h3g, Hist1h3g, Hist1h3g, Hist2h3b, Hist2h3c1, Hk2, Hmgn2, Hmgn2, Hmgn2, Hmgn2, Hnrnpl, Hpvc-ps, Hsd3b7, Hsf1, Hsh2d, Hsp90aa1, Hsp90ab1, Hspa5, Hspe1, Hspe1, Huwe1, Hyou1, Iars, Iars, Icam1, Ide, Ifih1, Ifitm1, Ifitm3, Ifng, Ifrd2, Ifrg15, Igf2r, Il12rb1, Il12rb2, Il18bp, Il2ra, Il6st, Ints7, Ipo4, Ipo5, Ipo7, Ipo9, Irf1, Irf7, Irf8, Irgm1, Isg20, Jun, Jund, Kat2a, Kpnb1, Krtap10-10, Ksr1, Lag3, Larp1, Larp1, Larp4, Larp4, Larp4, Lig1, Litaf, Lmf2, Lmnb1, LOC100044102, LOC100044416, LOC100047557, LOC433762, LOC641050, LOC641050, LOC641050, LOC641050, LOC670326, Lpp, Lrrc4, Luzp1, Lyar, Map2k4, Map2k7, Map3k8, Mapk6, Maz, Mcm10, Mcm3, Mcm4, Mcm5, Mcm6, Mcm7, Mcph1, Mctp2, Med13l, Med15, Mettl1, Mfsd2, Midn, Mink1, Mlkl, Mllt6, Morc2a, Mov10, Mpa2l, Ms4a6b, Msmp, Mtbp, Mthfd1l, Mthfd2, Muc1, Mx1, Mxd1, Mybl2, Myd88, Myo19, Nacc1, Nap1l1, Ncapg2, Ncl, Nefh, Nek6, Nf1, Nfil3, Nfkbib, Nfkbiz, Nkrf, Nle1, Nlrc5, Nlrc5, Nlrc5, Nlrc5, Noc4l, Nolc1, Nop58, Notch1, Nphp4, Npm1, Nr4a1, Nr4a2, Nr4a3, Nup107, Nup205, Nup98, Oas1a, Oas1g, Oas3, Oasl1, Oasl2, Obfc2a, Obfc2b, Odc1, Odc1, Orc6l, Osm, Otud4, P2ry14, P4hb, Pa2g4, Pabpc4, Pabpc4, Parp12, Parp14, Parp9, Patl1, Paxip1, Pcgf2, Pcna, Pcna, Pdia3, Pdia6, Pds5a, Pecam1, Phf11, Picalm, Piga, Pik3ap1, Pim1, Pitpnm2, Pkm2, Pkmyt1, Pla2g6, Plcg2, Plk1, Plk3, Plk4, Plod2, Pmepa1, Pmf1, Pml, Pnet-ps, Pola1, Pole2, Polq, Pols, Pom121, Pop1, Pou5f2, Ppm1h, Ppp1r14b, Ppp1r15b, Ppp1r16b, Ppp1r3b, Pprc1, Prim1, Prp2, Psmd1, Psme1, Psme3, Ptma, Ptpn2, Ptpre, Purb, Pus7, Pvr, Pyhin1, R3hdm1, Rad51, Rad54l, Ranbp1, Rbl1, Rcc1, Rcc2, Rexo1, Rfc3, Rgs16, Riok1, Rnaseh2b, Rnf126, Rnf19b, Rnf213, Rrbp1, Rrm1, Rrm2, Rrp1b, Rsad2, Rtp4, Runx1, Samhd1, Sbno2, Scarb1, Sco1, Sdc3, Sec24c, Sema7a, Senp1, Serpinb9, Serpinb9b, Setbp1, Sf1, Sf3a2, Sfrs2, Sfrs4, Sfrs6, Sh3bp2, Shmt1, Sipa1l1, Sipa1l3, Slamf7, Slc16a6, Slc1a5, Slc25a22, Slc29a1, Slc35b1, Slc35f2, Slc41a1, Slc7a6, Slfn8, Smarca4, Smc2, Smchd1, Smchd1, Snd1, Snhg1, Snhg1, Snrpa, Snx9, Socs1, Socs3, Socs3, Solh, Sos1, Spna2, Spred2, Srcap, Srf, Srrm1, Srxn1, Ssr1, Ssrp1, St6galnac4, Stat1, Stat2, Stat3, Stk39, Stk40, Stx11, Sulf2, Sult2b1, Suv39h1, Syncrip, Syvn1, Taf1d, Taf4b, Taf6, Tagln2, Tap1, Tbkbp1, Tbrg4, Tbx21, Tcerg1, Tcf19, Tcof1, Tfrc, Tgfb1, Tgm2, Thada, Thoc4, Thop1, Ticam1, Timeless, Tk1, Tk1, Tle3, Tmem106a, Tmem184b, Tmem2, Tmprss6, Tnfaip3, Tnks1bp1, Tomm40, Top2a, Topbp1, Tpst1, Tpx2, Trafd1, Trak1, Trak2, Treml2, Trim30, Trip13, Trp53, Ttll4, Tuba1b, Tuba1b, Tuba1c, Txn2, Ubap2, Ubap2l, Ube2m, Uck2, Uck2, Uhrf1, Ung, Usp18, Usp2, Usp25, Usp31, Usp37, Vac14, Vasp, Vps37b, Wars, Wbp7, Wdhd1, Wdr43,*

	Wdr62, Wee1, Whsc1, Wiz, Wnk1, Xaf1, Xcl1, Xdh, Xpot, Yrdc, Zbp1, Zbtb32, Zc3h4, Zcchc2, Zcchc7, Zfp335, Zfp367, Zfp384, Znhit1, Zranb3
Late effector	*1700017B05Rik, 1700066M21Rik, 1700081L11Rik, 2310034G01Rik, 2900026A02Rik, 4931440P22Rik, A530032D15Rik, A630072L19Rik, Arap3, Atxn1, Atxn7l1, Avpr2, BC059842, BC059842, Cbfa2t3, Cdc20, Cercam, Chd7, Chd7, Ckm, Cnnm2, Dennd1c, Depdc1b, Dnm1, Dock5, Fam117a, Fbrs, Foxk1, Fry, Ggnbp1, Gm10124, Gm10825, Gm10838, Gm2889, Gm5589, Gm8485, Gm8956, Gm8985, Gna15, Grm2, Haao, Hamp2, Hip1, Hmgb2, Hmgb2, Hmgb2, Inpp4a, Jarid2, Kifc1, Klf11, Klf13, Klrg1, LOC100046894, Lphn1, Lphn1, Maml2, Mef2d, Mlxip, Mnt, Mospd3, Mt1, Myo1e, Nacad, ND4L, Ngfr, Ntng2, Olfr566, Os9, Palm, Pdcd11, Pik3cb, Plekho1, Pltp, Prss27, Ptms, Ptp4a3, Ptprs, Racgap1, Rangrf, Rbm38, Rhbdf2, Rnf43, Setd1b, Sik1, Slain2, Slc36a1, Slc9a3r1, St3gal3, St6galnac6, Tet3, Tmem221, Trp73, Tspan31, Ttyh2, Ube2c, Zdhhc20, Zmiz1*
Sustained effector	*AF362573, Arhgef1, ATP6, Aurkb, B3gnt7, BC059842, BC059842, BC059842, BC059842, BC059842, BC059842, C330019G07Rik, Ccna2, Ccnb2, Cdc6, Cdca2, Chd7, Cyfip2, Dgkz, Diap3, Dock6, Dtl, E2f2, E2f7, E2f8, Eif3c, Eif4g3, Epn1, Foxm1, Fyb, G530012D18Rik, Glcci1, Gm6041, Gopc, Grb7, Grn, Hmgn2, Itpr1, Jak3, Kif11, Kif18b, Kif23, Lrdd, Map3k11, Mark2, Mbd6, Mki67, Mll2, Msl1, Ncapd2, Ncaph, Nlrc5, Nlrc5, Nlrc5, Nlrc5, Nlrc5, Nlrc5, Nlrc5, Nlrc5, Nlrc5, Nlrc5, Nlrc5, Nlrc5, Nlrc5, Nlrc5, Pctk1, Prkcz, Psme2, Rnf213, Runx3, Scaf1, Slc43a3, Stom, Thy1, Traf4, Trerf1, Troap, Tyms, Zfhx2*
Infection signature	*AY036118, BC049688, Chd7, F730043M19Rik, Gm12000, Gm7265, Gp49a, Hist1h1b, Hopx, Hsn2, Nlrc5, Trio, Trip11*
Memory	*1700029I01Rik, 2310001H12Rik, 2410080I02Rik, 2610020H08Rik, 3110052M02Rik, 4930444G20Rik, 4930522L14Rik, 4930522L14Rik, 4932438A13Rik, 5830415L20Rik, A830080D01Rik, AB010352, Ahsa2, Amotl1, Apoa2, Apold1, Arih2, Armc7, Arx, Atrx, B230307C23Rik, BC094916, Calm1, Camk2b, Casp1, Ccdc137, Ccdc85c, Ccnl1, Cdc20b, Cdkn2b, Cdv3, Cep57, Cetn4, Chadl, Chd7, Chd7, Chd7, Chd7, Chd7, Clock, Cnih2, Cog3, Dgkz, Dnajb9, Dnajc1, Dusp14, Efemp2, EG547347, ENSMUSG00000072643, Fam111a, Fam178a, Far1, Fasl, Fcho2, Fos, Gcc2, Gm10830, Gm11435, Gm12504, Gm13051, Gm13251, Gm15296, Gm15542, Gm4759, Gm6540, Gm6651, Gm7125, Gm8995, Gm9264, Gm9405, Gsc2, Gvin1, Hbb-b1, Hes1, Hmga1, Hmgb1, Hmgb1, Hmgb1, Hmox1, Hspa4l, Kif7, Klf12, Klra10, Klra6, Krt8, LOC100043371, LOC100044428, LOC100044517, LOC100045396, LOC638407, LOC640991, LOC676160, Lrrfip1, Ly6c1, Mdfic, Mdga1, Mrpl20, Nktr, OTTMUSG00000010657, Pisd-ps2, Pitx1, Pmaip1, Ppig, Ppp3cc, Ptpn4, Ptprv, Rab11fip4, Rab4a, Rbm25, Rpl17, Rsrc1, Sacs, Sltm, Stxbp3b, Thoc1, Top1, Tpr, Ttc14, Ypel1, Zfp125, Zfp182, Zfp292, Zfp599, Zfp871, Zfp97, Zufsp*

Supplementary Table 4. Common effector response of NK cell s and effector CD8$^+$ T cells

Significant Genes
ATP6, AY036118, BC049688, Ccl9, Dock5, E2f2, F730043M19Rik, Galnt3, Gm10785, Gna15, Gzmk, Hip1, Hmgb2, Hmgb2, Hmgb2, Hopx, Hpse, Itga1, Itpr1, Klrg1, Mark2, Palm, Ptms, Ptpn3, Runx3, Slc43a3, Smpdl3b, Stard10, Trio, Ttyh2, Zmiz1

Supplementary Table 5. Common memory signature of NK cell s and CD8$^+$ T cells

Significant Genes
F730043M19Rik, Gzmb, Hopx, Ly6c1, Mdfic, Pmaip1, Ptpn4, Sytl2