Supplementary information for:

MS4A3 Promotes Differentiation in Chronic Myeloid Leukemia Cells by Enhancing Common β Chain Cytokine Receptor Endocytosis

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SUPPLEMENTARY FIGURE LEGENDS

Figure S1. Expression of resistance classifier genes in CD34$^+$ cells from AP/BP-CML versus CP-CML patients. Relative mRNA expression for twenty genes with differential expression in CML disease progression and/or imatinib resistance were selected for validation by qRT-PCR in CD34$^+$ cells from an independent cohort of patients with AP/BP-CML (n=16) vs. CP-CML (n=17). (*p<0.05)

Figure S2. Myeloid-specific expression of the six-gene set from the combined meta-analysis. Hierarchical trees were generated with the BloodSpot online tool (http://servers.binf.ku.dk/bloodspot/) using the normal hematopoiesis vs. acute myeloid leukemia comparison.

Figure S3. Lentivirus-mediated *MS4A3* KD and overexpression, as well as their effect on colony formation by normal adult BM CD34$^+$ cells. (A-B) Relative *MS4A3* expression in LAMA-84 CML cell line **(A)** and in CD34$^+$ cells from a CP-CML patient **(B)** transduced with three different dox-shRNAs targeting *MS4A3* after ± 0.1 µg/mL dox treatment for 72 h. shRNA #1659 resulted in the best KD and was selected for use in subsequent experiments. Error bars represent SEM. **(C-D)** Relative *MS4A3* mRNA levels of CML and CB samples after lentiviral transduction and culture in the indicated conditions for 72 h. **(E)** Effect of *MS4A3* KD on colony formation of normal adult BM CD34$^+$ cells.

Figure S4. MS4A3 expression is regulated by DNA methylation in CML and is correlated with granulocytic lineage genes in AML. (A) *MS4A3* co-expression genes in TCGA AML cohort (NEJM, 2013) [1] analyzed by cBioPortal [2]. List shows the top positively correlated genes. Red font: *CEBPE* (C/EBPε) is the most significantly correlated transcription factor. Bold font: genes in the six-gene set identified in the combined meta-analysis. **(B-D)** Primary CML CD34$^+$ cells were treated with DNA methylation inhibitors as indicated, and MS4A3 expression level was analyzed by qRT-PCR.

Figure S5. MS4A3 does not regulate cell cycle progression or pCDK2 level; nor does it decrease with active cell proliferation in CML cells. (A) K562 cells, LAMA-84 cells, and primary CP-CML CD34$^+$ cells were lentivirally transduced for MS4A3 overexpression or KD, and analyzed for DNA content indicating the cell cycle stages using propidium iodide staining and flow cytometry. No obvious change in cell cycle distribution is observed with alterations of

MS4A3. **(B)** Immunoblot and flow cytometry analyses demonstrate no correlation between MS4A3 protein levels and pCDK2 levels in CML cell lines. **(C)** MS4A3 expression levels were detected in cells with or without active proliferation in $CD34^+$ cell cultures, using qRT-PCR. Active proliferation (more divisions) is labelled by reduced CFSE fluorescent intensity. No suppression of MS4A3 is observed in proliferating cells.

Figure S6. Confirmation of MS4A3 flow cytometry antibody specificity, and additional images for Fig.6H. (A) Relative mRNA level of *MS4A3* after dox-induced shRNA KD in M07e cells. Flow cytometry detection of MS4A3 protein using the monoclonal antibody specific to MS4A3 and PE-conjugated secondary antibody. Antibody labelling reduces as *MS4A3* mRNA decreases with incremental times of dox induction. **(B)** MS4A3 monoclonal antibody recognizes cell-free MS4A3-EGFP protein. MS4A3-EGFP fusion proteins were ectopically expressed in HEK293T cells, and then pulled down with agarose bead-bound polyclonal GFP antibody. MS4A3-EGFP-bound beads were then labelled by MS4A3 monoclonal antibody, GFP monoclonal antibody (positive control, different species from pulldown antibody), and CD3 monoclonal antibody (negative control), followed by corresponding fluorescent secondary antibodies. MS4A3 monoclonal antibody signal was comparable to the positive control. **(C)** LAMA-84 cells with or without GM-CSF stimulation (5 min) were fixed, stained for MS4A3 and CD116, and imaged by confocal microscopy. Arrows depict clusters of MS4A3 and CD116.

Figure S7. MS4A3 knockdown does not inhibit endocytosis of the βc independent receptor – Kit (CD117) and G-CSFR (CD114). (A) Representative flow cytometry plots showing the rapid endocytosis of CD117 after SCF stimulation in LAMA-84 cells. **(B)** Quantification of SCF induced CD117 endocytosis in LAMA-84 cells lentivirally transduced with dox-sh*MS4A3*, with or without dox mediated shRNA induction. **(C-D)** CP-CML $CD34^+$ cells were revived and lentivirally transduced for *MS4A3* KD or overexpression, then used for CD114 endocytosis assay. Cells were stimulated with 10 ng/mL G-CSF or PBS control for 5 minutes at 37°C, and surface CD114 were analyzed by flow cytometry. **(E)** Baseline CD114 surface expression on cells used in panel C-D. **(F)** CP-CML $CD34^+$ cells were revived and lentivirally transduced with empty GFP vector. GM-CSF-induced CD116 endocytosis was analyzed by flow cytometry. **(G-H)** GM-CSF/IL-3-induced intracellular kinase activation in cells used in panel F.

Figure S8. CD116 (*CSF2RA* / GM-CSFRα), and CD123 (*IL3RA* / IL-3Rα) expression in myeloid hematopoiesis. (A) CD116 and CD123 levels in various cells as shown by BloodSpot

illustration of the Dataset GSE42519. **(B)** Flow cytometry analysis of cell surface CD116 and CD123 expression in CML patient samples (N = 3).

Figure S9. Evolutionary phylogenetic trees of MS4A3-coding and M-CSF-coding gene orthologs. Gene orthologs were discovered in NCBI Gene database. One protein of each species was included in alignment and clustering using the Constraint-based Multiple Alignment Tool [3].

METHODS

Cell lines and patient samples.

All CML cell lines were maintained in RPMI1640 supplemented with 10% fetal bovine serum (FBS), 100 U/mL penicillin-streptomycin, and 2 mM L-glutamine (GIBCO, Thermo Fisher Scientific, Waltham, MA, USA). Mononuclear cells (MNCs) from normal cord blood (CB) or femoral head donors, or peripheral blood (PB) of CML patients were separated by density centrifugation on Ficoll-Hypaque (GE Healthcare, Waukesha, WI, USA). $CD34^+$ cells were selected using an autoMACS system (Miltenyi Biotec, Bergisch Gladbach, Germany), confirmed for >90% purity on a Guava easyCyte HT Flow Cytometer (Millipore, Billerica, MA), and cryopreserved. Additional normal adult BM $CD34^+$ cells collected from adult donors under 60 years old were purchased from AllCells (Alameda, CA, USA). Fresh or frozen $CD34^+$ cells were cultured in IMDM supplemented with 10% BIT9500 (StemCell Technologies, Vancouver, BC), 100 U/mL penicillin-streptomycin, 2 mM L-glutamine, and StemSpan cytokines (CC100; StemCell Technologies) for 24-48 h at 37˚C prior to use in biological assays. All cell lines used were authenticated by Short tandem repeat (STR) fingerprinting. CML cell lines were confirmed to harbor exclusively native *BCR-ABL1* by conventional Sanger sequencing in both directions using BigDye terminator chemistry on an ABI3730 instrument[71]. A complete list of patient samples used in this study can be found in Supplementary Table S1. All patients gave informed consent in accordance with the Declaration of Helsinki, and all studies with human specimens were approved by the University of Utah Institutional Review Board (IRB).

Scl-tTA$^+$;TRE-BCR-ABL1$^+$ compound transgenic mice.

Scl-tTA$^+$;TRE-BCR-ABL1$^+$ double transgenic mice were kindly provided by Emmanuelle Passegué [4]. These mice express tetracycline transactivator (tTA) in BM HSCs and CMPs, as well

as BCR-ABL1 under control of a tetracycline response element (TRE), such that BCR-ABL1 expression is repressed in the presence of doxycycline (tetracycline analog, 2 g/L, 5% sucrose, Gold Biotechnology, St. Louis, MO, USA) and expressed upon dox withdrawal. BM cells from double transgenic mice were used for *ex vivo* culture experiments. Lin^- BM cells were isolated from *Scl-tTA*$^+$*;TRE-BCR-ABL1*$^+$ mice maintained in the continuous presence of dox (0.1 µg/mL, Gold Biotechnology Inc.), and cultured for 72-96 hours without dox to turn on BCR-ABL1 expression. Resulting cells were assessed for *Ms4a3* mRNA expression by qRT-PCR. A list of primer sequences is available in Supplementary Table S2. Lin^- BM cells were also used for *ex vivo* shRNA-mediated *Ms4a3* KD experiments with scrambled RNA transfected cells as controls (GE Healthcare Dharmacon, Inc., Chicago, IL, USA). These mouse *Ms4a3* shRNA vectors are not dox-inducible. Lentivirus transduced (GFP^+) Lin^- BM cells were plated in semisolid culture (72 h) or colony formation assays ± doxycycline (0.1 µg/ml). For BM transplant, BM cells were flushed out from donor mice. RBC were lysed, and Lin^- BM hematopoietic cells were quantified by flow cytometry. Equal number ($6x10^5$) of Lin^- BM cells from *Ms4a3* knockout and control donors were i.v. injected into lethally irradiated *Ms4a3*$^+$ recipient mice. All animal experiments in this manuscript were approved by the University of Utah Institutional Animal Care and Use Committee (IACUC).

Xenograft in NSG mice.

$CD34^+$ cells from CP-CML (n=3) patients were lentivirally transduced with dox-inducible shRNA targeting human *MS4A3* (sh*MS4A3*) in tandem with GFP, and the resulting unsorted populations were injected into sub-lethally irradiated 8-week-old NSG recipients (NOD.Cg-*Prkdc*^{scid} *Il2rg*^{tm1Wjl}/SzJ, #005557, Jackson Laboratory, Bar Harbor, ME, USA; 6 mice/sample, $1.2x10^6$ cells/mouse) 72 hours post-infection. Following two weeks of engraftment, half of the mice remained on regular water, and half of the mice were placed on dox-containing water (2 g/L and changed twice a week, with 5% sucrose, Gold Biotechnology) to induce knockdown. All recipient mice received sulfadimethoxine (0.125 mg/mL, Vet One, Boise, ID, USA) in the drinking water for the duration of the study. At 12 weeks, all mice were sacrificed to assess for $hCD45^+$ GFP^+ cells in the PB, BM, and spleen.

mRNA expression analysis by qRT-PCR.

RNA extraction was performed using the RNeasy Mini Kit (Qiagen, Germantown, MD) and converted to cDNA with the iScript cDNA Synthesis Kit (Bio-Rad Laboratories, Hercules, CA). cDNAs of indicated genes were detected by qRT-PCR using gene-specific primers

with SsoAdvanced™ SYBR® Green Supermix (Bio-Rad Laboratories) or by using primer/probes in a CFX96 Real-Time PCR Detection System (Bio-Rad Laboratories). Human genes expression was referenced to human beta-glucuronidase (*GUSB*) or *GAPDH*, and mouse genes to *Gapdh* and analyzed in CFX Manager (Bio-Rad Laboratories) using the "ΔΔCt method". qRT-PCR analysis was done in triplicate for each experiment. All primers used with SYBR® Green Supermix were designed to have consistent amplification efficiency across genes in the same PCR program. A list of primers used can be found in Supplementary Table S2 and additional reagents and resources may be found in the Key Resources Table.

Western blotting analysis.

For LAMA-84 cell line, cells were treated as indicated in the experiments and then immediately chilled on ice-water mixture to stop enzymatic activities before being lysed in RIPA buffer. Protein lysates were denatured at 95 °C for 10 min prior to being electrophoresis on SDS-PAGE gels and being transferred to nitrocellulose membranes. Membranes were blocked in 5% non-fat milk in TBST buffer, and probed with primary antibody, followed by species matched secondary antibody-HRP conjugates. Blots were imaged with Pierce™ enhanced chemiluminescence substrate (Thermo Fisher Scientific, Waltham, MA) on ChemiDoc XRS+ imaging system (Bio-Rad Laboratories, Hercules, CA). A list of antibodies used can be found in Supplementary Table S3 and additional reagents and resources may be found in the Key Resources Table.

***Plasmids*.**

Inducible shRNAs targeting *MS4A3* (sh*MS4A3*) were purchased from Cellecta (Mountain View, CA, USA). Briefly, sh*MS4A3* was inserted into a tetracycline-inducible vector (pRSIT12-U6Tet-CMV-TetR-2A-TagGFP-2A-Puro), containing the wild-type tetracycline repressor (tetR); thus, transcription is blocked unless 0.1 µg/mL doxycycline is present in the culture medium. Construct #1659 resulted in the most efficient KD of *MS4A3* in CP-CML $CD34^+$ cells, and was chosen for further studies (Suppl. Fig. 3). For ectopic expression, human *MS4A3* was PCR amplified from mononuclear cells of a healthy donor, *CEBPE* from KBM5 cells, *MECOM* (transcript RefSeq NM_005241) from HEL cells, and subcloned into the XbaI- and NotI-digested pCDH-CMV-MCS-EF1-copGFP vector (System Biosciences, Mountain View, CA, USA). Gene inserts were Sanger sequenced (by Univ. of Utah Genomics Core) to verify authenticity.

Lentivirus.

Lentivirus-producing 293FT (#R70007, Thermo Fisher Scientific) cells were maintained in culture in DMEM plus 10% FBS, 2.0 mM L-glutamine, 100 U/mL penicillin-streptomycin, 1.0 mM sodium pyruvate, and 0.1 mM non-essential amino acids (GIBCO). Lentiviral constructs were packaged in combination with vesicular stomatitis virus glycoprotein (VSV-G) (Clontech, Mountain View, CA, USA) and psPax2 (for lentivirus production) using the ProFection® Mammalian Transfection System as recommended by the manufacturer (Promega, Madison, WI, USA). Lentivirus-containing supernatants were concentrated 100X using polyethylene glycol 8000 (Fisher Scientific, Lenexa, KS, USA). Derivative cells were generated by spinoculation of viral particles into cell lines, mouse BM, or primary $CD34^+$ samples, followed by FACS sorting of green fluorescent protein-positive (GFP^+) cells when indicated. Expression of *MS4A3*, *CEBPE, MECOM*, and shRNA-mediated KD were validated by qRT-PCR analysis 48-72 h following sorting or drug selection.

Colony formation assays.

Methylcellulose colony formation assays were performed by seeding CML cell lines or $CD34^+$ primary cells in 0.9% MethoCult (H4230; StemCell Technologies). 10^3 viable cells were plated in humid chambers at 37°C with 5% CO_2, and primary cells were cultured in the presence of CC100 cytokine cocktail (StemCell Technologies). Where indicated, cells were also incubated with or without 0.1 µg/mL dox and/or imatinib at the indicated concentrations in duplicates. Colony forming unit granulocyte-macrophage colonies (CFU-GM) were scored under an inverted microscope following two weeks in culture.

LTC-IC assays.

$CD34^+$ cells from CP-CML (n=3) patients were lentivirally transduced with shRNA targeting *MS4A3* (sh*MS4A3*), and resulting GFP^+ cells were sorted by FACS. Following 96 h culture ± imatinib and/or doxycycline (0.1 µg/ml), remaining $CD34^+$ cells were plated in MyeloCult (H5100; StemCell Technologies) on top of irradiated (80 Gy) M210B4 cells in LTC-IC assays as described[5-7]. After 6 weeks of culture with weekly half-medium changes, cells were trypsinized, plated into methylcellulose colony assays (H4435, StemCell Technologies), and scored after 21 days. BCR-$ABL1^+$ colonies were identified by FISH on individually plucked colonies as previously described [8]. Briefly, individual colonies were picked and resuspended in 100 µL PBS prior to cytospin and fixation, and cells were immersed in 10% pepsin for 6 minutes at 37°C prior to hybridization. To detect *BCR-ABL1*, the Vysis LSI BCR/ABL Dual Color Dual Fusion Translocation Probe (Abbott Laboratories, Abbott Park, Illinois, USA) was used according to the

manufacturer's instructions. Fluorescent signals were visualized using an Axioskop 2 mot *plus* equipped with an AxioCam microscope camera (Carl Zeiss Microscopy, LLC, Thornwood, NY, USA).

Digital PCR for BCR-ABL1 genotyping.

To detect low levels of *BCR-ABL1* transcripts in the BM, PB, and spleen of xenograft recipient mice, nanofluidic digital polymerase chain reaction was used [9]. Briefly, RNA was reverse transcribed followed by a pre-amplification step of 14 cycles. This is partitioned into three separate 765-well sections, followed by qRT-PCR using published primer pairs [9]. Copy number was calculated based on Poisson distribution.

DNA bisulfite conversion and patch PCR sequencing.

DNA bisulfite and patch PCR sequencing was performed on DNA from $CD34^+$ cells from normal donor CB or from CP-CML, or BP-CML patients (n=3 for each sample type), as described [10]. Briefly, the human *MS4A3* promoter CpG islands were analyzed between the transcription start site (TSS) and 2000 bp upstream of the TSS. These sequences were scanned for *Alu*I restriction fragments, and patch oligonucleotides were designed by sequentially including base pairs from the *Alu*I restriction sites into fragment sequences until the Tm of the patch oligo was between 62-67°C. Fragments whose patch oligos contained repetitive elements according to the RepeatMasker track were excluded. Patch oligos were then appended with the complement universal primer sequences, and resulting patch oligonucleotides were synthesized by SigmaGenosys. 149 pairs of patch oligos were ordered in a 96-well plate. Oligonucleotide sequences are listed in Supplementary Table S4. Additional sequences that were omitted due to amplification of repetitive elements are highlighted in grey. DNA bisulfite conversion (Zymo Research, Irvine, CA) was performed by the Molecular Diagnostics Section of the Biorepository and Molecular Pathology Shared Resource at Huntsman Cancer Institute (The University of Utah, Salt Lake City, UT). Resulting DNA sequences were analyzed on a HiSeq 50 Cycle Single-Read Sequencing v4 platform at the High-Throughput Genomics Shared Resource at Huntsman Cancer Institute (The University of Utah, Salt Lake City, UT).

32D-cl3 cells expressing BCR-ABL1.

32D-cl3 cells were cultured in complete RPMI1640 supplemented with 10% WEHI culture supernatant as a source of murine IL-3. To generate stable cells, parental 32D-cl3 cells were infected with retrovirus produced by standard procedures using either pMIG-BCR-ABL1-p210-

WT-IRES-EGFP, pMIG-BCR-ABL1-p210-K271R-IRES-EGFP, or the empty vector pMIG-MCS-IRES-EGFP. After infection, the cells expressing $p210^{BCR-ABL1}$, the kinase-inactive mutant ($p210^{BCR-ABL1-K271R}$) or the empty vector were sorted for EGFP using a BD FACSAria™ II flow cytometer (BD Biosciences, Franklin Lakes, NJ). Cells were only used with a few passages to avoid phenotypic drifting. To assess the effect of BCR-ABL1 on *Ms4a3* transcript levels, 1×10^6 cells/well were plated in a 12-well plate and incubated with and without imatinib (2 µM) for indicated time. Cells were pelleted and qRT-PCR was performed as described above.

ChIP-seq.

CP-CML and BP-CML samples ($CD34^+$, n=3 each, $1.2x10^6$ cells each), as well as CB samples ($CD34^+$, n=3, $0.9\text{-}1.5x10^6$ each) were thawed and immediately resuspended in 1% formaldehyde (diluted in PBS from a 37% stock, with 10-15% methanol, F8775-500ML, Sigma-Aldrich, St. Louis, MO) and incubated at room temperature for 10 minutes without shaking. Glycine was added to 125 mM to quench formaldehyde and cells were centrifuged at 2,400g for 5 minutes. The cell pellet was washed in 1 mL of cold PBS and centrifuged again. The supernatant was discarded and the cells were stored at -80°C until further processing. Chromatin immunoprecipitation was performed as previously described [11]. Cells were sonicated for 8 cycles of 30 seconds with 30 seconds of rest on an Epishear probe-in sonicator (Active Motif). An antibody against H3K27me3 (Active Motif, cat # 39155) was used for pulldown and input DNA was used as controls for each sample. Libraries were sequenced on a HiSeq 2500 as single-end 50 base pair reads. Sequence reads were aligned using Bowtie [12]. Peaks were called using MACS2 [13] and samples were excluded when less than 10,000 peaks were called. MACS2 was used to create read depth normalized bedgraphs to visualize the *MS4A3* locus on IGV [14].

Epigenetic drug library screening.

Primary $CD34^+$ cells from a CP-CML patient were used to screen an Epigenetics Screening Library (#11076, Cayman Chemicals, Ann Arbor, MI, USA). All cells were incubated in the presence of 1 µM compound or DMSO control for 72 h, followed by assessment of *MS4A3* mRNA by qRT-PCR using the *Power* SYBR Green RNA-to-C_T™ *1-Step* Kit (Thermo Fisher Scientific) according to the manufacturer's instructions. Resulting hits were confirmed with additional CML patient samples as indicated.

FACS and flow cytometry analysis.

Sorting of $CD34^+38^-$ stem cells from magnetically enriched $CD34^+$ cells was performed using FITC-anti-CD34 (#11-0341-81, eBioscience, San Diego, CA) and APC-anti-CD38 (#102712, BioLegend, San Diego, CA) antibodies. Antibody stained and GFP^+ cells were sorted by a FACSAria™ II flow cytometer. For cell cycle analysis following culture in the indicated conditions, cells were fixed in 70% ethanol, stained with propidium iodide (PI), and analyzed for DNA content. For multi-colored flow cytometry, cells were blocked with Human TruStain FcX Fc Receptor Blocking Solution (BioLegend) and then stained with manufacturer recommended concentrations of antibodies in PBS containing 0.5% BSA on ice for 30 minutes. After washing, cells were analyzed on BD FACSCanto, with corresponding single fluorophore instructed compensations. For FRET signal detection in EGFP-RFP double positive cells, cells were excited at 488 nm laser and detected by the 695/40 nm filter (RFP emission) on BD Fortessa. Data were analyzed using FlowJo V10 data analysis software (FlowJo).

Immunofluorescent (IF) staining and confocal microscopy

For HEK293, cells were cultured on poly-Lysine coated cover glass and IF staining was performed directly on the cover glass. For LAMA-84, IF staining was carried out in suspension and stained cells were pressed onto glass slides by Cytospin (1000 rpm for 2 minutes). For surface protein IF staining, cells were fixed with 2% paraformaldehyde in PBS on ice for 15 minutes. After washing with 0.5% BSA in PBS, cells were blocked with 0.5% normal serum of the secondary antibody matched species in PBS for 30 minutes. Primary antibodies and species-matching fluorescently labelled secondary antibodies were incubated with cells in 0.5% BSA in PBS for 1 hour each, with 3 washed in between. Then cell nucleus was stained with Hoechst 33342 (BD) for 5 minutes. For intracellular protein staining and total cell protein staining, cells were fixed with 2% paraformaldehyde in PBS on ice for 15 minutes. After washing with 0.5% BSA in PBS, cells were permeabilized with 0.2% saponin in PBS for 30 minutes, and washed with perm/wash buffer (0.5% BSA and 0.05% saponin in PBS). Primary antibodies and species-matching fluorescently labelled secondary antibodies were incubated with cells in perm/wash buffer for 1 hour each, with 3 washed in between. Then cell nucleus was stained with DAPI (Biolegend) for 5 minutes. All IF staining procedures were performed on ice. Stained cells on slides were mounted with VECTASHIELD® Antifade Mounting Medium (Vector Laboratories), and imaged with a Leica SP8 405-488-561-633 laser confocal microscopy system (Cell Imaging Core, University of Utah). Images are processed and analyzed using LAS X software (Leica). Pearson's coefficient values between EGFP signal and Alexa Fluor 647 conjugated secondary antibodies were calculated with MS4A3-EGFP positive cells in each field of imaging (N=20). Relative fluorescent intensity (/ Max)

of each marker was calculated by marker protein fluorescent intensity divided by the maximal intensity of each cell.

Cytokine receptor endocytosis analysis.

To assess the regulation of cytokine receptor endocytosis by MS4A3, we utilized the Ph^+ CML cell line, LAMA-84, or primary $CD34^+$ cells from CP-CML patients. Cells were transduced with indicated lentiviruses to overexpress or knockdown *MS4A3*. 48 hours later, LAMA-84 cells were selected by Puromycin (1 μg/mL) to obtain pure populations of transduced cells. After viral transduction, CML cells were cultured with or without dox (0.1 μg/mL) to induce knockdown in dox-sh*MS4A3* group for 72 hours. GFP^+ cells are positively transduced cells, while GFP^- cells serve as un-transduced internal control. To stimulate receptor endocytosis, GM-CSF (10 ng/mL) or IL-3 (40 ng/mL) were added to the cells, and cells were incubated at 37 °C for 5 – 15 minutes. After the stimulation, cells were immediately chilled on ice-water mixture to stop cellular activities, and all operations were performed at 4 °C or on ice from then on. Cells with or without cytokine stimulation were washed with ice-cold PBS (+ 0.5% BSA), and stained with CD116-APC antibody (clone REA211, Miltenyi Biotec) or CD123-BV711 antibody (clone 9F5, BD) on ice. After washing, the surface labelled receptor was analyzed by flow cytometry.

Nanoparticles.

The prototype liposomal nanoparticles used in this study were manufactured from LAMA-84 cells that naturally express CD62L and readily shed granular lipid particles from plasma membrane (unpublished data). For Nano-CD62L/MS4A3, particles were collected from the culture supernatant of LAMA-84 cells overexpressing MS4A3-EGFP. For Nano-CD62L (MS4A3-free), particles were collected from the culture supernatant of LAMA-84 cells after CRISPR-mediated MS4A3 knockout. All nanoparticles were pelleted from the supernatant by adding 10% PEG-8000 and 0.3M NaCl, resuspended in RPMI1640 to achieve 100X concentration, and then stored at -80°C in aliquots. Nanoparticles were added to $CD34^+$ cell cultures at 50 μL/mL. To facilitate initial nanoparticle uptake, 10 μg/mL polybrene was added to the cultures for 12h, and then diluted or washed off. Mock treatment is the addition of polybrene only. The standard curve coordinating FSC (flow cytometry) and particle size was generated using commercial reference microbeads of known sizes (BD). To titrate the dosage of nanoparticles for delivery into $CD34^+$ cells, Kasumi-1 ($CD34^+$ myeloblast, doubling time ~48h) cells were used as target cells.

QUANTIFICATION AND STATISTICAL ANALYSIS

Meta-analysis. Series matrix files for the McWeeney dataset (GSE14671), comparing TKI responders versus non-responders [15], and the Cramer-Morales dataset (GSE47927), comparing LSCs versus progenitor cells[16] were downloaded from the Gene Expression Omnibus (https://www.ncbi.nlm.nih.gov/geo/). The Zheng dataset (E-MEXP-480) comparing CP-CML versus BP-CML[17], Yong dataset (E-MIMR-17) comparing long versus short duration of CP-CML[18], and Graham dataset (E-MTAB-2508) comparing cycling versus quiescent CML cells[19] were downloaded from ArrayExpress (http://www.ebi.ac.uk/arrayexpress). Probe IDs were converted to gene symbols, and genes in each study having an absolute magnitude fold change ≥1.5 (for upregulated genes) and ≤-1.5 (for downregulated genes) were considered for overlapping gene detection if statistical significance (using non-parametric methods) at $p<0.05$ was observed. The genes identified as commonly up- or down-regulated compared with the McWeeney dataset were tallied and the statistical likelihood for the number of common genes observed compared to that expected by chance was determined using an exact Binomial test as previously described[20].

Kaplan-Meier Survival Curve. Correlation of *MS4A3* mRNA levels with survival in CML was established using survival data available for 35 patients from the original microarray training set[15]. All CEL files from the original study[15] were imported with Partek software (Partek, Inc.) followed by GC-RMA normalization (which included normalization of intensities to the median sample of the experiment). Expression levels were calculated from the microarray (HG-U133A, Affymetrix, Inc.) and dichotomized into high and low groups based on distribution of the data. OS was assessed with Kaplan-Meier curves generated in Prism version 6.04 (GraphPad Software, La Jolla, CA). All statistical analyses were performed in SAS version 9.3 (SAS Institute, Carey, NC), and P-values are 2-sided from a log-rank test.

***MS4A3 analysis by microarray*.** The microarray data presented here are a combination of two separate experiments from Oehler V. et al. (unpublished data) and Zheng et al.[17], which is available from ArrayExpress under accession number E-MEXP-480. In total, CML $CD34^+$ cells were analyzed for 8 CP-CML and 7 BP-CML samples by Oehler et al., and 11 CP-CML and 9 BP-CML samples by Zheng et al.[17], yielding a total of 19 CP-CML and 16 BP-CML samples. Briefly, RNA was extracted using the RNeasy Mini Kit (Qiagen, Hilden, Germany). Preparation of hybridization probes and HG-U133A microarray processing were performed according to the manufacturer's instructions (Affymetrix, Santa Clara, CA).

***Statistical analysis*.** Two-tailed *t* test (or with Welch's correction when SD is unequal) was used for experiments in Figure 1C, 1E, 2C-D, 2F-H, 3A-F, 4B-C, 4E-F, 7F-D, 8B-I. When comparing two groups, *t* test is replaced by Mann-Whitney non-parametric test if the sample values do not conform to a normal distribution. One-way ANOVA was used for experiments in Figure 1B, 7E. Fisher's exact test was used for the experiment in Figure 6E. For all assays, three independent experiments were performed unless otherwise noted.

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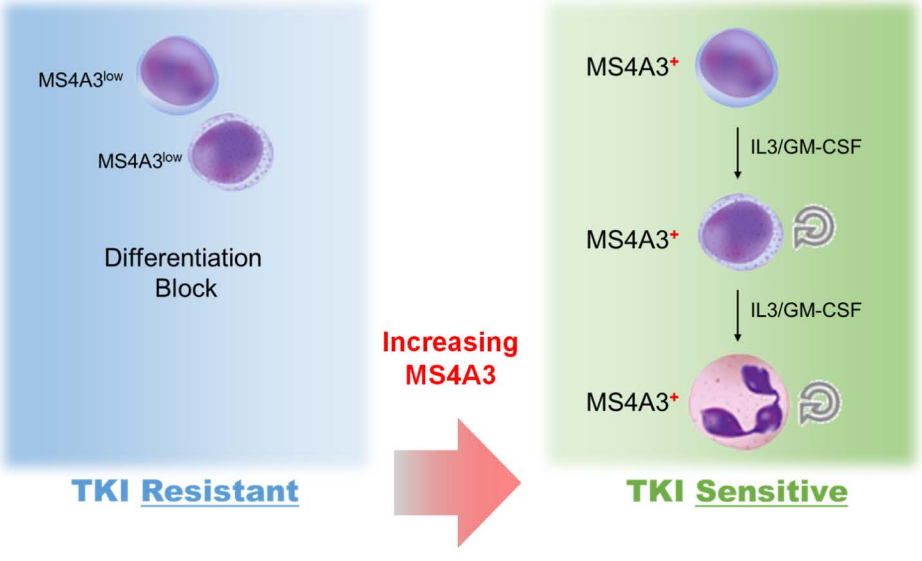
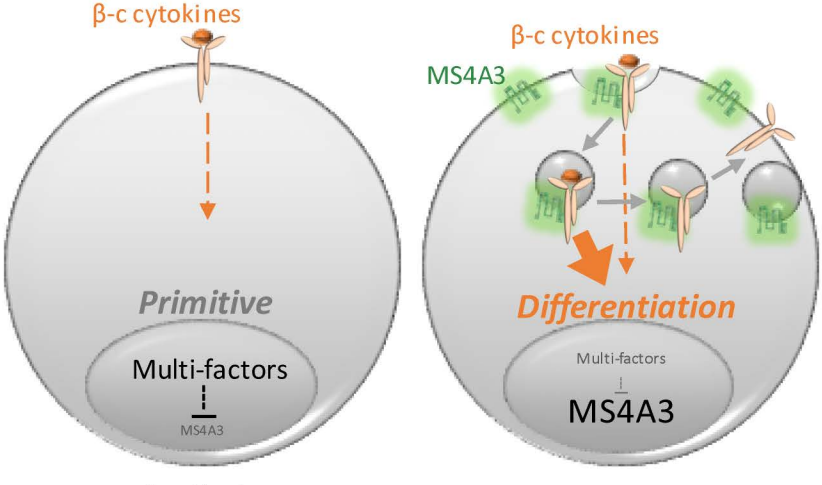
Graphic abstract



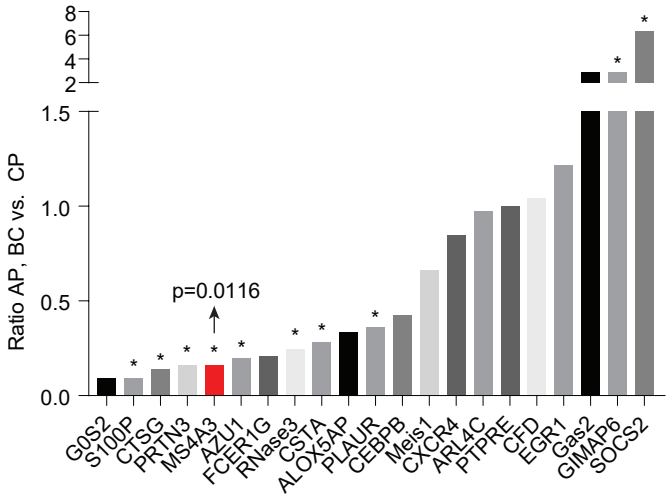


MS4A3low CML

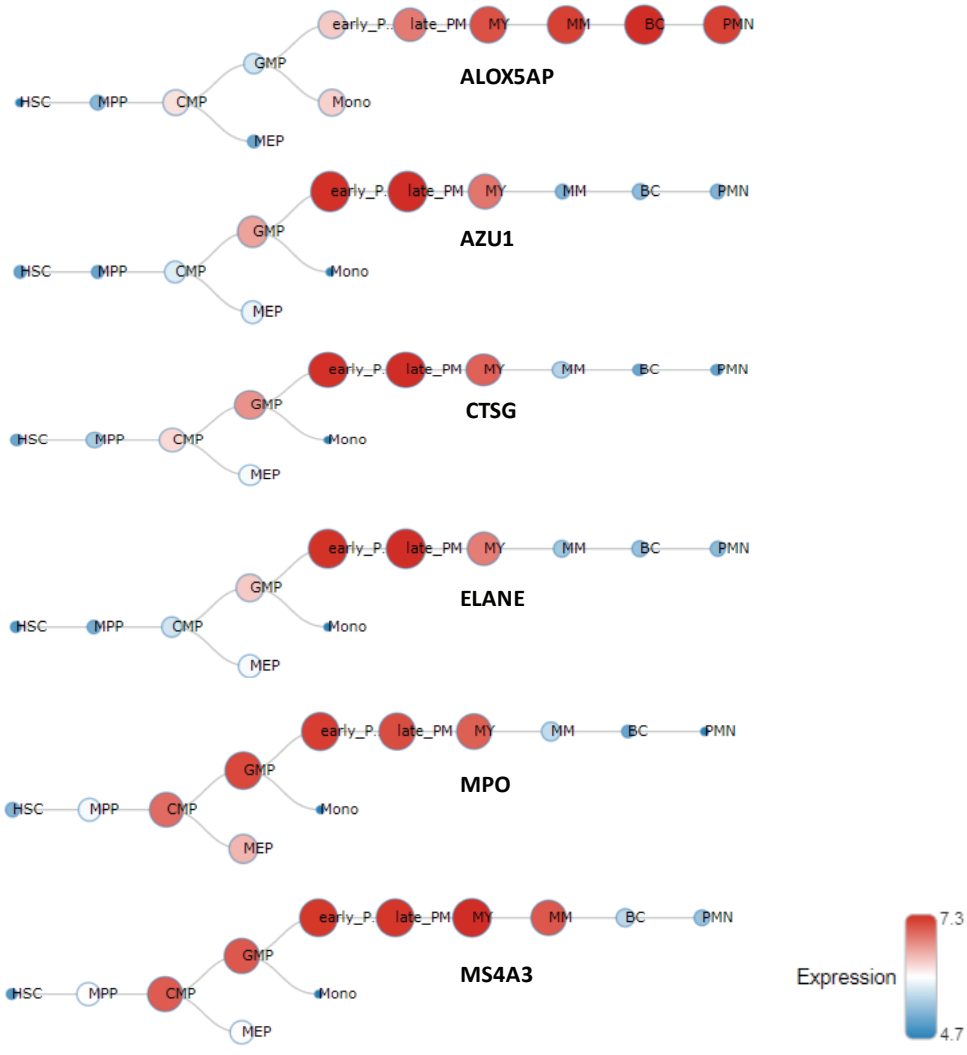
MS4A3+ CML

Multi-factors:
BCR-ABL1, MECOM, DNA methylation, EZH2/H3K27me3

Supplemental Figure 1



Supplemental Figure 2



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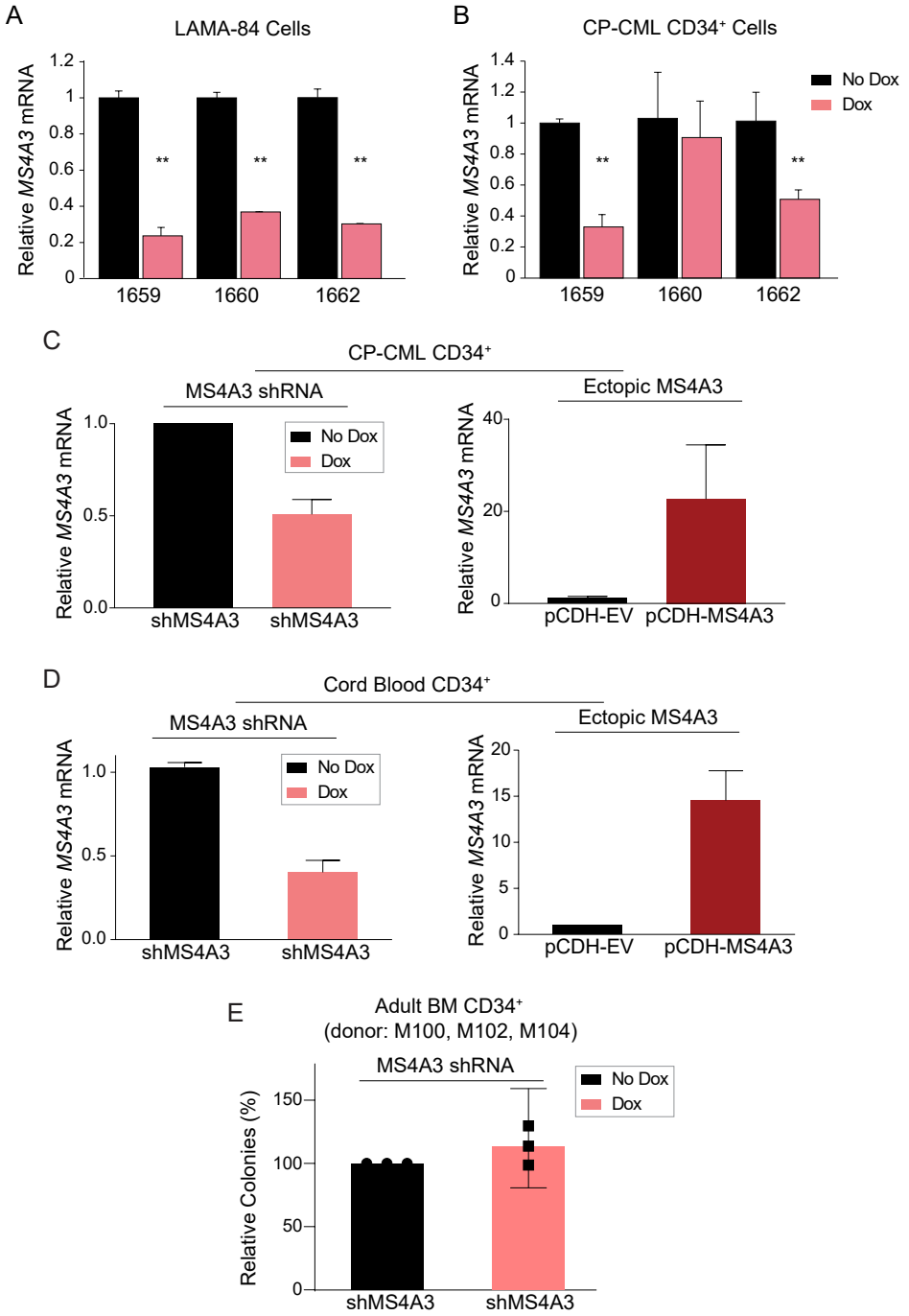


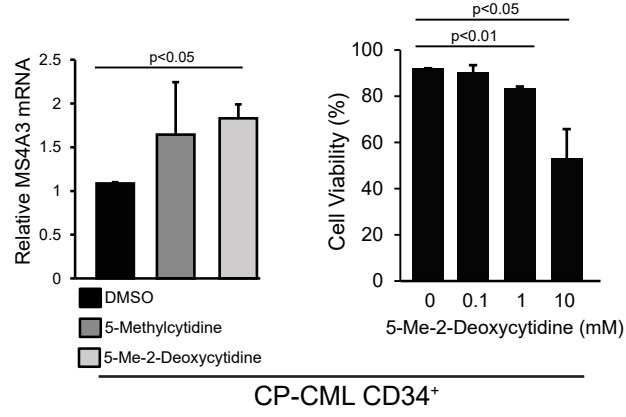
Supplemental Figure 4

A

Co-expression with *MS4A3*

Correlated Gene	Spearman's Correlation	-LOG10(q-value)
AFF2	0.695	19.640
CTSG	0.687	19.209
CEBPE	0.678	18.606
AZU1	0.662	17.384
ELANE	0.656	16.991
RNASE3	0.622	14.462
NOCT	0.620	14.427
P4HB	0.620	14.427
CILP2	0.613	14.024
HSP90B1	0.610	13.886
HAL	0.606	13.650
SERPINB10	0.597	13.088
LPO	0.592	12.780
CALR	0.591	12.740
P2RY2	0.587	12.553
RAB32	0.587	12.551
SRGN	0.586	12.551
ERLIN1	0.581	12.221
PLPPR3	0.569	11.511
SLC39A11	0.567	11.455
ATP23	0.565	11.362
RNASE2	0.563	11.243
S100P	0.562	11.194
MPO	0.556	10.863

B



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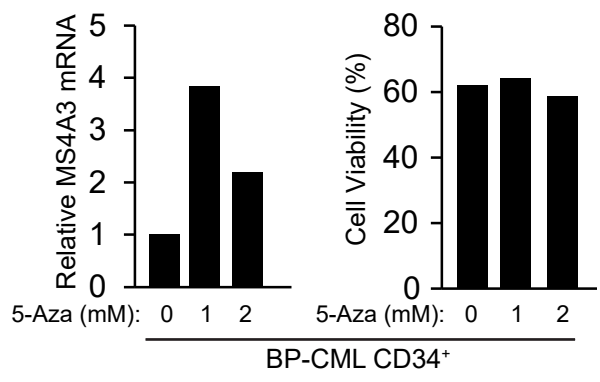

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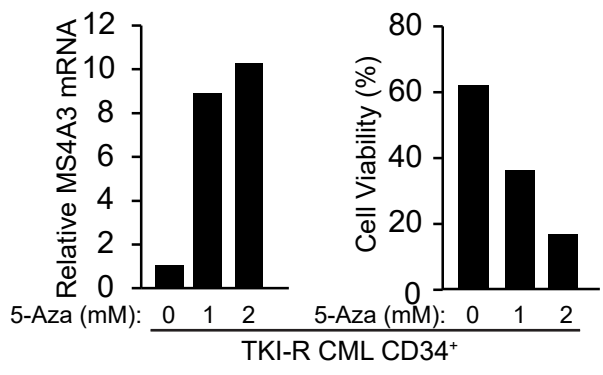
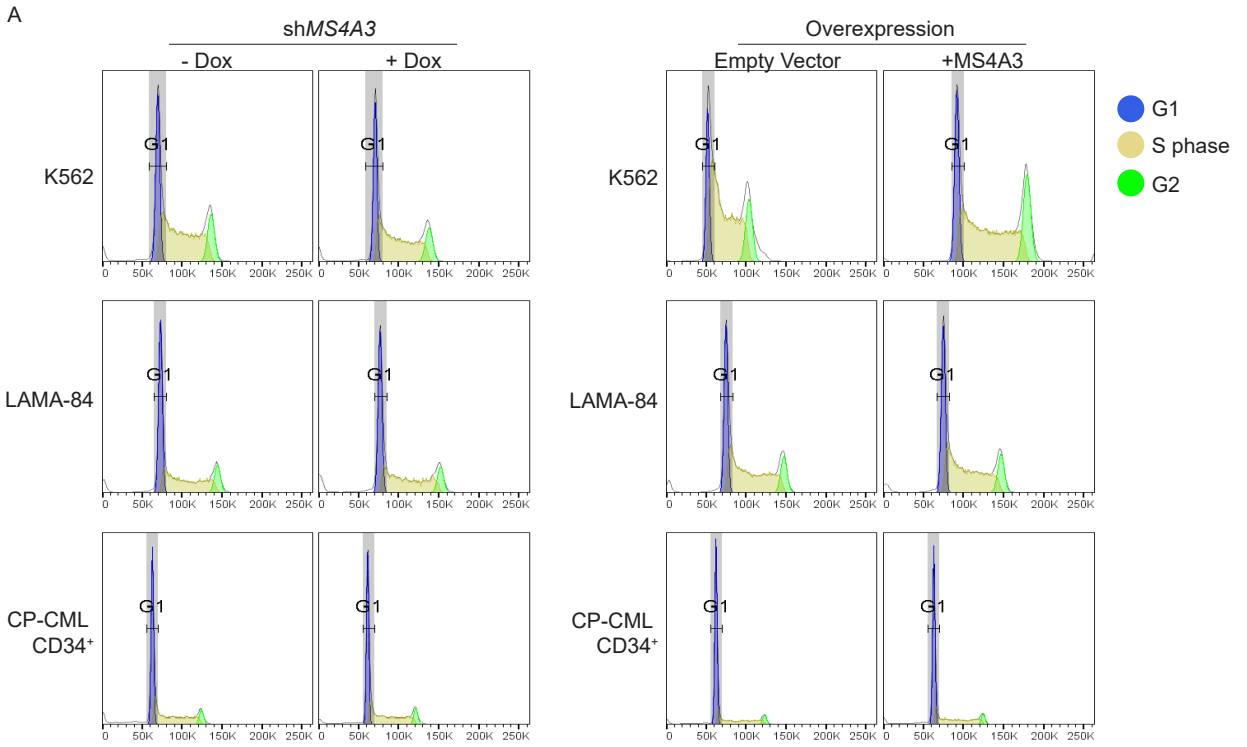
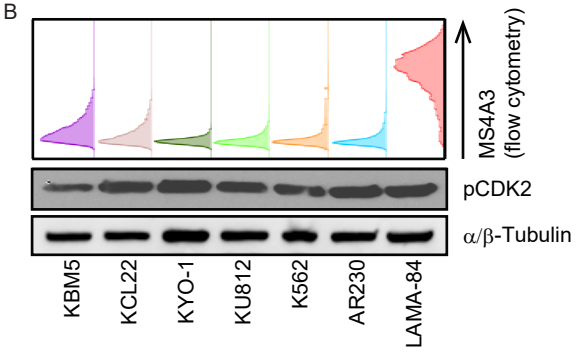
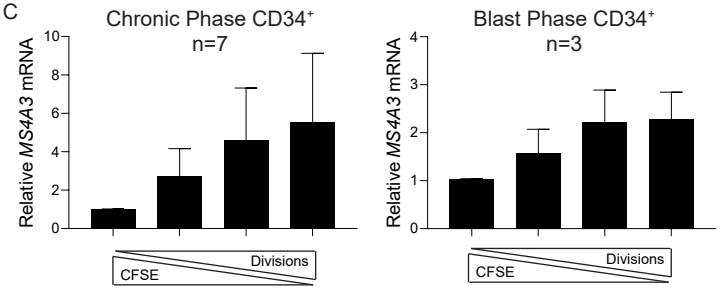


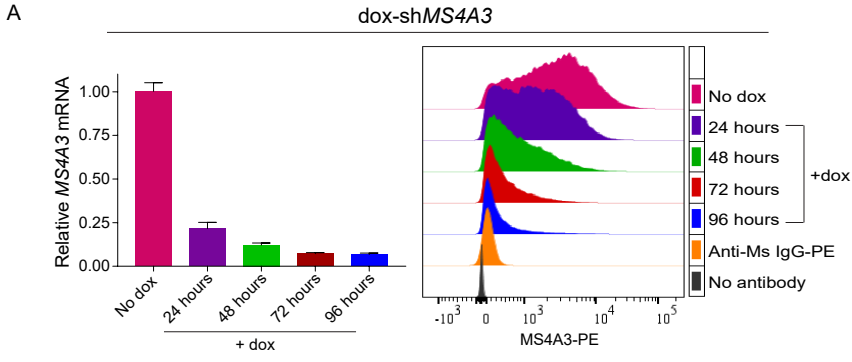
Supplemental Figure 5

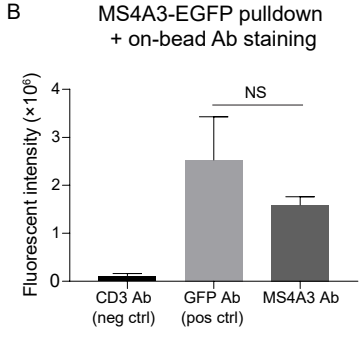


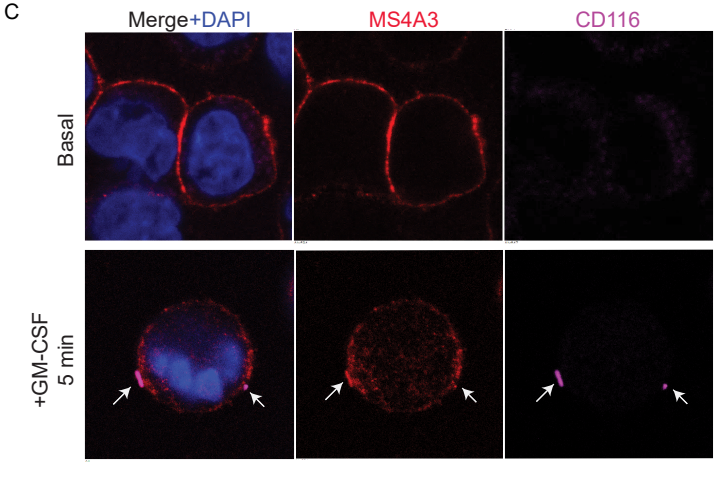




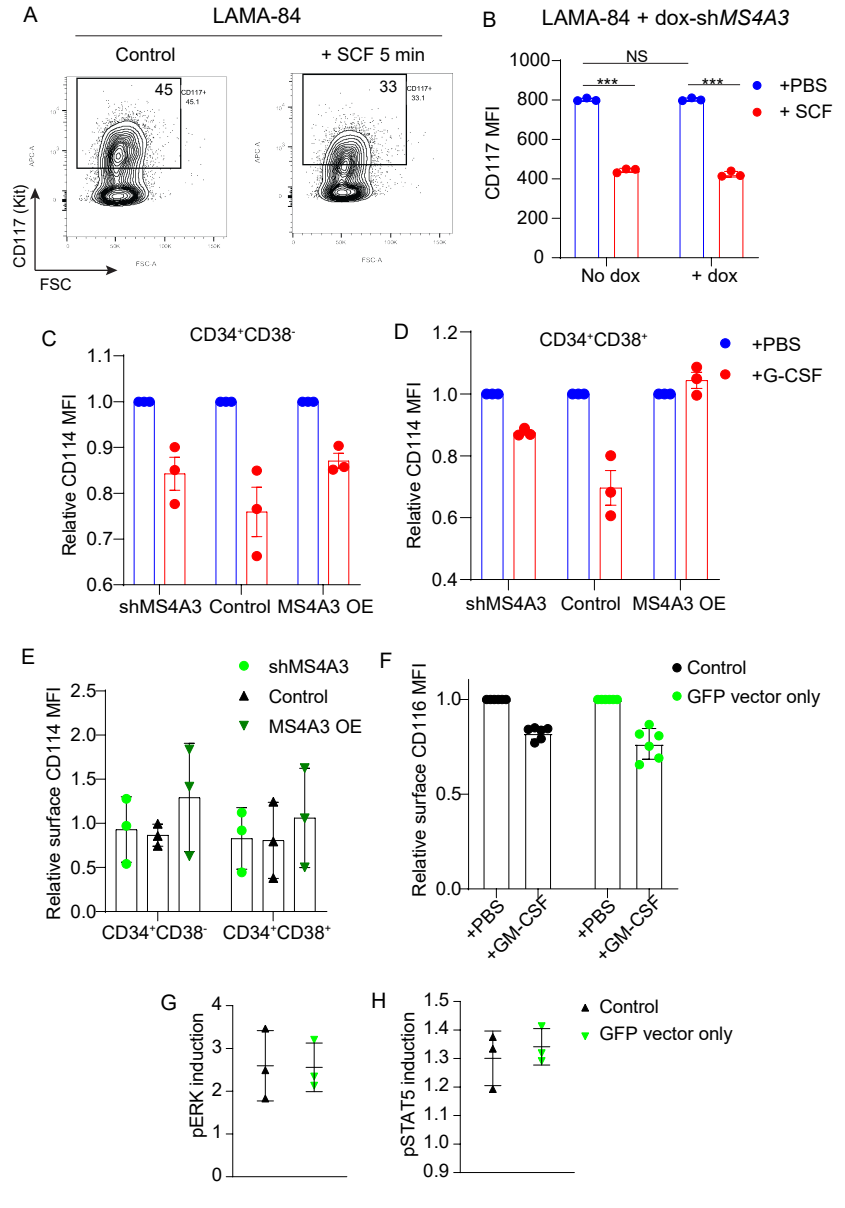
Supplemental Figure 6





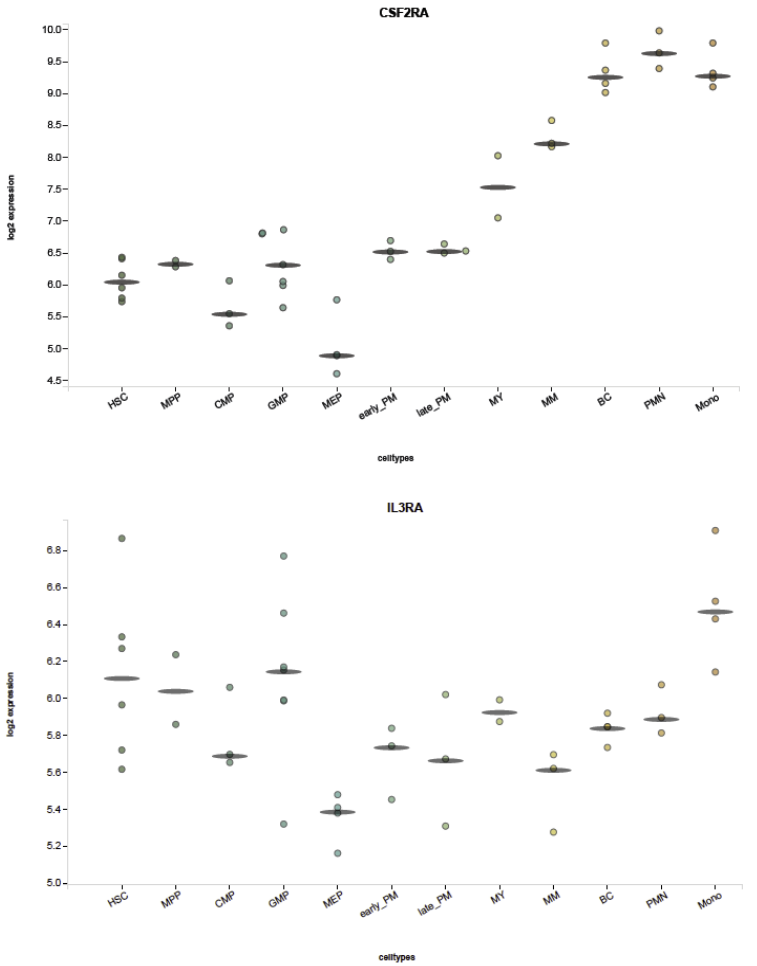


Supplemental Figure 7

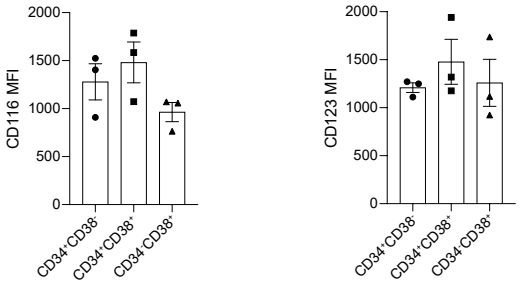


Supplemental Figure 8

A



B



Supplemental Figure 9

Supplementary Table S1. Patient sample summary

Category	Patient ID	CML Disease Phase	BCR-ABL1 Kinase Domain Mutations	Prior TKI Exposure	Type of Resistance	Assays
Newly Diagnosed	M003	CP-CML	None	None	N/A	DNA bisulfite conversion & patch PCR sequencing
	M009	CP-CML	None	None	N/A	qRT-PCR
	M010	CP-CML	None	None	N/A	qRT-PCR
	M011	CP-CML	None	None	N/A	qRT-PCR, shMS4A3, CFSE staining
	M014	CP-CML	None	None	N/A	qRT-PCR, shMS4A3, colony assays, immunoblot, LTC-IC, xenografts, CFSE staining, DNA bisulfite conversion & patch PCR sequencing
	M016	CP-CML	None	None	N/A	qRT-PCR, shMS4A3, colony assays, LTC-IC, xenografts
	M017	CP-CML	None	None	N/A	qRT-PCR, shMS4A3, colony assays
	M018	CP-CML	None	None	N/A	qRT-PCR, shMS4A3, colony assays
	M021	CP-CML	None	None	N/A	Immunoblot, shMS4A3
	M022	CP-CML	None	None	N/A	shMS4A3, colony assays
	M023	CP-CML	None	None	N/A	qRT-PCR, CFSE staining
	M024	CP-CML	None	None	N/A	qRT-PCR, shMS4A3, colony assays, DNA bisulfite conversion & patch PCR sequencing
	M025	CP-CML	None	None	N/A	qRT-PCR, immunoblot, shMS4A3, annexin V, CFSE staining
	M028	CP-CML	None	None	N/A	qRT-PCR, immunoblot, shMS4A3, colony assays, annexin V, LTC-IC, xenografts, CFSE staining, CD38 selection, DNA bisulfite conversion & patch PCR sequencing
	M029	CP-CML	None	None	N/A	Immunoblot
	M030	CP-CML	None	None	N/A	qRT-PCR
	M040	CP-CML	None	None	N/A	qRT-PCR, immunoblot, ectopic MS4A3, shMS4A3, annexin V, CD38 selection
	M041	CP-CML	None	None	N/A	qRT-PCR, immunoblot, shMS4A3
	M043	CP-CML	None	None	N/A	qRT-PCR, shMS4A3, CD38 selection
	M044	CP-CML	None	None	N/A	qRT-PCR, shMS4A3
	M045	CP-CML	None	None	N/A	Immunoblot, CD38 selection, qRT-PCR, shMS4A3
	M046	CP-CML	None	None	N/A	Immunoblot, CD38 selection, qRT-PCR
	M047	CP-CML	None	None	N/A	qRT-PCR, shMS4A3
	M051	CP-CML	None	None	N/A	Immunoblot
	M052	CP-CML	None	None	N/A	Immunoblot
	M055	CP-CML	None	None	N/A	qRT-PCR, differential sorting
	M059	CP-CML	None	None	N/A	qRT-PCR, ectopic MS4A3, CD38 selection, CFSE staining
	M060	CP-CML	None	None	N/A	qRT-PCR, differential sorting
	M066	CP-CML	None	None	N/A	qRT-PCR, CFSE staining
	M071	CP-CML	None	None	N/A	qRT-PCR, DNA bisulfite conversion & patch PCR sequencing
	M073	CP-CML	None	None	N/A	qRT-PCR, shMS4A3
	M074	CP-CML	None	None	N/A	qRT-PCR, differential sorting
	M078	CP-CML	None	None	N/A	qRT-PCR, shMS4A3
AP/BP-CML	M019	BP-CML	None		N/A	qRT-PCR, immunoblot, ectopic MS4A3, shMS4A3, annexin V, colony assays, CFSE staining
	M020	BP-CML	None		N/A	qRT-PCR, immunoblot, ectopic MS4A3, annexin V, colony assays
	M027	AP-CML	None		N/A	qRT-PCR, ectopic MS4A3, annexin V, colony assays
	M033	BP-CML	None		N/A	qRT-PCR, immunoblot, ectopic MS4A3, shMS4A3, annexin V, colony assays, CFSE staining, DNA bisulfite conversion & patch PCR sequencing
	M039	BP-CML	None		N/A	qRT-PCR, immunoblot, ectopic MS4A3, annexin V, colony assays, DNA bisulfite conversion & patch PCR sequencing
	M042	AP-CML	None		N/A	qRT-PCR, ectopic MS4A3, annexin V, DNA bisulfite conversion & patch PCR sequencing
	M049	BP-CML	None		N/A	qRT-PCR, ectopic MS4A3, annexin V, 5-aza treatment
	M050	BP-CML	None		N/A	qRT-PCR, ectopic MS4A3, annexin V, 5-aza treatment
	M065	BP-CML	None		N/A	qRT-PCR, CFSE staining, differential sorting
TKI-R CML	M001	TKI-R (CP-CML)	None	IM, NIL, DAS	Cytogenetic	qRT-PCR
	M002	TKI-R (AP-CML)	None	NIL	Cytogenetic	qRT-PCR, DNA bisulfite conversion & patch PCR sequencing
	M004	TKI-R (CP-CML)	None	IM, NIL, DAS	Cytogenetic	qRT-PCR
	M005	TKI-R (CP-CML)	E255K	IM, NIL, DAS	Cytogenetic	qRT-PCR, DNA bisulfite conversion & patch PCR sequencing
	M006	TKI-R (CP-CML)	None	IM, NIL, DAS	Cytogenetic	qRT-PCR
	M007	TKI-R (AP-CML)	None	IM, DAS	Cytogenetic	qRT-PCR, DNA bisulfite conversion & patch PCR sequencing
	M008	TKI-R	None		Cytogenetic	qRT-PCR
	M012	TKI-R	None		Cytogenetic	qRT-PCR, DNA bisulfite conversion & patch PCR sequencing
	M013	TKI-R (CP-CML)	None	NIL, DAS	Cytogenetic	qRT-PCR, DNA bisulfite conversion & patch PCR sequencing
	M015	TKI-R (CP-CML)	T315I	IM, DAS	Cytogenetic	qRT-PCR, DNA bisulfite conversion & patch PCR sequencing
Healthy Donors	M026	CB	N/A	N/A		qRT-PCR, immunoblot, ectopic MS4A3, shMS4A3, colony assays
	M031	CB	N/A	N/A		qRT-PCR, CFSE staining
	M032	CB	N/A	N/A		qRT-PCR
	M034	CB	N/A	N/A		qRT-PCR, CFSE staining

M035	CB	N/A	N/A	immunoblot
M036	CB	N/A	N/A	immunoblot
M037	CB	N/A	N/A	qRT-PCR, DNA bisulfite conversion & patch PCR sequencing
M038	CB	N/A	N/A	qRT-PCR, immunoblot, ectopic MS4A3, shMS4A3, colony assays, DNA bisulfite conversion & patch PCR sequencing
M048	CB	N/A	N/A	immunoblot
M053	FH	N/A	N/A	qRT-PCR
M054	FH	N/A	N/A	qRT-PCR, CFSE staining
M056	CB	N/A	N/A	qRT-PCR, differential sorting
M057	CB	N/A	N/A	qRT-PCR, CD38 selection
M058	CB	N/A	N/A	qRT-PCR, CD38 selection
M061	CB	N/A	N/A	qRT-PCR, differential sorting
M062	CB	N/A	N/A	qRT-PCR, immunoblot, ectopic MS4A3, colony assays, CFSE staining
M063	CB	N/A	N/A	qRT-PCR, immunoblot, CFSE staining
M067	CB	N/A	N/A	qRT-PCR, CD38 selection
M068	CB	N/A	N/A	qRT-PCR, CD38 selection
M069	CB	N/A	N/A	qRT-PCR, CD38 selection
M070	CB	N/A	N/A	qRT-PCR, DNA bisulfite conversion & patch PCR sequencing
M072	CB	N/A	N/A	qRT-PCR
M075	CB	N/A	N/A	qRT-PCR, CD38 selection
M076	CB	N/A	N/A	qRT-PCR, shMS4A3, CD38 selection
M077	CB	N/A	N/A	qRT-PCR, CD38 selection

Supplementary Table S2. Primer sequences

Gene	Forward Primer	Reverse Primer
	Human	
BCR-ABL1	GGT ACC AGG AGT GTT TCT CCA	GAG CGT GCA GAG TGG AGG GA
CEBPB	GACAAGCACAGCGACGAGTA	AGCTGCTCCACCTTCTTCTG
CEBPE	GCAAGAAGGCAGTGAACAAAG	CTCTGCCATGTACTCCAGCA
CSTA	ATACCTGGAGGCTTATCTG	CCAGTAAGTACCAAGTCCTCATT
CTSG	CCTGCTGTGTAACAATGTGG	AAGGCTCTGGCAACACTGTG
CXCR4	GGTGGTCTATGTTGGCGTCT	TGGAGTGTGACAGCTTGGAG
EGR1	GGGAGAGGCAGGAAAGACATAA	TCTGAGATCTTCCATCTGACCTAAGA
G0S2	CGTGCCACTAAGGTCATTCC	GCACGTACAGCTTCACCATC
GAS2	GAAGGTTTGGTCCTCCACAA	GAAGGAGAAGGGGCAGAAAG
GUS	GAAAATATGTGGTTGGAGAGCTCATT	CCGAGTGAAGATCCCCTTTTTA
MECOM	ACCAGCCCCTGGATCTAAGT	TTCGACGTTGCTTCCTTTTT
MS4A3	AGCAGGGATAAAACCCACAA	AATTGCATAGGTCCGGTGAC
PLAUR	GACCCTGAGCTATCGGACTG	CATCCAGGCACTGTTCTTCA
PRTN3	ACGCGGAGAACAAACTGAAC	GGGACGAAAGTGCAAATGTT
PTPRE	AGCACCAGCGACAAGAAGAT	ATGTGTCCAGATGGCAATGA
RNase3	AGGTGAACTGGAACCACAGG	AGATTCCGGGTGCCTTTACT
	Mouse	
Ms4a3	TGCTGAGGAATTGCACAAAG	ACCAGTCTCCTCTGGCTTCA
Gapdh	GGCATTGCTCTCAATGACAA	TGTGAGGGAGATGCTCAGTG

Supplementary Table S3. Antibodies

Protein	Source	Catalog #
	Immunoblot	
Rabbit anti-MS4A3	Aviva Systems Biology	ARP62012-P050
Rabbit anti-α/β-tubulin	Cell Signaling Technology	2148
Rabbit anti-pCDK2 (Thr160)	Cell Signaling Technology	2561S
	Immunofluorescent staining	
Rabbit anti-Rab4	Invitrogen	PA3-912
Rabbit anti-Rab5	Cell Signaling Technology	3547
Rabbit anti-Rab7	Cell Signaling Technology	9367
Rabbit anti-Rab11	Cell Signaling Technology	5589
Rabbit anti-LAMP1	Cell Signaling Technology	9091
Rabbit anti-LC3B	Cell Signaling Technology	3868
Rabbit anti-Clathrin	Cell Signaling Technology	4796
Rabbit anti-Caveolin	Cell Signaling Technology	3267
Rabbit anti-58K Golgi protein	Invitrogen	PA5-83166
Rabbit anti-alpha tubulin	Cell Signaling Technology	2125
Alexa Fluor™ 594 Phalloidin	Invitrogen	A12381
Goat anti-Rabbit IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor 647	Invitrogen	A-21245
	Flow Cytometry	
APC anti-human CD45	BioLegend	368512
FITC anti-human CD34	eBioscience	11-0341-81
APC anti-human CD38	BioLegend	102712
BV421 anti-human CD117	BD Biosciences	562435
APC anti-human CD11b	eBioscience	17-0112-82
	ChIP	
Rabbit anti-Histone H3K27me3	Active Motif	39155

Supplementary Table S4. Patch Oligonucleotide Sequences

Patch_L1

Well Position	Name	Sequence
A1	chr1:151958613-151958784	ggctacttaacaaaggaggacctgaACTCCCCACCTTCCTCATTCTCT
A2	chr1:151962717-151962873	acatatttttccttttgcgtatggaatgtgACTCCCCACCTTCCTCATTCTCT
A3	chr1:151966081-151966153	gtggggaatccgctgctcaACTCCCCACCTTCCTCATTCTCT
A4	chr1:151966154-151966313	tgcccggggaaaaccctgACTCCCCACCTTCCTCATTCTCT
A5	chr1:151966314-151966577	cacccgccgcacgtactaaACTCCCCACCTTCCTCATTCTCT
A6	chr1:153329674-153329767	ggcaattctgatgataccttcctcttgACTCCCCACCTTCCTCATTCTCT
A7	chr1:153329926-153330006	ccttttagtccaacaaggatggtctgaACTCCCCACCTTCCTCATTCTCT
A8	chr1:153330088-153330317	tggttgtttagttcatttcccttctatcctaaACTCCCCACCTTCCTCATTCTCT
A9	chr1:153330318-153330500	acagagtgtttgccagagctgtgACTCCCCACCTTCCTCATTCTCT
A10	chr1:153330768-153330894	gcgttccagctgcgacattttgACTCCCCACCTTCCTCATTCTCT
A11	chr1:153348337-153348415	cctgggccctggctcaACTCCCCACCTTCCTCATTCTCT
A12	chr1:153362881-153363077	aattgctagagaccgagtgtcctcaACTCCCCACCTTCCTCATTCTCT
B1	chr1:153363139-153363248	tgctggtttggttatttggagagtgACTCCCCACCTTCCTCATTCTCT
B2	chr1:153363438-153363550	gaagtggagcagccttcctgaACTCCCCACCTTCCTCATTCTCT
B3	chr1:153363557-153363691	cgctataaaaaggagctgcctctcaACTCCCCACCTTCCTCATTCTCT
B4	chr1:161184287-161184369	ggagacgagcaggaaaaattgctaaACTCCCCACCTTCCTCATTCTCT
B5	chr1:161184396-161184474	gtttaccaagttatgtgggcactgaACTCCCCACCTTCCTCATTCTCT
B6	chr1:161184475-161184585	ctgcccgtcaacattccctcaACTCCCCACCTTCCTCATTCTCT
B7	chr1:161184586-161184671	gctggtcttgaactcctgatctcaACTCCCCACCTTCCTCATTCTCT
B8	chr1:161184987-161185063	ggccccttcccctttcctgACTCCCCACCTTCCTCATTCTCT
B9	chr1:161185076-161185223	gccgttctgacagcactgtgACTCCCCACCTTCCTCATTCTCT
B10	chr1:161186799-161186880	cgaaaccaaggctcggaaaagctaaACTCCCCACCTTCCTCATTCTCT
B11	chr1:161188811-161188906	gccagctggtgttaatggcatgACTCCCCACCTTCCTCATTCTCT
B12	chr1:186642099-186642206	actctgcctatattttcttacctgaacttttgACTCCCCACCTTCCTCATTCTCT
C1	chr1:186650355-186650456	gctcacattaactatttacagggtaactgcttaACTCCCCACCTTCCTCATTCTCT
C2	chr1:209847625-209847712	ttagctgtaatcacctggggctgaACTCCCCACCTTCCTCATTCTCT
C3	chr1:209848398-209848506	cttcttactggtgtcagcgggtgACTCCCCACCTTCCTCATTCTCT
C4	chr1:209848507-209848581	cgtgggaaggccagtgtgACTCCCCACCTTCCTCATTCTCT
C5	chr1:209848582-209848716	gtggccacgcgctgaACTCCCCACCTTCCTCATTCTCT
C6	chr1:209848717-209848789	ggggccgcttatatcttttctctgaACTCCCCACCTTCCTCATTCTCT
C7	chr1:209848891-209848994	gctcatagaaaggcggactaccttaACTCCCCACCTTCCTCATTCTCT
C8	chr2:64677694-64677801	ccgtggtactatggagataggtgaaaatgACTCCCCACCTTCCTCATTCTCT
C9	chr2:64680293-64680366	gtggcccaggctggagtgACTCCCCACCTTCCTCATTCTCT
C10	chr2:64683514-64683698	cctctccccagatatacaagaatttctgaACTCCCCACCTTCCTCATTCTCT
C11	chr2:64685929-64686047	ggttgtgctacacaattccactttagtgACTCCCCACCTTCCTCATTCTCT
C12	chr2:113587642-113587785	aaaccacggccacatttggttctaaACTCCCCACCTTCCTCATTCTCT
D1	chr2:113593790-113593883	cagccatggcagaagtacctgaACTCCCCACCTTCCTCATTCTCT
D2	chr2:113594250-113594412	tgactttaatcttccttacaactaggtgctaaACTCCCCACCTTCCTCATTCTCT
D3	chr2:113594413-113594489	tgaaatcaggtattcaacagagaaatttctcaACTCCCCACCTTCCTCATTCTCT
D4	chr2:113594618-113594718	gaaaatccagtattttaatgtggacatcaactgACTCCCCACCTTCCTCATTCTCT
D5	chr2:136872117-136872217	gctagaaatgatccccagctgtttatgACTCCCCACCTTCCTCATTCTCT
D6	chr2:136873290-136873443	ggtcatgggttaccagaagaaactgaACTCCCCACCTTCCTCATTCTCT
D7	chr2:136873749-136873819	ccaagatgtgactttgaaaccctcaACTCCCCACCTTCCTCATTCTCT
D8	chr2:136874486-136874584	cccagcggagcccctgACTCCCCACCTTCCTCATTCTCT
D9	chr2:136874585-136874693	ttgctagggagtttttggtttcctgACTCCCCACCTTCCTCATTCTCT
D10	chr3:122044160-122044233	tggcgggtttggcctcaACTCCCCACCTTCCTCATTCTCT
D11	chr3:122058093-122058177	ctgcgaagtagattattaccctcattgtgACTCCCCACCTTCCTCATTCTCT
D12	chr4:6695222-6695366	tgctgacacgaggagacatctgaACTCCCCACCTTCCTCATTCTCT

E1	chr4:6695367-6695479	gtctcggcgccatcactgaACTCCCCACCTTCCTCATTCTCT
E2	chr4:6698030-6698255	gcatggagcaagcaccctgaACTCCCCACCTTCCTCATTCTCT
E3	chr4:90815871-90815966	gctgaagggtctctgacaaagctaaACTCCCCACCTTCCTCATTCTCT
E4	chr4:90816031-90816118	gctgcttccacactgaatctgctaaACTCCCCACCTTCCTCATTCTCT
E5	chr4:90816279-90816377	gacccgagtggttggcagtatttgACTCCCCACCTTCCTCATTCTCT
E6	chr4:90823160-90823235	tgtcaggctttcccagcgtgACTCCCCACCTTCCTCATTCTCT
E7	chr4:90836562-90836635	gctgatccctcaatatcaagtgaaaacttgACTCCCCACCTTCCTCATTCTCT
E8	chr4:156549424-156549498	ctttctgactggcccctcttcttgACTCCCCACCTTCCTCATTCTCT
E9	chr4:156585604-156585709	tgaatctttctaaattcagggatttttagaacctgACTCCCCACCTTCCTCATTCTCT
E10	chr4:156587988-156588084	cgcaggaaaagtgtaggaaaactctgACTCCCCACCTTCCTCATTCTCT
E11	chr4:156588085-156588219	cccggctggggtctctaaACTCCCCACCTTCCTCATTCTCT
E12	chr4:156588586-156588666	gacccgcgtggggatgACTCCCCACCTTCCTCATTCTCT
F1	chr4:156589214-156589300	acgaaaacagaaatgggactgctaaACTCCCCACCTTCCTCATTCTCT
F2	chr4:156589354-156589437	agcctgaaatcacatgaccacattgACTCCCCACCTTCCTCATTCTCT
F3	chr5:88017774-88017907	catatttaattaaataaataaataatctgggtctgACTCCCCACCTTCCTCATTCTCT
F4	chr5:88017908-88018019	catcccaagaatgctcacaaacctgACTCCCCACCTTCCTCATTCTCT
F5	chr5:88018385-88018459	tcagattattacttactagttttttttttttttcttgACTCCCCACCTTCCTCATTCTCT
F6	chr5:88018460-88018715	ggacgaaagggaaagtccctcaACTCCCCACCTTCCTCATTCTCT
F7	chr6:130686016-130686122	gggtgggggagagccatgACTCCCCACCTTCCTCATTCTCT
F8	chr6:130686123-130686195	gtgatagaaggcaagtatgatattctggtgACTCCCCACCTTCCTCATTCTCT
F9	chr6:130690524-130690712	aaccttatgtctctctcctgtttactcaACTCCCCACCTTCCTCATTCTCT
F10	chr6:130747455-130747602	gtcctgtttcatcttttgcgtgctgACTCCCCACCTTCCTCATTCTCT
F11	chr6:130757713-130757869	tctagaatgagtgaatctacaggctctgACTCCCCACCTTCCTCATTCTCT
F12	chr6:130758118-130758262	atggggatgctaacggcagttgACTCCCCACCTTCCTCATTCTCT
G1	chr6:132987332-132987408	ggtcttgttcatggtattcaaaacactgaACTCCCCACCTTCCTCATTCTCT
G2	chr6:132987409-132987478	ggcaagacaaagtcatctgaatttgattgACTCCCCACCTTCCTCATTCTCT
G3	chr6:132987492-132987573	ggaggaaggtaatctaaaaaagagtccctgACTCCCCACCTTCCTCATTCTCT
G4	chr6:133003614-133003784	agaggaaggacaactctttacaagctaaACTCCCCACCTTCCTCATTCTCT
G5	chr6:133004825-133004937	agagacaggagatgacagatgctcaACTCCCCACCTTCCTCATTCTCT
G6	chr6:133035164-133035249	tcattggacttcagcatgactactcaACTCCCCACCTTCCTCATTCTCT
G7	chr6:133035250-133035333	gttttcttaattaacttccgtagtttaaggtactaaACTCCCCACCTTCCTCATTCTCT
G8	chr6:133035334-133035444	acatagagttcttgagttaatcttcacaaattactgACTCCCCACCTTCCTCATTCTCT
G9	chr7:150211739-150211909	tttcgcttcaggttatagtgatggatgACTCCCCACCTTCCTCATTCTCT
G10	chr7:150323041-150323184	cgatcaatttcccattgaactgaacatgACTCCCCACCTTCCTCATTCTCT
G11	chr7:150328732-150328802	agggaggtgccttgcgtgACTCCCCACCTTCCTCATTCTCT
G12	chr8:30209251-30209362	ccaggctgatctcaaactcctgaACTCCCCACCTTCCTCATTCTCT
H1	chr8:30209363-30209450	gcaggaagtttctcgacacctcaACTCCCCACCTTCCTCATTCTCT
H2	chr8:30209451-30209538	cggggcaagaaaataagtaatttttttttctctgACTCCCCACCTTCCTCATTCTCT
H3	chr8:30209539-30209649	gctgaccagcctggatgtgACTCCCCACCTTCCTCATTCTCT
H4	chr8:30210276-30210522	gggaccatgttaactgccaacttgACTCCCCACCTTCCTCATTCTCT
H5	chr8:30262205-30262359	cccgggaggtggaggttgACTCCCCACCTTCCTCATTCTCT
H6	chr8:30264605-30264707	acgtgactgctattcaggagactgaACTCCCCACCTTCCTCATTCTCT
H7	chr8:30272512-30272647	acaaaggacaccatccatgggaatgACTCCCCACCTTCCTCATTCTCT
H8	chr8:30279880-30279964	ccccagcactttgaaaggctgaACTCCCCACCTTCCTCATTCTCT
H9	chr8:30279965-30280034	ctgggtaacatagcaagacctctattactaaACTCCCCACCTTCCTCATTCTCT
H10	chr8:48648672-48648902	gcaaatatccgactgactgctccttaACTCCCCACCTTCCTCATTCTCT
H11	chr8:48649023-48649130	cgggactttgctttcactttcctcaACTCCCCACCTTCCTCATTCTCT
H12	chr8:48649131-48649216	gggggcccctgctgaACTCCCCACCTTCCTCATTCTCT

Patch_L2

Well Position	Name	Sequence
A1	chr8:48649309-48649539	gcaggcccgagctactcaACTCCCCACCTTCCTCATTCTCT
A2	chr8:48649623-48649763	agctttttctacatcttactcctgttgatgACTCCCCACCTTCCTCATTCTCT
A3	chr11:59822619-59822847	ggcccagttgccagaaaatttctgACTCCCCACCTTCCTCATTCTCT
A4	chr11:59824073-59824143	ccacagacttaacgttatctttgccttatgACTCCCCACCTTCCTCATTCTCT
A5	chr11:59824144-59824297	cttgtcgcaagtaggagacactcaACTCCCCACCTTCCTCATTCTCT
A6	chr12:69743601-69743702	ccgtgctcccatccctcaACTCCCCACCTTCCTCATTCTCT
A7	chr13:31256700-31256846	cttgaagatcccctcaaaggtctcaACTCCCCACCTTCCTCATTCTCT
A8	chr13:31264669-31264779	cttttcccctctgctccctcaACTCCCCACCTTCCTCATTCTCT
A9	chr13:31305958-31306085	cagaatccggagccgctgaACTCCCCACCTTCCTCATTCTCT
A10	chr13:31306157-31306256	cgcgcacattaagattctggctgACTCCCCACCTTCCTCATTCTCT
A11	chr13:31308427-31308520	caatgccctcggttcagctgaACTCCCCACCTTCCTCATTCTCT
A12	chr13:31308521-31308612	ggcagcagggagggctgACTCCCCACCTTCCTCATTCTCT
B1	chr14:25042640-25042723	acaaatttatttctcacaggtctagaggctaaACTCCCCACCTTCCTCATTCTCT
B2	chr14:25043403-25043546	ggagagaggggcccgtgACTCCCCACCTTCCTCATTCTCT
B3	chr14:25043773-25043883	ggagggcatgggatgtgtactgACTCCCCACCTTCCTCATTCTCT
B4	chr14:25044917-25045008	gcaaagcattctcctcaatacctgaACTCCCCACCTTCCTCATTCTCT
B5	chr14:25045492-25045582	ccacccctttccttcctctctcaACTCCCCACCTTCCTCATTCTCT
B6	chr14:25045583-25045665	cagtttgtgggcaaacttcctgaACTCCCCACCTTCCTCATTCTCT
B7	chr14:94854933-94855052	gacagggccctgtctcctcaACTCCCCACCTTCCTCATTCTCT
B8	chr14:94855161-94855233	cacaggacgctgtggtttctgaACTCCCCACCTTCCTCATTCTCT
B9	chr17:53340951-53341040	ggcaaaagggtaaggcaacattctaaACTCCCCACCTTCCTCATTCTCT
B10	chr17:53341041-53341201	gcaagtgcctttctgccctgaACTCCCCACCTTCCTCATTCTCT
B11	chr17:53341202-53341275	cctttgtgaccccaggctgaACTCCCCACCTTCCTCATTCTCT
B12	chr17:53341569-53341721	gcgcttgggtcaagttattaggtttgACTCCCCACCTTCCTCATTCTCT
C1	chr17:53341848-53342046	ggccccggccaagcttaACTCCCCACCTTCCTCATTCTCT
C2	chr17:53342047-53342128	catagttttcaagctgggaataacctgaACTCCCCACCTTCCTCATTCTCT
C3	chr17:53342679-53342771	agaaaaaaattacttatatctttataaatacatctgACTCCCCACCTTCCTCATTCTCT
C4	chr17:53342910-53343164	gttctccagcagggacctgaACTCCCCACCTTCCTCATTCTCT
C5	chr17:53345556-53345685	ggagcagaagaaggtacctctcttaACTCCCCACCTTCCTCATTCTCT
C6	chr17:56345755-56345894	gtttttgagcacttctaatgtgctgtgACTCCCCACCTTCCTCATTCTCT
C7	chr17:56349058-56349181	ggcccactcctcgcctgACTCCCCACCTTCCTCATTCTCT
C8	chr17:56352856-56353022	cgggatccagatgtgtccctgACTCCCCACCTTCCTCATTCTCT
C9	chr17:56354467-56354732	accagacattttccagtgttttttttttttctaaACTCCCCACCTTCCTCATTCTCT
C10	chr17:56355246-56355465	ctgctgccctttgacaacctgACTCCCCACCTTCCTCATTCTCT
C11	chr17:56356893-56357035	gcaccatcaccgggatgtgACTCCCCACCTTCCTCATTCTCT
C12	chr18:61553980-61554107	cgtgttaagtgcccctttgtccttaACTCCCCACCTTCCTCATTCTCT
D1	chr18:61557698-61557783	gctgtatgttttgctttcatcatagcttgACTCCCCACCTTCCTCATTCTCT
D2	chr19:826530-826639	cgaaatgtccagaacaagcaaatctgACTCCCCACCTTCCTCATTCTCT
D3	chr19:827348-827467	ttgttgcccaggctggagtgACTCCCCACCTTCCTCATTCTCT
D4	chr19:827468-827539	gcaccgggggctcaACTCCCCACCTTCCTCATTCTCT
D5	chr19:827570-827660	cagcacatggcgggcatgACTCCCCACCTTCCTCATTCTCT
D6	chr19:827673-827749	ctgggctccccctacattctgACTCCCCACCTTCCTCATTCTCT
D7	chr19:827750-827824	cagggacagccccactcaACTCCCCACCTTCCTCATTCTCT
D8	chr19:827825-827967	ggggcaggtctgtggctaaACTCCCCACCTTCCTCATTCTCT
D9	chr19:839649-839771	ctcctggcagggccctgACTCCCCACCTTCCTCATTCTCT
D10	chr19:840607-840754	gacgtagcaggggacaggatgACTCCCCACCTTCCTCATTCTCT
D11	chr19:840755-840992	caacatggccacagccctcaACTCCCCACCTTCCTCATTCTCT
D12	chr19:840993-841063	catggtggggtccagggtgACTCCCCACCTTCCTCATTCTCT

E1	chr19:841064-841176	gtggctcactcaccgctcaACTCCCCACCTTCCTCATTCTCT
E2	chr19:44152949-44153103	ctacagacttgctgtgtgacctcaACTCCCCACCTTCCTCATTCTCT
E3	chr19:44159620-44159775	acaccttccacttcctgaaatgctgACTCCCCACCTTCCTCATTCTCT
E4	chr19:44173928-44174036	gtcgcccaggctggagtgACTCCCCACCTTCCTCATTCTCT
E5	chr20:48805984-48806131	cctctgctgggtaggctcaACTCCCCACCTTCCTCATTCTCT

Patch_R1

Well Position	Name	Sequence
A1	chr1:151958613-151958784	AACACCAACTACCCTCCCACACTcataaagtctgccaaaaaaagttaatgtagac
A2	chr1:151962717-151962873	AACACCAACTACCCTCCCACACTgcagtgagatagcagcactagaaa
A3	chr1:151966081-151966153	AACACCAACTACCCTCCCACACTcacccggcttcgcg
A4	chr1:151966154-151966313	AACACCAACTACCCTCCCACACTggaaggcgcacagcc
A5	chr1:151966314-151966577	AACACCAACTACCCTCCCACACTgggtggggatgccctg
A6	chr1:153329674-153329767	AACACCAACTACCCTCCCACACTgcaaggtcacatagctggttg
A7	chr1:153329926-153330006	AACACCAACTACCCTCCCACACTggacctatgggggcctga
A8	chr1:153330088-153330317	AACACCAACTACCCTCCCACACTcaggctcggcatttataggcag
A9	chr1:153330318-153330500	AACACCAACTACCCTCCCACACTgaaaatgtgaaagaagctttaaagtaggc
A10	chr1:153330768-153330894	AACACCAACTACCCTCCCACACTcagatcttttcgcaccagctcttt
A11	chr1:153348337-153348415	AACACCAACTACCCTCCCACACTggctgtaaagtttgttctcctagtct
A12	chr1:153362881-153363077	AACACCAACTACCCTCCCACACTcaaattccctgccatgggattcc
B1	chr1:153363139-153363248	AACACCAACTACCCTCCCACACTcacatgtctctgtgtgaatggacc
B2	chr1:153363438-153363550	AACACCAACTACCCTCCCACACTcatgtctcttgtcagctgtctttc
B3	chr1:153363557-153363691	AACACCAACTACCCTCCCACACTcacagtgattgccacattcacct
B4	chr1:161184287-161184369	AACACCAACTACCCTCCCACACTggcgaaagaggaaatggggaatag
B5	chr1:161184396-161184474	AACACCAACTACCCTCCCACACTgaccccactatagccctttcc
B6	chr1:161184475-161184585	AACACCAACTACCCTCCCACACTggtgatccatccgcctcg
B7	chr1:161184586-161184671	AACACCAACTACCCTCCCACACTcaccaccacgcccg
B8	chr1:161184987-161185063	AACACCAACTACCCTCCCACACTgcgagcagttccctgacc
B9	chr1:161185076-161185223	AACACCAACTACCCTCCCACACTgacccaagctctggacttcc
B10	chr1:161186799-161186880	AACACCAACTACCCTCCCACACTcacaaatcttaaaactaccctgtgagg
B11	chr1:161188811-161188906	AACACCAACTACCCTCCCACACTgcattagtctttaacagggaggagg
B12	chr1:186642099-186642206	AACACCAACTACCCTCCCACACTgagacacagtcttctcatcacttcg
C1	chr1:186650355-186650456	AACACCAACTACCCTCCCACACTcaaattctggccatcgccg
C2	chr1:209847625-209847712	AACACCAACTACCCTCCCACACTggtaagaatccagagtgtgagtactc
C3	chr1:209848398-209848506	AACACCAACTACCCTCCCACACTcacgcgaaggtcccactc
C4	chr1:209848507-209848581	AACACCAACTACCCTCCCACACTgcacgctccgactgtgt
C5	chr1:209848582-209848716	AACACCAACTACCCTCCCACACTgacacgcctcctgggc
C6	chr1:209848717-209848789	AACACCAACTACCCTCCCACACTcagctctcccagttggagact
C7	chr1:209848891-209848994	AACACCAACTACCCTCCCACACTcaggaggagcagcaggaga
C8	chr2:64677694-64677801	AACACCAACTACCCTCCCACACTcacatggaatttctaatattgggaggaag
C9	chr2:64680293-64680366	AACACCAACTACCCTCCCACACTgaggctccttttttttttttttttttttttttaa
C10	chr2:64683514-64683698	AACACCAACTACCCTCCCACACTcagaaattctggctgcttcaagtg
C11	chr2:64685929-64686047	AACACCAACTACCCTCCCACACTcaaaacaaaaacaaaaacaaaaacaaaaaacaaaa
C12	chr2:113587642-113587785	AACACCAACTACCCTCCCACACTgaggatctcctgtccatcagcc
D1	chr2:113593790-113593883	AACACCAACTACCCTCCCACACTgagaaatcacacatgaacgtagcc
D2	chr2:113594250-113594412	AACACCAACTACCCTCCCACACTgcctcctacttctgcttttgaaag
D3	chr2:113594413-113594489	AACACCAACTACCCTCCCACACTgaagcttccaccaatactcttttcc
D4	chr2:113594618-113594718	AACACCAACTACCCTCCCACACTcatgtataaatctgtgtgtcttccacttt
D5	chr2:136872117-136872217	AACACCAACTACCCTCCCACACTgttgctgtatgtctcgtggtagga
D6	chr2:136873290-136873443	AACACCAACTACCCTCCCACACTggggactatgactccatgaaggaa
D7	chr2:136873749-136873819	AACACCAACTACCCTCCCACACTggaaggttttttttcttccctctagtg
D8	chr2:136874486-136874584	AACACCAACTACCCTCCCACACTcagcggcgcgcaattc
D9	chr2:136874585-136874693	AACACCAACTACCCTCCCACACTcaagtggggaaaccgtttgg
D10	chr3:122044160-122044233	AACACCAACTACCCTCCCACACTgacttttttcctgaatggcatcaact
D11	chr3:122058093-122058177	AACACCAACTACCCTCCCACACTcatagtgaattataagtgctcaataaatttccagc
D12	chr4:6695222-6695366	AACACCAACTACCCTCCCACACTgccacagtggcatcctcattc
E1	chr4:6695367-6695479	AACACCAACTACCCTCCCACACTcatcgttgtgatgacgtttctgga
E2	chr4:6698030-6698255	AACACCAACTACCCTCCCACACTcactgctaacttcatgggcctc
E3	chr4:90815871-90815966	AACACCAACTACCCTCCCACACTggaagttcggtttcctgtttctgt

E4	chr4:90816031-90816118	AACACCAACTACCCTCCCACACTgtagtttgaagcaaggtagctcatg
E5	chr4:90816279-90816377	AACACCAACTACCCTCCCACACTgggaggcagtgttgatttaagaag
E6	chr4:90823160-90823235	AACACCAACTACCCTCCCACACTcaaaactgtgacttgagcatattccg
E7	chr4:90836562-90836635	AACACCAACTACCCTCCCACACTgaaccagaaaaccttcctgtgtgg
E8	chr4:156549424-156549498	AACACCAACTACCCTCCCACACTcatttatctaggtcaggcctccat
E9	chr4:156585604-156585709	AACACCAACTACCCTCCCACACTcacattaaagtttgaaaagcactggtc
E10	chr4:156587988-156588084	AACACCAACTACCCTCCCACACTgctcctccaggcgctc
E11	chr4:156588085-156588219	AACACCAACTACCCTCCCACACTcagttcctttccataaggcattcg
E12	chr4:156588586-156588666	AACACCAACTACCCTCCCACACTggagaggaaggagacccagc
F1	chr4:156589214-156589300	AACACCAACTACCCTCCCACACTcagacaggcgcggagac
F2	chr4:156589354-156589437	AACACCAACTACCCTCCCACACTcaaaatgaaagaataaccatgtgaaaatcagt
F3	chr5:88017774-88017907	AACACCAACTACCCTCCCACACTcaggcatatcattggcgtatggc
F4	chr5:88017908-88018019	AACACCAACTACCCTCCCACACTcaacatatagaaaaatgtatagatgcttggaca
F5	chr5:88018385-88018459	AACACCAACTACCCTCCCACACTgtcaagcgcatgcgactttc
F6	chr5:88018460-88018715	AACACCAACTACCCTCCCACACTgagttcaaatctctccctgccttc
F7	chr6:130686016-130686122	AACACCAACTACCCTCCCACACTcagtgtatttgtttatttcggcgtgt
F8	chr6:130686123-130686195	AACACCAACTACCCTCCCACACTcacaaggtgtgtgctatgcttgt
F9	chr6:130690524-130690712	AACACCAACTACCCTCCCACACTgaggaggagtgggcacagaa
F10	chr6:130747455-130747602	AACACCAACTACCCTCCCACACTcagaaaggattcttctccttaacctaatttaca
F11	chr6:130757713-130757869	AACACCAACTACCCTCCCACACTcagtgagttatgatcatgccactact
F12	chr6:130758118-130758262	AACACCAACTACCCTCCCACACTcaatttatacacatctgccatggagtt
G1	chr6:132987332-132987408	AACACCAACTACCCTCCCACACTcaggtcaaaattagaatgtcaaccct
G2	chr6:132987409-132987478	AACACCAACTACCCTCCCACACTcaaaatgggccttacgaagtggaa
G3	chr6:132987492-132987573	AACACCAACTACCCTCCCACACTcagtatatttagtctgtgggaaaaactgaag
G4	chr6:133003614-133003784	AACACCAACTACCCTCCCACACTgaatgtgactgtatttggagacaggg
G5	chr6:133004825-133004937	AACACCAACTACCCTCCCACACTcaagttctcctcccactccc
G6	chr6:133035164-133035249	AACACCAACTACCCTCCCACACTgttctggacaccacgtgtcttc
G7	chr6:133035250-133035333	AACACCAACTACCCTCCCACACTcaataaggtagggtcttttgttatgtaacaa
G8	chr6:133035334-133035444	AACACCAACTACCCTCCCACACTcaaagcaataaatttttttatttttttacaccaccc
G9	chr7:150211739-150211909	AACACCAACTACCCTCCCACACTggctgggtggagccac
G10	chr7:150323041-150323184	AACACCAACTACCCTCCCACACTgaaagcttcagcatttctcttgct
G11	chr7:150328732-150328802	AACACCAACTACCCTCCCACACTcacactgtggccaacatgg
G12	chr8:30209251-30209362	AACACCAACTACCCTCCCACACTgcttcttgagtagccgggacta
H1	chr8:30209363-30209450	AACACCAACTACCCTCCCACACTcaggtcgcaggctggaag
H2	chr8:30209451-30209538	AACACCAACTACCCTCCCACACTcacgatttccctcatggttaaaatttaatttt
H3	chr8:30209539-30209649	AACACCAACTACCCTCCCACACTcaggtcgctgtccccg
H4	chr8:30210276-30210522	AACACCAACTACCCTCCCACACTcacgttaaacatctgctcatcgac
H5	chr8:30262205-30262359	AACACCAACTACCCTCCCACACTggtcaggagttcgagattagcct
H6	chr8:30264605-30264707	AACACCAACTACCCTCCCACACTggagttcaagaccagcctgg
H7	chr8:30272512-30272647	AACACCAACTACCCTCCCACACTcaggttagatggtggggataaggg
H8	chr8:30279880-30279964	AACACCAACTACCCTCCCACACTgaaaatttagtattattattatttaagaaaatttc
H9	chr8:30279965-30280034	AACACCAACTACCCTCCCACACTggcaggaggactgcttaagc
H10	chr8:48648672-48648902	AACACCAACTACCCTCCCACACTcagtgctttaagatttaattaaaaagccgc
H11	chr8:48649023-48649130	AACACCAACTACCCTCCCACACTgaacagttcaagagctccctaact
H12	chr8:48649131-48649216	AACACCAACTACCCTCCCACACTggtaagctagcagctttccagc

Patch_R2

Well Position	Name	Sequence
A1	chr8:48649309-48649539	AACACCAACTACCCTCCCACACTgcatgctcacttttttatattaatttttacagtat
A2	chr8:48649623-48649763	AACACCAACTACCCTCCCACACTcagtttcttgggacataggagcg
A3	chr11:59822619-59822847	AACACCAACTACCCTCCCACACTgagaaagaatgagggcacagcc
A4	chr11:59824073-59824143	AACACCAACTACCCTCCCACACTgaaaagatcactacagcatcttttccc
A5	chr11:59824144-59824297	AACACCAACTACCCTCCCACACTcagacatccccagtagtccactg
A6	chr12:69743601-69743702	AACACCAACTACCCTCCCACACTcaaatcatcttgtaacaccaacgaaca
A7	chr13:31256700-31256846	AACACCAACTACCCTCCCACACTcattcagttaggttcattatcacacactc
A8	chr13:31264669-31264779	AACACCAACTACCCTCCCACACTcactccgcggctgc
A9	chr13:31305958-31306085	AACACCAACTACCCTCCCACACTgacagaacaaaaagacaaggggca
A10	chr13:31306157-31306256	AACACCAACTACCCTCCCACACTcagaggcccggggatg
A11	chr13:31308427-31308520	AACACCAACTACCCTCCCACACTcatctcggcacggaagagg
A12	chr13:31308521-31308612	AACACCAACTACCCTCCCACACTgctatttggcattggttaagaggt
B1	chr14:25042640-25042723	AACACCAACTACCCTCCCACACTgtttgtttggattgctacaacaaaatagc
B2	chr14:25043403-25043546	AACACCAACTACCCTCCCACACTcagagggataggcagtgcct
B3	chr14:25043773-25043883	AACACCAACTACCCTCCCACACTcaggtaccacctacctggc
B4	chr14:25044917-25045008	AACACCAACTACCCTCCCACACTgagggctctgggaagctc
B5	chr14:25045492-25045582	AACACCAACTACCCTCCCACACTgcagccttgggtgatgaaac
B6	chr14:25045583-25045665	AACACCAACTACCCTCCCACACTgcagctgctcaagagctcac
B7	chr14:94854933-94855052	AACACCAACTACCCTCCCACACTgcccctgtttgctcctcc
B8	chr14:94855161-94855233	AACACCAACTACCCTCCCACACTgtggtactctcccagagactgtc
B9	chr17:53340951-53341040	AACACCAACTACCCTCCCACACTgctgtaggttcttcataaaaggacac
B10	chr17:53341041-53341201	AACACCAACTACCCTCCCACACTgtcgctggggaaggatgtg
B11	chr17:53341202-53341275	AACACCAACTACCCTCCCACACTcaagaacgaatgggcacaaatgaa
B12	chr17:53341569-53341721	AACACCAACTACCCTCCCACACTcagagaggtgttaacggtggg
C1	chr17:53341848-53342046	AACACCAACTACCCTCCCACACTggagttttaaaaaaatcgcgataccca
C2	chr17:53342047-53342128	AACACCAACTACCCTCCCACACTgatttttttttttttttttggtctgggtgg
C3	chr17:53342679-53342771	AACACCAACTACCCTCCCACACTgcttttcctccgtcctttgc
C4	chr17:53342910-53343164	AACACCAACTACCCTCCCACACTggaggggtccctcccc
C5	chr17:53345556-53345685	AACACCAACTACCCTCCCACACTcaaaatcagaatttctaggggtagatacaaag
C6	chr17:56345755-56345894	AACACCAACTACCCTCCCACACTgtggtaagacatgtatggcctgta
C7	chr17:56349058-56349181	AACACCAACTACCCTCCCACACTggaacctgaaattggcgaggaaa
C8	chr17:56352856-56353022	AACACCAACTACCCTCCCACACTcacaccctcttacttcgggag
C9	chr17:56354467-56354732	AACACCAACTACCCTCCCACACTgcggtgctaaccacatttcaaatg
C10	chr17:56355246-56355465	AACACCAACTACCCTCCCACACTcatcccgttcttccgctcc
C11	chr17:56356893-56357035	AACACCAACTACCCTCCCACACTgctcccccattgttctttccc
C12	chr18:61553980-61554107	AACACCAACTACCCTCCCACACTcactccagcctgggtgac
D1	chr18:61557698-61557783	AACACCAACTACCCTCCCACACTcatgctcacacccaaggtgtg
D2	chr19:826530-826639	AACACCAACTACCCTCCCACACTcactccagcctgggtgac
D3	chr19:827348-827467	AACACCAACTACCCTCCCACACTgggcagtggagctggc
D4	chr19:827468-827539	AACACCAACTACCCTCCCACACTgagtcccagtctccccatcc
D5	chr19:827570-827660	AACACCAACTACCCTCCCACACTgtttccctctctagaagatggcca
D6	chr19:827673-827749	AACACCAACTACCCTCCCACACTgtgggaacacgggaaattgc
D7	chr19:827750-827824	AACACCAACTACCCTCCCACACTggcggcggctgc
D8	chr19:827825-827967	AACACCAACTACCCTCCCACACTgttctgccctggcagc
D9	chr19:839649-839771	AACACCAACTACCCTCCCACACTgagtctcttggggtctgtggaat
D10	chr19:840607-840754	AACACCAACTACCCTCCCACACTgagcaacacatgcccacgt
D11	chr19:840755-840992	AACACCAACTACCCTCCCACACTcacccacggtcaagctcc

D12	chr19:840993-841063	AACACCAACTACCCTCCCACACTgcagcaaggccagcag
E1	chr19:841064-841176	AACACCAACTACCCTCCCACACTgtttccccagctgtgcca
E2	chr19:44152949-44153103	AACACCAACTACCCTCCCACACTgcctcaccatcaccctgc
E3	chr19:44159620-44159775	AACACCAACTACCCTCCCACACTgtccctcattcacaatctgacatct
E4	chr19:44173928-44174036	AACACCAACTACCCTCCCACACTggaaatattagtggagcaaaggcat
E5	chr20:48805984-48806131	AACACCAACTACCCTCCCACACTcaccccgaggttcaacttttttca