A comprehensive analysis of gene expression profiles in distal parts of the mouse renal tubule.

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Abstract

The distal parts of the renal tubule play a critical role in maintaining homeostasis of extracellular fluids. In this review, we present an in-depth analysis of microarray-based gene expression profiles available for microdissected mouse distal nephron segments, i.e., the distal convoluted tubule (DCT) and the connecting tubule (CNT), and for the cortical portion of the collecting duct (CCD) (Zuber et al., 2009). Classification of expressed transcripts in 14 major functional gene categories demonstrated that all principal proteins involved in maintaining of salt and water balance are represented by highly abundant transcripts. However, a significant number of transcripts belonging, for instance, to categories of G protein-coupled receptors (GPCR) or serine-threonine kinases exhibit high expression levels but remain unassigned to a specific renal function. We also established a list of genes differentially expressed between the DCT/CNT and the CCD. This list is enriched by genes related to segment-specific transport functions and by transcription factors directing the development of the distal nephron or collecting ducts. Collectively, this *in silico* analysis provides comprehensive information about relative abundance and tissue specificity of the DCT/CNT and the CCD expressed transcripts and identifies new candidate genes for renal homeostasis.

Introduction

The final adjustment of urine composition takes place in the distal parts of the renal tubule, i.e. in the distal nephron and in the collecting duct. Over the last decades, research efforts in the field allowed identification of many essential proteins (channels, transporters, receptors, etc.) involved in this process. The majority of these proteins were first discovered by expression cloning, an approach based on the *a priori* available information about function and tissue expression distribution of the candidate gene. The aquaporin-2 water channel (aqp-2), the V_2-type of vasopressin receptor (Avpr2), the Ca^{2+}-sensing receptor (CaSR), the thiazide-sensitive sodium-chloride co-transporter (NCC), the secretory potassium channel (ROMK), the amiloride-sensitive sodium channel (ENaC) and the epithelial calcium channel (Trpv5) are just a few out of many examples of proteins identified by this approach. Moreover, a growing list of functionally important genes has been added from human genetic association studies. The latter includes WNK1 and WNK4 serine-threonine kinases [1], the FXYD2 subunit of the Na,K-ATPase [2], the KCNJ10 and KCNA1 potassium channels and the pro-EGF [3-5]. Significant progress in deciphering regulatory pathways in the distal nephron and/or collecting ducts has been made with the development of methods allowing global view of all expressed transcripts (transcriptome) or proteins (proteome) and their dynamics. For example, the aldosterone or vasopressin signaling pathways were extensively characterized by the serial analysis of gene expression (SAGE) and microarray hybridization [6, 7]. Various proteome tools were used for identification, of vasopressin-dependent phosphorylation sites within aqp-2 or for detection of lithium-induced changes in the proteome of the inner medullary collecting ducts (IMCD) [8, 9].

In order to identify new genes involved in renal homeostatic mechanisms we used an *in silico* approach based on the analysis of transcript abundance in several major functional gene categories most relevant to secretion/reabsorption processes in the distal nephron and/or the collecting duct. This analysis was performed on a recently obtained microarray-based dataset of gene expression profiles of the mouse distal convoluted tubule (DCT), the connecting tubule (CNT) and the cortical collecting duct (CCD) [10]. The principal characteristics of this dataset are the following: (i) the DCT/CNT and the CCD samples were obtained by microdissection; the DCT and CNT were microdissected together because of the gradual transition between these two segments in mice; (ii) samples were prepared from animals sacrificed for microdissection every four hours throughout a 12 h/12 h light-dark cycle (a total of 6 time-points); this protocol allows detection of all expressed transcripts independently of diurnal variations in their expression levels; (iii) a total of 30 animals were used for microdissection of DCT/CNT and CCD samples (5 animals/time-point); (iv) 12 microarray hybridizations were performed for both DCT/CNT and CCD (2 hybridizations/time-point). The quality of microdissection was validated by the analysis of expression levels of several nephron segment-enriched transcripts (see [10] and below). Altogether, this dataset represents a complete and reliable source of information on the genes expressed in the distal nephron and the CCD (see below).

Functional classification and analysis of transcript abundance allowed us to identify a new set of highly abundant transcripts encoding proteins potentially relevant to the homeostasis of water and/or electrolytes. Finally, comparison of the DCT/CNT and the CCD transcriptomes revealed a number of previously uncharacterized transcripts exhibiting significantly different expression levels between these parts of the renal tubule. These data could be further used for the functional characterization of the identified candidates.

1. Functional classification of DCT/CNT and CCD transcripts. Functional classification of DCT/CNT and CCD transcripts was performed using the PANTHER Classification System, a database allowing subdivision of proteins and mRNA transcripts into functionally related categories (www.pantherdb.org). A similar approach was previously used by Uawithya et al. for the transcriptional profiling of rat inner medullary collecting ducts (IMCD) [11]. The classification data are presented in tables in which only the 20 most abundant transcripts per category are listed for space purposes. If more than 20 transcripts per category fitted the cut-off criteria (see below), a full list of transcripts can be viewed in associated supplementary tables. The transcripts are ranked by their abundance calculated as log2 normalized microarray hybridization signal intensity (A-values) [12]. Hence, a difference in one unit of A_values corresponds to the 2-fold difference in the transcript expression levels. The median microarray signal intensity (5.8 units of A_value, for both the DCT/CNT and the CCD transcriptomes) was chosen as an arbitrary cut-off value above which expression of a transcript was assigned as significant. The data are discussed in terms of expression levels or transcripts abundance. However, we have to emphasize that microarray signal intensities and sequencing-based quantification of mRNA abundance have been shown to exhibit a correlation coefficient of ~ 0.7 [13]. To assess this correlation in the DCT/CNT and the CCD datasets we performed qPCR analysis of transcripts abundance in one of the selected gene categories, namely G protein-coupled receptors (GPCR). As shown in Figure 1A and 1B, both, DCT/CNT and CCD datasets exhibit a good correlation between microarray signal intensities and Ct values of qPCR amplification (correlation coefficients of 0.769 and 0.823, respectively). These data also demonstrate that transcripts with A-values below the median cut-off level exhibit significantly lower correlation between microarray and qPCR data.

1.1. G protein-coupled receptors (GPCRs). Most GPCRs that have been previously identified in the DCT/CNT and/or the CCD are abundantly represented in the respective transcriptomes (Table 1 and Supplemental Table 1). These include vasopressin receptors type 1a (Avpr1a) and type 2

(Avpr2), prostaglandin E receptors type 3 (Ptger3), type 1 (Ptger1) and type 4 (Ptger4), prostaglandin F receptor (Ptgfr), glucagon receptor (Gcgr), proteinase-activated receptor 2 (F2rl1), calcium-sensing receptor (Casr), endothelin receptor type B (Ednrb), parathyroid hormone receptor 1 (Pth1r), adenosine A1 receptor (Adora1) and adrenergic receptors type beta 1 (Adrb1), beta 2 (Adrb2) and alpha 2a (Adra2a). This analysis also revealed the presence of a number of highly abundant GPCRs with yet unassigned function in the kidney. For instance, both, DCT/CNT and CCD exhibit high expression levels of several chemokine GPCRs, including Ccrl1, Cxcr4 and Gpr146. The Cxcr4 receptor has been shown to bind SDF-1, a chemokine involved in a multitude of functions, including epithelial patterning and renal morphogenesis [14]. However, the role of chemokine GPCRs in the adult kidney remains unknown. The DCT/CNT and the CCD transcriptomes are enriched by orphan receptors belonging to a subclass of adhesion-GPCRs (Celsr2, Gpr116, Gpr56 and Celsr1). Adhesion-GPCRs constitute a novel subclass of GPCRs characterized by the presence in their N-termini of cadherin-like cell adhesion modules. These receptors are critical for the normal development of the central nervous system and for the immune response. Several adhesion-GPCRs are involved in human diseases. For example, deletion of the Gpr56 gene in human causes the autosomal recessive bilateral frontoparietal polymicrogyria (BFPP), a disease characterized by severe neurological dysfunction [15]. However, a renal phenotype in these patients, if any, has not yet been communicated. Both the DCT/CNT and the CCD transcriptomes revealed high expression levels of Gprc5C and Gprc5B, two receptors related to the family C of GPCRs, which also includes the metabotropic glutamate receptors, the GABA(B) receptors, several pheromone receptors and the calcium sensing receptor [16]. However, in contrast to other members of the family, both, Gprc5C and Gprc5B still remain orphan. Our analysis also revealed a high expression of three receptors belonging to the class A of the rhodopsin-like GPCRs, namely the oxoglutarate receptor 1

(Oxgr1), the estrogen receptor (Gper or Gpr30) and the apelin receptor. Several pieces of evidence indicate that these receptors may have an important role in the regulation of tubular solute transport. Oxgr1 (also known as Gpr80 or Gpr99) is a specific receptor to α-ketoglutarate, a citric acid cycle intermediate [17]. Interestingly, urinary concentration of α-ketoglutarate varies significantly upon perturbation of systemic acid-base balance, being significantly increased in alkalosis and significantly decreased in acidosis [18]. This suggests a possible role for Oxgr1 in sensing acid-base disequilibrium. Gper is a recently identified plasma membrane estrogen receptor which mediates non-genomic effect of estrogen. As it was recently hypothesized, Gper may be involved in the rapid magnesiotropic effects of estrogen in the distal nephron [19]. Apelin is a recently discovered peptide which mediates a multitude of biological functions including vasoconstriction, cardiac myogenesis, glucose metabolism and vasopressin synthesis/release in the brain. Knockout of apelin receptor in mice leads to abnormal fluid homeostasis, resulting in disturbance of both, kidney urinary concentration capacity and drinking behaviour [20]. The role of this receptor in the renal tubules has not yet been elucidated.

1.2 Heterotrimeric G proteins. GPCRs transduce signals from extracellular stimuli by activating heterotrimeric G proteins. These latter can be grouped in four subfamilies Gαs, Gαi, Gαq/11 and Gα12/13, according to the structural and functional properties of their α subunits. Gαs and Gαi regulate intracellular cAMP levels by activating (Gαs) or inhibiting (Gαi1, Gαi2 and Gαi3) adenylyl cyclase; Gαq and Gα11 increase intracellular Ca^{2+} level via activation of phospholipase C; and, Gα12 and Gα13 couple GPCRs to the small GTPases of the Rho family. As shown in Table 2, all α subunits, at the exception of Gα12, are well represented in both transcriptomes, thereby providing molecular basis for a variety of intracellular signalling pathways activated by GPCRs in these parts of the renal tubule.

1.3 Nucleotide cyclases. Chabardès et al. have shown that cortical and outer medullary collecting ducts exhibit high expression levels of Ca^{2+}-inhibitable adenylyl cyclases 6 (Adcy6) and 5 (Adcy5) [21]. Our data support these findings and extend the Adcy6 and Adcy5 distribution to the DCT/CNT (Table 3). Both the DCT/CNT and the CCD also show a high expression of Adcy9, a cyclase which can be either potentiated or inhibited by the intracellular Ca^{2+} [22]. Collectively, these cyclases represent a point of cross-talk between the cAMP- and Ca^{2+}-dependent signalling pathways. Similar to what was found in the IMCD, both, the DCT/CNT and the CCD exhibit low expression of guanylate cyclases (only Gucy1a3 fit the cut-off criteria) and none of the nitric acid synthase isoforms were detected (data not shown) [11].

1.4 Cyclic nucleotide phosphodiesterases. Cyclic nucleotide phosphodiesterases (Pde) participate in attenuation of GPCR signalling by degrading cellular cAMP and/or cGMP. As shown in Table 4, both, the DCT/CNT and the CCD exhibit high expression levels of several cAMP-specific phosphodiesterases, including Ca^{2+}-activated Pde1a and cGMP-inhibited Pde3b. A significant expression of 3-isobutyl-1-methylxanthine (IBMX)-insensitive Pde8a and Pde8b provides a molecular basis for the IBMX-insensitive fraction of phosphodiesterase activity. The rolipram-sensitive cAMP-specific Pde4b and Pde4a have been proposed as important regulators of Avpr2-induced signalling cascade [23]. However, in the DCT/CNT and the CCD transcriptomes presented here they are expressed only at moderate levels.

1.5 Protein kinases. More than 350 protein kinases have been found in the transcriptomes of the DCT/CNT and the CCD (Table 5 and Supplemental Table 2). Most of them (~ 300, Table 5A and Supplemental Table 2) belong to the class of serine/threonine protein kinases. Importantly, kinases that have been previously reported to strongly influence the secretion/reabsorption processes in DCT/CNT and/or the CCD are abundantly represented. WNK1, WNK4, SPAK (STK39) and Sgk1 have been involved in maintaining salt balance and are present within the 20 most abundant serine-threonine kinases. Both, the DCT/CNT and the CCD also exhibit moderate to high expression levels of protein kinase A (Prkaa2, Prkacb, Prkaca and Prkaa1), protein kinase C (Prkcd, Prkci, Prkch, Prkca and Prkcz), casein kinases (Csnk1d, Csnk1a1, Csnk2a1, Csnk1g2 and Csnk2a2), Gsk3β and G protein-coupled receptor kinases 6, 5 and 4. Interestingly, several *in vitro* studies have demonstrated that the activity of the DCT-specific sodium-chloride co-transporter (NCC) is regulated by WNK3 [24], a kinase which is expressed at background levels in our data (A_values of 3.8 and 2.8 in DCT/CNT and CCD, respectively). Accordingly, WNK3 is also absent in microarray-based rat IMCD transcriptome [11]. Collectively, these results indicate that WNK3 distribution in the kidney requires a detailed re-evaluation. By contrast, both the DCT/CNT and the CCD exhibit strong expression of various serine-threonine kinases with yet unattributed function in the kidney. These include Pctk1, Pim3, Pak4, Aak1, Taok3, Rock1 and several MAP kinases. In the kidney, tyrosine kinases (Table 5B) and receptor tyrosine kinases (Table 5C) have been mostly involved in tubulogenesis, cell differentiation and in maintaining cell polarity. However, the fibroblast growth factor receptor 1 (Fgfr1), which is specifically expressed in the distal nephron and the collecting duct, has been recently shown as the predominant receptor for the hypophosphatemic action of FGF23 [25].

1.6 Protein phosphatases. Protein phosphatases participate in intracellular signalling by reversing protein kinases-dependent events. All protein phosphatases can be grouped into three subfamilies: serine/threonine phosphatases, phosphotyrosine-specific protein tyrosine phosphatases and dual specificity (serine/threonine/tyrosine) phosphatases. As shown in Table 6 and Supplemental Table 3, both, DCT/CNT and CCD express a variety of highly abundant phosphatases representing all three subfamilies. However, despite high expression levels and, presumably, significant functional role, only a limited number of phosphatases have been characterized in the kidney. Several studies have shown that calcineurin (Ppp3ca), a serine/threonine phosphatase with broad substrate specificity, is involved in the regulation of transport proteins, including the Na,K-ATPase, aqp-2, ROMK and acid-base transporters [26-29]. The ROMK has been also shown as a substrate of tyrosine phosphatases [30]. Dual specificity phosphatases are thought to participate in renal function mainly by dephosphorylating kinases involved in the stress response (e.g. MAP kinases).

1.7 A kinase anchoring proteins. A kinase anchoring proteins (AKAPs) constitute a family of scaffold proteins involved in the targeting of protein kinase A to its substrates. The AKAPs have been extensively studied for their role in the PKA-dependent regulation of aqp-2 and ENaC activity. Henn et al., and Okutsu et al., have demonstrated that aqp-2 is co-localized with AKAP7 (AKAP18) and AKAP11 (AKAP220) in subapical vesicles of the principal cell [31, 32]. Bengrine et al., have shown that AKAP7 is also involved in the feedback inhibition of ENaC [33]. It has been proposed that these AKAPs are required for compartmentalization of cAMP signalling in the principal cell. As shown in Table 7, we found both AKAP7 and AKAP11 in the DCT/CNT and CCD transcriptomes. However, the role of the more abundant AKAPs 2, 9 and 8 has not yet been assessed.

1.8 Phospholipases. Phospholipases play important roles in transmembrane signaling processes activated by GPCRs and receptor tyrosine kinases. Receptor-mediated activation of phospholipases results in hydrolysis of membrane phospholipids and generation of phospholipid-derived second messengers. Phospholipases C (PLC) is a family of enzymes which catalyses the hydrolysis of phosphatidylinositol 4,5-biphosphate to produce diacyglycerol (DAG) and inositol 1,4,5-trisphosphate (IP3). In the DCT/CNT and/or the CCD several targets of PLC/DAG/PKC cascade have been identified, including TRPV5 calcium channel, aqp-2, ROMK and ENaC [34-37]. We found that the most abundant phospholipase in the DCT/CNT and the CCD is Plcg1, a PLC activated by a variety of growth factors including platelet-derived growth factor (PDGF), hepatocyte growth factor (HGF) and fibroblast growth factor (FGF) (Table 8). Recently, Irarrazabal et al., have shown that Plcg1 contributes to the osmoprotective effect of TonEBP/OREBP transcriptional factor in the kidney [38]. Analysis of both transcriptomes also revealed expression of Ca^{2+}-sensitive PLC isoforms Plcd3 and Plcd1 but only a low amount of Gq-activated Plcb1. Phospholipases A2 (PLA2) catalyze the hydrolysis of phospholipids to generate free fatty acids and lysophospholipids. One of the principal products of PLA2 activity is the arachidonic acid, a precursor in the biosynthesis of prostaglandins and other eicosanoids. Prostaglandins are known to regulate water and solutes transport in an autocrine or paracrine manner by activating apical or basolateral GPCRs. According to our data, the principal PLA2 isoforms expressed in the DCT/CNT and the CCD are Pla2g4a, Pla2g15 and Pla2g6 (Table 8). Phospholipase D (PLD) isoforms which are also abundantly represented in both trancriptomes have been recently shown to be important regulators of endocytosis and endosomal recycling pathways [39].

1.9 Small GTP-binding proteins. Small GTP-binding proteins are low-molecular weight GTPases (20-25 kDa) that control a variety of cellular processes including vesicle transport, cytoskeleton dynamics, cell division and immune response. All small GTPases can be divided in five subfamilies, namely the Rab subfamily, the Arf subfamily, the Rho/Rac/Cdc42 subfamily, the Ras/Ral/Rap subfamily and the Ran GTPase. More than 50 members of the Rab subfamily were found to be expressed at significant levels (Table 9A and Supplemental Table 4). The members of this family are implicated in the transport, docking and fusion of endocytotic vesicles. Van de Graaf et al. have shown that Rab11a is required for the intracellular trafficking of TRPV5 and TRPV6 calcium channels to the cell surface [40]. Curtis and Gluck have demonstrated that Rab11 and Rab20 are mainly expressed in V-ATPase expressing intercalated cells of the collecting duct, whereas principal cells of the collecting duct and of the distal nephron are enriched in Rab18 and Rab5a [41]. Several evidence indicate that Rab(s) could be involved in trafficking of CFTR, ENaC and aqp-2 [42]. However, functional role of many highly abundant Rab(s) in DCT/CNT and CCD remains unknown. ADP-ribosylating factors (Arfs) are participating in the formation of coated transport vesicles. El-Annan et al. have shown abundant expression of Arf1 and Arf6 in the distal nephron and the collecting duct and have demonstrated that Arf1 is mostly localized to the apical membrane whereas Arf6 appeared to be mainly expressed at the basolateral membrane [43]. Arf6 was further demonstrated as a factor promoting Avpr2 recycling [44]. Our data confirm high expression levels of Arf1 and Arf6 and reveal abundant expression of several Arf(s) (Arf3, Arl1, Arl3, etc., see Table 9B) with yet unassigned function in the renal tubule. As shown in Table 9C, both the DCT/CNT and the CCD also exhibit high expression levels of several Rho GTPases, including Cdc42, RhoA and Rac1. The main function of Rho GTPases consists in the control of cytoskeleton dynamics and assembly. Thus, it was logically proposed that Rho(s) could be involved in trafficking of aqp-2, a process which requires remodelling of microtubules and filaments. However, evidence that support this hypothesis remains limited to a few *in vitro* studies [45, 46]. Members of Ras subfamily share the highest degree of homology with Ras, one of the most frequently mutated oncogenes in cancer. Ras, Ral and Rap have been shown to play an important role in cellular proliferation and differentiation by influencing a number of intracellular signalling pathways. Ras GTPases have been also shown to influence activity or expression of several important DCT/CNT and/or CCD transporters, including NCC (H-ras), H,K-ATPase (Rap1), ENaC (K-ras) and aqp-2 (Rap1) [47-50]. As shown in Table 9D, H-ras, K-ras and Rap1 are present within the 10 most abundant members of the Ras subfamily. However, role of several other highly abundant Ras GTPases, including the most abundant Rragd, remain unknown.

1.10 SNAREs and SNARE-related proteins. SNARE proteins participate in trafficking of renal transporters by mediating fusion of intracellular vesicles to the target membranes. Molecular composition of SNARE complexes has been extensively studied for aquaporins involved in renal urine concentration mechanism. Mistry et al., have shown that aqp-2 sorting to the apical membrane requires snapin (SNAPAP), SNAP23 and syntaxin-3, whereas syntaxin-4 is preferentially involved in cell surface expression of aqp-3 [51]. SNAP23/syntaxin-1a complex has been also proposed to regulate cell surface expression of ENaC. However, in our data, expression levels of syntaxin-1a are low (A_values of 4.7 and 5.0 in the DCT/CNT and the CCD, respectively). Accordingly, only a low signal intensity for syntaxin-1a was detected in the IMCD hybridization data [11]. As shown in Table 10 and Supplemental Table 5, both the DCT/CNT and the CCD exhibit high expression of SNAPAP, SNAP23, syntaxin-3 and syntaxin-4. High expression levels were also detected for vesicle associated membrane proteins (VAMP) – 2, 8 and 3. VAMP2 and VAMP3 proteins were previously identified in aqp-2-containing intracellular vesicles indicating their involvement in aqp-2 trafficking [52]. Recently, Wang et al. have shown that mice devoid of *VAMP8* gene exhibit a diabetes insipidus-like phenotype and a significantly reduced membrane expression of aqp-2 in collecting duct cells [53].

1.11 Clathrin, clathrin adaptors and dynamin-like GTPases. Clathrin-coated vesicles are major protein carriers in protein endocytotic pathways. Clathrin-coated vesicles mediate endocytosis of many essential DCT/CNT and/or CCD transporting proteins including ROMK, Na,K-ATPase, ENaC, aqp-2 and Trpv5 [54-58]. As shown in Table 11A, both the DCT/CNT and the CCD exhibit high expression levels of clathrin light and heavy chains (Clta, Cltb and, Cltc, respectively) as well as several clathrin adaptor subunits (Ap1s3, Ap2s1 and Ap3s1). Similar to the IMCD [11], our data show a high abundance of Picalm, a clathrin adaptor which was recently shown to direct VAMP2 trafficking during endocytosis [59]. Dynamins are high molecular weight GTPases (~ 100 kDa) that mediate the fission of clathrin-coated vesicles from the membrane. As shown in Figure 11B, both transcriptomes reveal a high expression of dynamin 2 (Dnm2) and dynamin 1-like (Dnm1l) and low expression of dynamins 1 and 3 (Dnm1 and Dnm3, respectively). Interestingly, this distribution of dynamins differs significantly from that of IMCD in which only dynamin-like GTPases Mx1 and Mx2 demonstrated high signal intensities [11]. In the DCT/CNT and the CCD transcriptomes, both Mx1 and Mx2 exhibit low expression levels (Mx1: A_values of 4.3 and 3.8 in DCT/CNT and CCD, respectively; Mx2: A_values of 3.5 and 3.0 in DCT/CNT and CCD, respectively).

1.12 Cytoskeletal proteins and cytoskeletal regulators. Cytoskleletal proteins mediate a wide variety of essential renal functions. During foetal kidney development, the assembly and contraction of microtubules and microfilaments has been proposed as part of a mechanism that drives branching morphogenesis of the uteric bud [60]. In the adult kidney, cytoskeleton remodelling has been shown to influence cell surface expression and/or activity of a number of proteins involved in maintaining balance of water and electrolytes, including ENaC, aqp-2, Na,K-ATPase, secretory K channels and chloride channels [61-65]. A significant number of cytoskeletal proteins have been recently identified by a proteomic approach in the aqp-2-containing vesicles in the IMCD [52]. As shown in Table 12 and Supplemental Table 6, ~ 300 different transcripts encoding cytoskeletal and cytoskeletal-related proteins are present in our data. The overall distribution and abundance of cytoskeletal transcripts in the DCT/CNT and the CCD is largely similar to that identified in the IMCD. However, for several major transcripts a significant difference was observed. For instance, moesin, an actin-binding protein which has been shown to modulate activity of aqp-2, Na,K-ATPase and CFTR in different models of epithelial cells, was undetectable in IMCD transcriptome [11, 66-68]. In our study, moesin is abundantly present in both the DCT/CNT and the CCD (see subcategory *actin and actin-binding* *proteins*, Table 12A). Also our data reveal high expression of myosin VI (Myo6), a myosin which has been shown as a prerequisite for the clathrin-dependent endocytosis of CFTR in the intestine [69] (see subcategory *myosin and myosin-like proteins*, Table 12B). The role of Myo6 in the kidney has not yet been investigated. In subcategory *microtubule and microtubule-related proteins* (Table 12C) we found strong expression of tubulins 1b and 1a (Tuba1b and Tuba1a), two tubulins that were not detected in the IMCD. Again, despite a high abundance of these transcripts, their role in the kidney remains unknown. Finally, in subcategory *intermediate filaments and related proteins* (Table 12D), we detected several keratins not present in the IMCD transcriptome (Krt10, Krt80, Krt23 and Krt34).

1.13 Transporters and channels. As shown in Table 13 and Supplemental Table 7, more than 250 transcripts encoding water/solutes transporting proteins are expressed at significant levels in the DCT/CNT and/or the CCD, confirming the variety of solutes transported across the epithelium of these segments. In subcategory *water channels* (Table 13A), aquaporins are abundantly represented by plasma membrane expressed aquaporins 2, 3 and 4, as well as by the intracellular aquaporins 6 and 11. As expected, expression of aquaporins 2 and 4 is significantly lower in the DCT/CNT than in the CCD, whereas aquaporin-3 is equally represented in both transcriptomes. Surprisingly, our analysis also revealed a low, but significant, expression of aquaporin 1, a channel which is present, according to immunohistochemical analyses, only in the proximal tubule and descending thin limb. Interestingly, the aquaporin 1 RNA has also been detected in human DCT, at levels of ~ 10% of those in the proximal tubule [70]. However, in both, human and mouse transcriptomes, the expression levels of aquaporin 1 RNA in the distal nephron are significantly lower than those of other water channels. For instance, in mouse DCT/CNT the difference between the aquaporin 3 and aquaporin 1 RNA expression is ~ 130-fold (13.11 units of A-value vs. 6.09 units of A-value, respectively, Table 13A).

In subcategory *ion channels and transporters excluding SLC* (Table 13B), all principal genes involved in maintaining ion balance are represented (e.g. Na,K-ATPase, αβγENaC (Scnn1), ROMK (Kcnj1), Kir5.1 (Kcnj16), Kir 4.1 (Kcnj10), Clcnkb, Clc3, Trpv5, PMCA2 (ATP2b2), Trpm6 and various H^+-ATPases). Analysis of the transcripts belonging to this subcategory also revealed a number of highly abundant transcripts with yet unassigned function in the kidney. For instance, both the DCT/CNT and the CCD exhibit high expression levels of Tmem16f, a functionally uncharacterized paralogue of a recently identified calcium-activated chloride channel Tmem16a [71]. Also, both transcriptomes reveal abundant expression of several voltage-gated ion channels, including Kcnq1, Kcne1, Kcnj10, Cacna1d, Cacnab4, Kcnh3 and Cacna2d1. Importantly, mutations in two voltage-gated potassium channels (Kcnj10 and Kcna1) have been recently shown to cause electrolyte imbalance in human [3, 4]. To what extent other voltage-gated channels identified in our study can participate in the physiology/pathophysiology of distal nephron and/or collecting duct remains to be established.

In subcategory *solute carrier proteins (SLC)* (Table 13C), the most abundant transcript is pendrin (Slc26a4), a chloride/bicarbonate exchanger located at the apical membrane of the CNT and CCD cells. Also highly abundant is Slc2a9, a recently identified urate transporter [72]. Interestingly, analysis of the SLC(s) expressed in the DCT/CNT and/or the CCD revealed the presence of several transcripts whose expression was previously considered as restricted to the proximal tubule or to Henle's loop. For example, a high expression of the glucose transporter Glut1 (Slc2a1) and the sodium-glucose co-transporter Sglt2 (Slc2a5) and, a moderate expression of the sodium-potassium-chloride co-transporter NKCC2 (Slc12a1) and the sodium-phosphate co-transporter NaPi-IIa (Slc34a2) were detected in distal nephron. Glut1 and NKCC2 transcripts were also detected in the IMCD transcriptome [11]. Expression of NaPi-IIa, NKCC2 and Sglt2 in the DCT has been validated by RT-PCT analysis (D.Firsov, unpublished observations). The correlation between transcript and protein expression of these genes remains unknown. However, this information might be important for selection of tissue-specific promoters in transgenic experiments.

1.14 Transcription factors. More than 1'000 transcription factors are expressed in DCT/CNT and/or CCD above median levels (Table 14 and Supplemental Table 8). Only a small fraction of them has been assigned to a specific renal function. For instance, Homeobox-containing transcriptional factors (*Hox*) are largely involved in morphogenesis of different parts of the renal tubule (see below). Mineralocorticoid receptor (Nr3c2), glucocorticoid receptor (Nr3c2), vitamin D receptor (Vdr), cAMP response element-binding proteins (Creb(s) and Atf(s)), peroxisome proliferator-activated receptors (PPARs), TonEBP (Nfat5), Jun, Fos, Edf1, Jag have been shown to participate in the regulation of secretion/reabsorption processes along the distal nephron and the collecting duct. Recently, we have shown that transcriptional factors of the circadian clock (arntl (bmal1), clock, npas2, dbp, hlf, tef) are playing a major role in DCT/CNT and CCD homeostatic function [10].

2. Comparison of DCT/CNT and CCD transcriptomes. To identify genes differentially expressed between the DCT/CNT and the CCD we performed a comparative analysis of the normalized DCT/CNT and CCD transcriptomes. A 3-fold difference in expression levels and a false discovery rate (FDR) of 5% were used as cut-off criteria. Overall, 122 DCT/CNT transcripts (corresponding to 82 distinct genes) and 118 CCD transcripts (corresponding to 91 distinct genes) met this criterion (Supplemental Figure 1).

2.1 Transcripts enriched in DCT/CNT. Analysis of differentially expressed transcripts revealed two major groups of genes enriched in DCT/CNT: (i) genes of the Homeobox (*Hox*) family of transcriptional factors that play an essential role during embryonic kidney development

[73] and, (ii) genes involved in the secretion/reabsorption of different solutes along the nephron (Table 15 and Supplemental Table 8). The *Hox* genes have been shown to determine the segment identity of the renal tubule, being principal genes of formation and patterning of the uteric bud and the metanephric mesenchyme. However, their role in the adult kidney is less clear. Our data demonstrate that *Hox* genes which are specifically involved in the nephron formation during the embryogenesis (*Hoxa9, Hoxd10, Hoxd11, Hoxa10, Hoxa3* and *Hoxc9*) remain enriched in the DCT/CNT of the adult kidney [74]. In contrast, analysis of the CCD enriched transcripts (Table 16) shows that *Hox* genes specifically involved in the development of the uteric bud are either not expressed in the CCD of the adult kidney (*Hoxd1*) or show comparable expression levels in the DCT/CNT and CCD (*Hoxb7*, *Hoxd8*) [74].

At least 15 out of 83 DCT/CNT enriched genes have been shown to participate in renal solute homeostasis. For instance, the thiazide-sensitive sodium-chloride cotransporter (NCC or Slc12a3) and the WNK1 (with-no-lysine (K)) serine-threonine kinase are critically involved in sodium/chloride reabsorption and potassium secretion in the distal nephron segments [75]. The Glut9 (Slc2a9) transporter has been recently shown as a principal transporter involved in the renal handling of urate in both human and mice [76]. A significant number of the DCT/CNT enriched genes are involved in the transepithelial reabsorption of calcium and magnesium. These latter include the genes coding for the sodium-calcium exchanger (Slc8a1), parvalbumin (Pvalb), the tissue kallikrein (Klk1), the parathyroid hormone 1 receptor (Pth1r), klotho (Kl), the vitamin D receptor (Vdr), the calcium binding proteins calbindin-28K (Calb1) and S100 (S100g), the epidermal growth factor (Egf), the FXYD domain-containing ion transport regulator 2 (Fxyd2), the transient receptor potential cation channels Trpv5 and Trpm6 [77]. A secreted species of klotho has been shown to mediate the paracrine regulation of phosphate reabsorption in the proximal tubule [78].

This analysis also revealed several DCT/CNT-enriched transcripts potentially involved in renal solutes handling. For example, the Secreted Frizzled-Related Protein 1 (Sfrp1) belongs to a small family of secreted proteins acting as antagonist of the Wnt signaling pathway. Importantly, one of the Sfrp, namely Sfrp4, is one of the most potent tumor-derived antagonists of phosphate reabsorption in the proximal tubule As Sfrp1 strongly expressed in the kidney in normal physiological state, we believe that this gene might be an interesting candidate for maintaining phosphate balance by the kidney. Another interesting transcript is the cytochrome P450 2j11 (Cyp2j11) which shares a high degree of homology (80%) with the human Cyp2j2 protein. Several studies have provided evidence for an association of Cyp2j2 polymorphisms with a susceptibility to essential hypertension in man [79-81]. The Cyp2j2 has been proposed to regulate renal fluid-electrolyte transport by catalyzing production of cis-epoxyeicosatrienoic acids (EETs) from the arachidonic acid. *In vitro*, the EETs have been shown to inhibit the activity of ENaC [82]. However, other renal targets of EETs as well as the *in vivo* role of Cyp2j2/Cyp2j11 in the kidney remain unknown. Two other remarkable DCT/CNT enriched genes are the small GTPase Rab27a which is involved in the intracellular vesicle docking and membrane trafficking and, the Uscher syndrome 1C homolog (Ush1C), a ciliary protein which contributes to establishing the sensitivity to displacement of mechanotransduction channels in the hair cells [83, 84]. The functional relevance of these two proteins in the kidney remains unclear.

2.2 *Transcripts enriched in CCD.* The CCD transcriptome is also enriched in transcripts involved in different stages of tubulogenesis (Table 16 and Supplemental Table 9). These include an agonist of the frizzled receptors (Wnt9b), the enzymes of retinoic acid synthetic pathway (Aldh1a1 and Aldh1a7), the metallopeptidase inhibitor 2 (Timp2), the insulin-like growth factor 1 (Igf1), a ligand of the epidermal growth factor receptor (betacellulin), the arginase 2 (Arg2) and the axon guidance receptor homolog 1 (Robo1). Several enriched transcripts encode proteins participating in tubular water/solute transport (aqp-4, aqp-2, Fxyd4, Fxyd3, Slc26a7 and Ptger1). Interestingly, CCD cells exhibit significant expression of Gpr126, an orphan GPCR controlling the Gs/cAMP signaling pathway in Schwann cells [85]. In the kidney, neither function nor cellular localization of Gpr126 had been determined thus far. However, this receptor is expressed at high levels in mCCD cells, a model of principal cells of the collecting duct (Heidi Fodstad, unpublished microarray hybridization data, personal communication). This finding, if confirmed in human principal cells, raises an interesting possibility of using Gpr126 for bypassing malfunctioning V2R signaling pathway in X-linked nephrogenic diabetes insipidus (NDI). Both, the DCT/CNT and the CCD transcriptomes are enriched by enzymes involved in sulfation of glycoproteins (Sulf2 and Chst11 in DCT/CNT and, Chst9 and Hs3st3b1 in CCD). Sulfation is a posttranslational modification known to contribute to the functional heterogeneity of glycoproteins by modifying their binding capacities to glycans, glycolipids or to other glycoproteins. In the kidney, sulfation has been shown to affect many important biological processes including immune response, cell-cell adhesion and hormonal signaling. Yet, the specific targets of the above-mentioned enzymes along the nephron and in the collecting duct remain unknown.

Overall, this in-depth analysis of the mouse transcriptomes of the DCT/CNT and CCD opens new avenues in the comprehensive interpretation of molecular mechanisms underlying renal homeostasis. More studies are needed that will decipher the exact roles and interactions of the genes expressed in the distal part of the nephron and in the CCD.

FIGURE LEGEND

Figure 1. Correlation between qPCR- and microarray- based expression levels of GPCRs expressed in the DCT/CNT (**A**) and the CCD (**B**). Negative mean normalized Ct values (x-axis) are plotted against normalized expression values measured by Affymetrix microarrays (y-axis).

Genes with the Ct values of 36 or above are not plotted. Loess curves are indicated with a red line. Genes considered as expressed from the microarray data are indicated with a red dot. Several genes discussed in the text are indicated with a green dot. Two outliers are Cxcr7 (a) and S1pr3 (b). The qPCR was performed on Mouse GPCR array from Applied Biosystems.

Supplementary Figure 1

A. Scatter plot of average expression value in the DCT/CNT samples versus average expression value in CCD samples. Dashed red lines: 2-fold change cut-off. Solid green line: loess curve. **B**. Density distribution of the moderated t-statistics for the expression in DCT/CNT versus CCD. Black line: t-statistics calculated on the normalized values not corrected for batch effect. Red line: t-statistics calculated on the normalized values after correction for batch effect.

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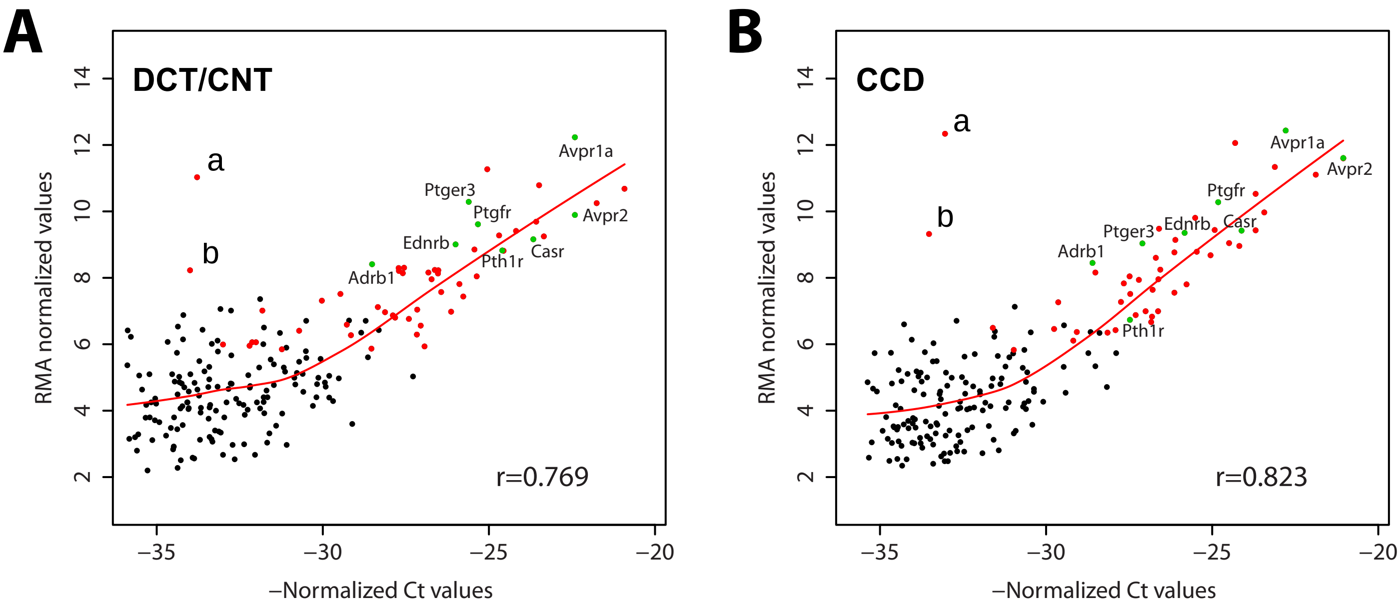

A
DCT/CNT
RMA normalized values
2
4
6
8
10
12
14
−35
−30
−25
−20
−Normalized Ct values
a
b
Avpr1a
Ptger3
Ptgfr
Avpr2
Ednrb
Casr
Pth1r
Adrb1
r=0.769
B
CCD
RMA normalized values
2
4
6
8
10
12
14
−35
−30
−25
−20
−Normalized Ct values
a
b
Avpr1a
Avpr2
Ptgfr
Ptger3
Ednrb
Casr
Adrb1
Pth1r
r=0.823

Supplemental Table 1. G protein-coupled receptors (GPCR)

Gene Name	Gene Symbol	DCT/CNT A_Value	CCD A_Value
arginine vasopressin receptor 1A	Avpr1a	12.23	12.44
cadherin, EGF LAG seven-pass G-type receptor 2	Celsr2	11.27	12.06
chemokine (C-X-C motif) receptor 7	Cxcr7	11.03	12.34
G protein-coupled receptor 116	Gpr116	10.79	11.34
G protein-coupled receptor 56	Gpr56	10.68	11.60
chemokine (C-X-C motif) receptor 4	Cxcr4	10.39	10.65
prostaglandin E receptor 3 (subtype EP3)	Ptger3	10.29	9.04
G protein-coupled receptor, family C, group 5, member C	Gprc5c	10.25	11.11
arginine vasopressin receptor 2	Avpr2	9.89	11.61
oxoglutarate (alpha-ketoglutarate) receptor 1	Oxgr1	9.69	9.44
xenotropic and polytropic retrovirus receptor 1	Xpr1	9.68	9.92
prostaglandin F receptor	Ptgfr	9.61	10.28
G protein-coupled receptor, family C, group 5, member B	Gprc5b	9.41	10.53
glucagon receptor	Gcgr	9.28	8.77
coagulation factor II (thrombin) receptor-like 1	F2rl1	9.25	9.97
calcium-sensing receptor	Casr	9.16	9.42
endothelin receptor type B	Ednrb	9.01	9.35
prostaglandin E receptor 1 (subtype EP1)	Ptger1	8.85	9.43
parathyroid hormone 1 receptor	Pth1r	8.82	6.73
G protein-coupled receptor 108	Gpr108	8.81	9.05
G protein-coupled estrogen receptor 1	Gper	8.43	8.64
adrenergic receptor, beta 1	Adrb1	8.41	8.45
prostaglandin E receptor 4 (subtype EP4)	Ptger4	8.30	9.48
adrenergic receptor, beta 2	Adrb2	8.29	8.16
adrenergic receptor, alpha 2a	Adra2a	8.24	8.79
apelin receptor	Aplnr	8.24	7.45
sphingosine-1-phosphate receptor 3	S1pr3	8.23	9.32
smoothened homolog (Drosophila)	Smo	8.23	8.25
gamma-aminobutyric acid (GABA) B receptor, 1	Gabbr1	8.21	7.83
coagulation factor II (thrombin) receptor	F2r	8.16	7.94
adenosine A1 receptor	Adora1	8.14	9.81
G protein-coupled receptor 146	Gpr146	8.13	9.14
RIKEN cDNA 2310046K01 gene	2310046K01Rik	8.09	9.51
G protein-coupled receptor 89	Gpr89	8.09	8.50
cadherin, EGF LAG seven-pass G-type receptor 1	Celsr1	8.04	8.68
G protein-coupled receptor 172B	Gpr172b	8.03	7.91
latrophilin 1	Lphn1	7.96	8.60
G protein-coupled receptor 107	Gpr107	7.90	8.35
vomeronasal 2, receptor 29	Vmn2r29	7.84	7.37
EGF, latrophilin seven transmembrane domain containing 1	Eltd1	7.81	7.80
component of Sp100-rs /// predicted gene, EG665317	Csprs	7.59	7.04
G protein-coupled receptor 125	Gpr125	7.57	7.64
complement component 5a receptor 1	C5ar1	7.51	7.26
neuropeptide Y receptor Y6	Npy6r	7.44	8.96
vomeronasal 2, receptor 4	Vmn2r4	7.33	6.10
adrenergic receptor, alpha 2c	Adra2c	7.31	7.51
lysophosphatidic acid receptor 1	Lpar1	7.30	9.04
transducin (beta)-like 3	Tbl3	7.30	7.75
G protein-coupled receptor 126	Gpr126	7.18	9.40
progestin and adipoQ receptor family member VIII	Paqr8	7.13	8.07
KISS1 receptor	Kiss1r	7.12	6.37
CD97 antigen	Cd97	7.04	6.99

histamine receptor H2	Hrh2	7.01	6.49
purinergic receptor P2Y, G-protein coupled, 5	P2ry5	6.98	7.55
G protein-coupled receptor 63	Gpr63	6.97	7.96
calcitonin receptor-like	Calcrl	6.87	6.35
lysophosphatidic acid receptor 2	Lpar2	6.80	7.27
secretin receptor	Sctr	6.76	6.11
vomeronasal 1 receptor, D14	V1rd14	6.64	5.41*
purinergic receptor P2Y, G-protein coupled, 14	P2ry14	6.59	8.04
calcitonin gene-related peptide-receptor component protein	Crcp	6.56	6.83
sphingosine-1-phosphate receptor 4	S1pr4	6.41	5.83
G protein-coupled receptor 39	Gpr39	6.29	6.88
5-hydroxytryptamine (serotonin) receptor 1B	Htr1b	6.27	6.99
Melanin-concentrating hormone receptor 1 (Mchr1), mRNA	Mchr1	6.18	6.21
sphingosine-1-phosphate receptor 1	S1pr1	6.06	5.70*
G protein-coupled receptor 135	Gpr135	6.06	3.38*
opsin 3	Opn3	6.04	6.20
chemokine (C-C motif) receptor 5	Ccr5	5.99	4.76*
cannabinoid receptor 1 (brain)	Cnr1	5.95	5.03*
G protein-coupled receptor 97	Gpr97	5.94	6.67
G protein-coupled receptor 37	Gpr37	5.94	6.57
Bradykinin receptor, beta 2 (Bdkrb2), mRNA	Bdkrb2	5.87	5.73*
complement component 3a receptor 1	C3ar1	5.85	5.64*
G protein-coupled receptor 110	Gpr110	5.81	4.75*
G protein-coupled receptor 64	Gpr64	5.15*	6.46
purinergic receptor P2Y, G-protein coupled 2	P2ry2	4.86*	6.43

* - the A-value is below the cut-off level

Supplemental Table 2. Protein kinases

Gene Name	Gene Symbol	DCT/CNT A_Value	CCD A_Value
Table 5A. Serine/threonine kinases			
calcium/calmodulin-dependent protein kinase II, beta	Camk2b	12.95	13.41
PCTAIRE-motif protein kinase 1	Pctk1	12.51	12.68
WNK lysine deficient protein kinase 1	Wnk1	12.48	11.27
proviral integration site 3	Pim3	12.43	12.20
serum/glucocorticoid regulated kinase 1	Sgk1	11.98	12.86
mitogen-activated protein kinase kinase kinase 12	Map3k12	11.85	11.90
MAP kinase-interacting serine/threonine kinase 2	Mknk2	11.54	12.23
p21 (CDKN1A)-activated kinase 4	Pak4	11.53	12.31
AP2 associated kinase 1	Aak1	11.50	11.93
serum/glucocorticoid regulated kinase 2	Sgk2	11.42	10.91
TAO kinase 3	Taok3	11.34	10.85
glycogen synthase kinase 3 beta	Gsk3b	11.28	12.04
casein kinase 1, delta	Csnk1d	11.20	11.79
Rho-associated coiled-coil containing protein kinase 1	Rock1	11.13	11.28
mitogen-activated protein kinase-activated protein kinase 3	Mapkapk3	11.07	11.40
NIMA (never in mitosis gene a)-related expressed kinase 7	Nek7	11.02	11.20
casein kinase 1, alpha 1	Csnk1a1	11.01	11.56
WNK lysine deficient protein kinase 4	Wnk4	10.99	10.46
p21 (CDKN1A)-activated kinase 2	Pak2	10.91	11.60
pyruvate dehydrogenase kinase, isoenzyme 2	Pdk2	10.80	10.80
serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	Stk39	10.75	11.46
homeodomain interacting protein kinase 2	Hipk2	10.71	10.91
serine/threonine kinase 24 (STE20 homolog, yeast)	Stk24	10.58	11.01
mitogen-activated protein kinase 14	Mapk14	10.53	11.07
calcium/calmodulin-dependent protein kinase kinase 2, beta	Camkk2	10.40	11.59
mitogen-activated protein kinase kinase 7	Map2k7	10.35	10.47
CDC like kinase 4	Clk4	10.33	10.54
cyclin-dependent kinase-like 1 (CDC2-related kinase)	Cdkl1	10.29	11.16
STE20-like kinase (yeast)	Slk	10.28	11.05
mitogen-activated protein kinase kinase kinase 5	Map3k5	10.28	10.80
protein kinase N2	Pkn2	10.27	10.50
nemo like kinase	Nlk	10.26	10.87
bone morphogenetic protein receptor, type 1B	Bmpr1b	10.22	11.13
CDC-like kinase 3	Clk3	10.21	10.92
cyclin G associated kinase	Gak	10.18	10.61
protein kinase, AMP-activated, alpha 2 catalytic subunit	Prkaa2	10.18	10.61
MAPK scaffold protein 1	Mapksp1	10.10	10.30
protein kinase C, delta	Prkcd	10.09	10.58
pyruvate dehydrogenase kinase, isoenzyme 1	Pdk1	10.02	9.71
bone morphogenic protein receptor, type II (serine/threonine kinase)	Bmpr2	10.02	10.57
mitogen-activated protein kinase kinase kinase kinase 3	Map4k3	10.01	10.76
serine/threonine kinase 17b (apoptosis-inducing)	Stk17b	10.00	10.35
leucine-rich PPR-motif containing	Lrpprc	9.99	9.98
CDC42 binding protein kinase gamma (DMPK-like)	Cdc42bpg	9.96	10.60
tousled-like kinase 2 (Arabidopsis)	Tlk2	9.89	10.60
NIMA (never in mitosis gene a)-related expressed kinase 9	Nek9	9.88	10.46
CDC-like kinase 1	Clk1	9.87	10.79
protein kinase, X-linked	Prkx	9.85	10.42
casein kinase 2, alpha 1 polypeptide	Csnk2a1	9.83	10.37
homeodomain interacting protein kinase 3	Hipk3	9.81	10.10
serine/threonine kinase 38	Stk38	9.80	10.53

large tumor suppressor 2	Lats2	9.76	10.35
integrin linked kinase	Ilk	9.74	10.27
mitogen-activated protein kinase kinase kinase 3	Map3k3	9.72	9.88
nuclear receptor binding protein 2	Nrbp2	9.69	10.16
MAP/microtubule affinity-regulating kinase 2	Mark2	9.68	10.50
tousled-like kinase 1	Tlk1	9.68	9.92
mitogen-activated protein kinase kinase kinase 7	Map3k7	9.65	9.97
Rous sarcoma oncogene	Src	9.65	9.35
activin receptor IIA	Acvr2a	9.63	10.01
serine/arginine-rich protein specific kinase 1	Srpk1	9.61	9.89
homeodomain interacting protein kinase 1	Hipk1	9.58	10.66
SNF related kinase	Snrk	9.55	10.13
mitogen-activated protein kinase 3	Mapk3	9.54	9.97
adrenergic receptor kinase, beta 2	Adrbk2	9.52	9.68
similar to Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	Lyn	9.52	10.33
transforming growth factor, beta receptor II	Tgfbr2	9.50	10.89
translocated promoter region	Tpr	9.47	10.48
mitogen-activated protein kinase kinase kinase 1	Map3k1	9.45	10.45
CDC2-related kinase, arginine/serine-rich	Crkrs	9.42	9.95
serine/threonine kinase 3 (Ste20, yeast homolog)	Stk3	9.41	9.38
serine/threonine kinase 11	Stk11	9.40	10.54
mitogen-activated protein kinase kinase 2	Map2k2	9.35	9.68
protein kinase, cAMP dependent, catalytic, beta	Prkacb	9.33	9.32
mitogen-activated protein kinase 9	Mapk9	9.31	9.24
cyclin-dependent kinase 9 (CDC2-related kinase)	Cdk9	9.29	9.82
FK506 binding protein 12-rapamycin associated protein 1	Frap1	9.27	9.47
serine/threonine kinase 4	Stk4	9.27	9.70
protein kinase C, iota	Prkci	9.26	9.77
receptor-interacting serine-threonine kinase 4	Ripk4	9.24	9.53
3-phosphoinositide dependent protein kinase-1	Pdpk1	9.22	9.94
eukaryotic translation initiation factor 2-alpha kinase 2	Eif2ak2	9.22	9.28
PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Prpf4b	9.22	9.57
kinase insert domain protein receptor	Kdr	9.21	9.22
serine/threonine kinase 40	Stk40	9.18	9.28
interleukin-1 receptor-associated kinase 1	Irak1	9.18	9.07
oxidative-stress responsive 1	Oxsr1	9.12	10.15
conserved helix-loop-helix ubiquitous kinase	Chuk	9.12	9.97
v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	Erbb3	9.12	9.94
RIO kinase 2 (yeast)	Riok2	9.12	9.45
mitogen-activated protein kinase kinase kinase 2	Map3k2	9.10	9.49
plexin B1	Plxnb1	9.06	10.17
casein kinase 1, gamma 2	Csnk1g2	9.02	9.31
mitogen-activated protein kinase 6	Mapk6	9.01	9.66
protein kinase, cAMP dependent, catalytic, alpha	Prkaca	9.01	9.51
serum/glucocorticoid regulated kinase 3	Sgk3	8.98	8.57
cyclin-dependent kinase 7	Cdk7	8.97	9.02
pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	8.95	9.65
myosin, light polypeptide kinase	Mylk	8.95	10.12
mitogen-activated protein kinase kinase 1	Map2k1	8.94	9.34
protein kinase C, eta	Prkch	8.94	10.04
Unc-51 like kinase 1 (C. elegans)	Ulk1	8.94	9.03
plexin B2	Plxnb2	8.93	10.28
phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 4,p150	Pik3r4	8.93	9.38
kit oncogene	Kit	8.91	9.80
CDC-like kinase 2 /// secretory carrier membrane protein 3	Clk2 /Scamp3	8.86	9.21
RIO kinase 3 (yeast)	Riok3	8.86	9.31

Braf transforming gene	Braf	8.86	9.44
activin A receptor, type 1B	Acvr1b	8.85	9.04
large tumor suppressor	Lats1	8.85	9.49
TAO kinase 1	Taok1	8.85	9.61
testis-specific kinase 2	Tesk2	8.84	8.95
eukaryotic elongation factor-2 kinase	Eef2k	8.84	10.36
protein kinase D3	Prkd3	8.78	9.31
microtubule associated serine/threonine kinase 2	Mast2	8.76	9.13
dual serine/threonine and tyrosine protein kinase	Dstyk	8.75	9.44
TAF1 RNA polymerase II	Taf1	8.75	9.37
calcium/calmodulin-dependent protein kinase I	Camk1	8.74	9.21
CDC42 binding protein kinase alpha	Cdc42bpa	8.72	9.13
protein kinase C, alpha	Prkca	8.71	9.10
NUAK family, SNF1-like kinase, 2	Nuak2	8.71	10.00
protein kinase C, zeta	Prkcz	8.68	9.20
NIMA (never in mitosis gene a)-related expressed kinase 4	Nek4	8.68	8.76
eukaryotic translation initiation factor 2 alpha kinase 1	Eif2ak1	8.67	8.97
SH3-domain binding protein 4	Sh3bp4	8.66	9.12
doublecortin-like kinase 3	Dclk3	8.64	9.84
cyclin-dependent kinase 4	Cdk4	8.63	9.27
Yamaguchi sarcoma viral (v-yes) oncogene homolog 1	Yes1	8.62	9.07
mitogen-activated protein kinase 1	Mapk1	8.61	9.10
cDNA sequence BC033915	BC033915	8.61	8.75
TANK-binding kinase 1	Tbk1	8.61	9.01
serine/arginine-rich protein specific kinase 2	Srpk2	8.60	8.97
serine/threonine kinase 16	Stk16	8.59	8.90
pyruvate dehydrogenase kinase, isoenzyme 3	Pdk3	8.59	8.86
casein kinase 2, alpha prime polypeptide	Csnk2a2	8.59	9.20
Fyn proto-oncogene	Fyn	8.55	9.65
cyclin-dependent kinase (CDC2-like) 10	Cdk10	8.55	9.09
cell division cycle 2-like 1	Cdc2l1	8.54	9.16
cyclin-dependent kinase 6	Cdk6	8.53	8.98
death associated protein kinase 1	Dapk1	8.50	7.62
colony stimulating factor 1 receptor	Csf1r	8.48	8.46
Endoplasmic reticulum (ER) to nucleus signalling 1 (Ern1), mRNA	Ern1	8.48	8.49
cyclin-dependent kinase 8	Cdk8	8.42	8.45
MAP kinase-activated protein kinase 5	Mapkapk5	8.40	8.84
G protein-coupled receptor kinase 6	Grk6	8.40	8.08
salt inducible kinase 2	Sik2	8.39	8.62
mitogen-activated protein kinase kinase kinase kinase 4	Map4k4	8.37	8.48
ribosomal protein S6 kinase polypeptide 3	Rps6ka3	8.37	8.97
serine/threonine kinase 25 (yeast)	Stk25	8.35	9.60
v-raf murine sarcoma 3611 viral oncogene homolog	Araf	8.33	8.83
v-raf-leukemia viral oncogene 1	Raf1	8.32	8.67
RIKEN cDNA B230120H23 gene	B230120H23	8.32	8.90
mitogen-activated protein kinase kinase kinase 9	Map3k9	8.32	8.46
mitogen-activated protein kinase kinase kinase 4	Map3k4	8.32	8.89
glycogen synthase kinase 3 alpha	Gsk3a	8.31	8.61
cyclin-dependent kinase 5	Cdk5	8.30	8.76
proviral integration site 1	Pim1	8.28	9.18
ataxia telangiectasia mutated homolog (human)	Atm	8.27	9.11
mitogen-activated protein kinase kinase kinase kinase 5	Map4k5	8.24	8.59
protein serine kinase H1	Pskh1	8.21	8.38
microtubule associated serine/threonine kinase 3	Mast3	8.17	9.24
vaccinia related kinase 1	Vrk1	8.14	8.50
phosphorylase kinase, gamma 2 (testis)	Phkg2	8.14	8.37

protein kinase C, epsilon	Prkce	8.14	8.00
adrenergic receptor kinase, beta 1	Adrbk1	8.14	8.39
casein kinase 1, gamma 3	Csnk1g3	8.11	9.15
receptor (TNFRSF)-interacting serine-threonine kinase 1	Ripk1	8.06	8.45
mitogen-activated protein kinase kinase 3	Map2k3	8.02	8.32
membrane protein, palmitoylated	Mpp1	8.01	8.17
NIMA (never in mitosis gene a)-related expressed kinase 1	Nek1	8.01	8.68
WEE 1 homolog 1 (S. pombe)	Wee1	8.00	7.63
Fas-activated serine/threonine kinase	Fastk	7.99	8.56
inhibitor of kappaB kinase beta	Ikbkb	7.98	8.73
v-erb-b2 erythroblastic leukemia viral oncogene homolog 2	Erbb2	7.97	8.47
plexin A1	Plxna1	7.97	8.50
serine/threonine kinase 38 like	Stk38l	7.97	8.58
tribbles homolog 3 (Drosophila)	Trib3	7.97	7.93
cDNA sequence BC021891	BC021891	7.95	8.84
interleukin-1 receptor-associated kinase 4	Irak4	7.95	8.97
Rho-associated coiled-coil containing protein kinase 2	Rock2	7.94	8.76
vaccinia related kinase 3	Vrk3	7.93	8.23
mitogen-activated protein kinase kinase kinase 10	Map3k10	7.93	8.75
mitogen-activated protein kinase kinase 4	Map2k4	7.92	8.64
thymoma viral proto-oncogene 3	Akt3	7.92	8.15
Unc-51 like kinase 2 (C. elegans)	Ulk2	7.92	8.23
PCTAIRE-motif protein kinase 2	Pctk2	7.88	8.35
thymoma viral proto-oncogene 1	Akt1	7.87	8.69
tribbles homolog 1 (Drosophila)	Trib1	7.86	8.87
ribosomal protein S6 kinase polypeptide 1	Rps6ka1	7.82	8.69
v-abl Abelson murine leukemia viral oncogene homolog 2	Abl2	7.80	8.30
cyclin-dependent kinase-like 2 (CDC2-related kinase)	Cdkl2	7.79	8.11
protein kinase N3	Pkn3	7.76	7.46
leucine-rich repeat kinase 1	Lrrk1	7.76	8.62
PFTAIRE protein kinase 1	Pftk1	7.75	8.38
CDC42 binding protein kinase beta	Cdc42bpb	7.75	8.20
SMG1 homolog, phosphatidylinositol 3-kinase-related kinase	Smg1	7.73	8.39
BMP2 inducible kinase	Bmp2k	7.73	7.78
nuclear receptor binding protein 1	Nrbp1	7.65	8.00
testis specific protein kinase 1	Tesk1	7.65	8.38
salt inducible kinase 1	Sik1	7.64	7.16
branched chain ketoacid dehydrogenase kinase	Bckdk	7.63	8.01
LIM motif-containing protein kinase 2	Limk2	7.62	7.81
misshapen-like kinase 1 (zebrafish)	Mink1	7.60	7.70
ribosomal protein S6 kinase, polypeptide 1	Rps6kb1	7.60	8.16
thymoma viral proto-oncogene 2	Akt2	7.59	8.29
NIMA (never in mitosis gene a)-related expressed kinase 8	Nek8	7.53	8.34
calcium/calmodulin-dependent protein kinase II, delta	Camk2d	7.52	8.15
mitogen-activated protein kinase kinase kinase 11	Map3k11	7.51	7.86
serine/threonine kinase 32B	Stk32b	7.48	5.65
mitogen-activated protein kinase 13	Mapk13	7.46	8.18
RIKEN cDNA C230081A13 gene	C230081A13	7.43	8.41
G protein-coupled receptor kinase 5	Grk5	7.42	8.18
tau tubulin kinase 2	Ttbk2	7.41	7.71
cell division cycle 2-like 5	Cdc2l5	7.39	7.99
SPEG complex locus	Speg	7.38	6.90
mitogen-activated protein kinase kinase 6	Map2k6	7.37	7.61
mitogen-activated protein kinase kinase kinase kinase 2	Map4k2	7.36	8.01
vaccinia related kinase 2	Vrk2	7.34	8.10
MAP/microtubule affinity-regulating kinase 4	Mark4	7.34	7.79

SH3-binding kinase 1	Sbk1	7.28	7.06
mitogen-activated protein kinase 8	Mapk8	7.27	7.97
p21 (CDKN1A)-activated kinase 6	Pak6	7.26	8.86
Death-associated protein kinase 3 (Dapk3), mRNA	Dapk3	7.23	7.40
serine/threonine kinase 35	Stk35	7.21	7.24
ribosomal protein S6 kinase polypeptide 1	Rps6kc1	7.21	8.05
renal tumor antigen	Rage	7.21	7.51
NIMA (never in mitosis gene a)-related expressed kinase 6	Nek6	7.19	7.13
cell division cycle 2-like 6 (CDK8-like)	Cdc2l6	7.19	7.87
STE20-related kinase adaptor alpha	Strada	7.18	7.70
RIO kinase 1 (yeast)	Riok1	7.17	7.54
protein kinase, AMP-activated, alpha 1 catalytic subunit	Prkaa1	7.17	7.27
MAP kinase-interacting serine/threonine kinase 1	Mknk1	7.16	7.67
dystrophia myotonica-protein kinase	Dmpk	7.14	6.75
LIM-domain containing, protein kinase	Limk1	7.12	6.71
ribosomal protein S6 kinase, polypeptide 2	Rps6kb2	7.09	7.50
MAP kinase-activated protein kinase 2	Mapkapk2	7.09	7.69
serine/threonine kinase 10	Stk10	7.08	7.61
phosphorylase kinase gamma 1	Phkg1	7.08	8.63
PDLIM1 interacting kinase 1 like	Pdik1l	7.08	7.82
polo-like kinase 4 (Drosophila)	Plk4	7.04	6.75
casein kinase 1, gamma 1	Csnk1g1	6.99	7.54
ATM interactor	Atmin	6.99	7.62
mitogen-activated protein kinase kinase 5	Map2k5	6.94	7.37
plexin A2	Plxna2	6.92	6.12
protein kinase C, theta	Prkcq	6.90	8.32
STE20-related kinase adaptor beta	Stradb	6.86	7.08
protein kinase D2	Prkd2	6.80	7.49
cell division cycle 2 homolog A (S. pombe)	Cdc2a	6.80	6.65
activin A receptor, type II-like 1	Acvrl1	6.79	6.80
leucine-rich repeat kinase 2	Lrrk2	6.77	7.15
pigeon homolog (Drosophila)	Pion	6.76	6.24
casein kinase 1, epsilon	Csnk1e	6.69	7.31
cell division cycle 7 (S. cerevisiae)	Cdc7	6.69	6.12
unc-51-like kinase 3 (C. elegans)	Ulk3	6.67	6.14
MAP/microtubule affinity-regulating kinase 1	Mark1	6.67	6.41
kinase suppressor of ras 1	Ksr1	6.66	6.25
PCTAIRE-motif protein kinase 3	Pctk3	6.58	7.46
calcium/calmodulin-dependent protein kinase II alpha	Camk2a	6.56	5.99
mitogen-activated protein kinase kinase kinase 14	Map3k14	6.54	6.50
mitogen-activated protein kinase kinase kinase kinase 1	Map4k1	6.51	6.85
ribosomal protein S6 kinase, polypeptide 4	Rps6ka4	6.51	7.53
tribbles homolog 2 (Drosophila)	Trib2	6.50	6.28
mitogen-activated protein kinase 4	Mapk4	6.50	6.71
NUAK family, SNF1-like kinase, 1	Nuak1	6.50	6.67
protein kinase N1	Pkn1	6.49	6.29
microtubule associated serine/threonine kinase family member 4	Mast4	6.48	6.86
eukaryotic translation initiation factor 2 alpha kinase 4	Eif2ak4	6.46	7.40
receptor-interacting serine-threonine kinase 3	Ripk3	6.43	6.09
cyclin-dependent kinase 2	Cdk2	6.36	7.03
activin receptor IIB	Acvr2b	6.35	6.41
PDZ binding kinase	Pbk	6.35	6.15
ribosomal protein S6 kinase, polypeptide 5	Rps6ka5	6.34	6.73
microtubule associated serine/threonine kinase-like	Mastl	6.33	6.09
aurora kinase A	Aurka	6.30	6.21
plexin D1	Plxnd1	6.25	6.49

polo-like kinase 2 (Drosophila)	Plk2	6.21	7.35
protein kinase, cGMP-dependent, type II	Prkg2	6.21	5.04*
intestinal cell kinase	Ick	6.16	6.83
ribosomal protein S6 kinase, polypeptide 2	Rps6ka2	6.07	5.76*
budding uninhibited by benzimidazoles 1 homolog, beta	Bub1b	6.06	5.99
DnaJ (Hsp40) homolog, subfamily C, member 6	Dnajc6	6.05	4.44*
mitogen-activated protein kinase 12	Mapk12	6.05	6.93
citron	Cit	6.04	6.37
p21 (CDKN1A)-activated kinase 1	Pak1	6.03	6.19
anti-Mullerian hormone type 2 receptor	Amhr2	6.01	6.13
NIMA (never in mitosis gene a)-related expressed kinase 3	Nek3	6.00	6.67
protein kinase, DNA activated, catalytic polypeptide	Prkdc	5.99	7.21
WNK lysine deficient protein kinase 2	Wnk2	5.99	6.00
PAS domain containing serine/threonine kinase	Pask	5.93	5.75*
zeta-chain (TCR) associated protein kinase	Zap70	5.82	5.24*
testis-specific serine kinase 3	Tssk3	5.80	5.27*
plexin A4	Plxna4	5.72*	6.37
serine/threonine kinase 36 (fused homolog, Drosophila)	Stk36	5.65*	6.59
CHK2 checkpoint homolog (S. pombe)	Chek2	5.63*	6.46
G protein-coupled receptor kinase 4	Grk4	5.58*	5.84
calcium/calmodulin-dependent protein kinase IV	Camk4	5.48*	6.02
p21 (CDKN1A)-activated kinase 3	Pak3	5.47*	6.92
mitogen-activated protein kinase 11	Mapk11	4.83*	5.98

Table 5B. Non-receptor tyrosine kinases

fyn-related kinase	Frk	10.1	10.91
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	Dyrk1a	9.55	10.59
PTK2 protein tyrosine kinase 2	Ptk2	9.15	10.02
PTK2 protein tyrosine kinase 2 beta	Ptk2b	8.81	8.85
lemur tyrosine kinase 2	Lmtk2	8.73	9.99
fer (fms/fps related) protein kinase, testis specific 2	Fert2	8.73	9.47
Janus kinase 2	Jak2	8.66	9.12
Janus kinase 1	Jak1	8.46	9.24
tyrosine kinase, non-receptor, 1	Tnk1	8.25	8.78
FMS-like tyrosine kinase 1	Flt1	8.24	7.46
FMS-like tyrosine kinase 4	Flt4	8.18	7.82
tyrosine kinase, non-receptor, 2	Tnk2	7.83	8.34
tec protein tyrosine kinase	Tec	7.76	7.94
tyrosine kinase 2	Tyk2	7.18	7.53
c-mer proto-oncogene tyrosine kinase	Mertk	7.12	6.24
c-src tyrosine kinase	Csk	7.02	7.59
serine/threonine/tyrosine kinase 1	Styk1	6.99	8.85
PTK7 protein tyrosine kinase 7	Ptk7	6.53	6.49
Aatyk3 mRNA for apoptosis-associated tyrosine kinase 3	Lmtk3	6.29	6.04

Table 5C. Tyrosine kinase receptors

met proto-oncogene	Met	11.36	11.87
discoidin domain receptor family, member 1 receptor	Ddr1	11.35	11.45
fibroblast growth factor receptor 2	Fgfr2	10.31	11.30
insulin receptor	Insr	9.52	9.83
insulin receptor-related receptor	Insrr	9.50	10.06
insulin-like growth factor I receptor	Igf1r	9.04	9.99
endothelial-specific receptor tyrosine kinase	Tek	8.85	9.32
fibroblast growth factor receptor 1	Fgfr1	8.82	8.93
Eph receptor B4	Ephb4	8.63	8.87
receptor-like tyrosine kinase	Ryk	8.21	8.45

Eph receptor A1	Epha1	7.37	7.72
Eph receptor B2	Ephb2	7.14	7.07
fibroblast growth factor receptor 3	Fgfr3	7.04	7.03
epidermal growth factor receptor	Egfr	7.01	8.54
tyrosine kinase with immunoglobulin-like and EGF-like domains 1	Tie1	6.91	6.73
Eph receptor B3	Ephb3	6.63	6.11
c-abl oncogene 1, receptor tyrosine kinase	Abl1	6.62	7.24
AXL receptor tyrosine kinase	Axl	6.23	5.93
receptor tyrosine kinase-like orphan receptor 1	Ror1	5.84	6.21
Eph receptor A4	Epha4	5.74*	6.31
Eph receptor B6	Ephb6	5.20*	6.04
TXK tyrosine kinase	Txk	4.15*	5.80

* - the A-value is below the cut-off level

Supplemental Table 3. Protein phosphatases

Gene Name	Gene Symbol	DCT/CNT A_Value	CCD A_Value
Table 6A. Serine-threonine phosphatases			
protein phosphatase 2 (formerly 2A), alpha isoform	Ppp2r1a	12.51	12.72
protein phosphatase 1, catalytic subunit, gamma isoform	Ppp1cc	11.76	12.14
protein phosphatase 1, catalytic subunit, beta isoform	Ppp1cb	11.35	11.90
protein phosphatase 1, catalytic subunit, alpha isoform	Ppp1ca	11.17	11.79
protein phosphatase 1B, magnesium dependent, beta isoform	Ppm1b	11.15	11.49
protein phosphatase 1H (PP2C domain containing)	Ppm1h	10.87	11.35
protein phosphatase 2, alpha isoform	Ppp2r5a	10.85	11.19
protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	Ppp2ca	10.68	10.96
PTC7 protein phosphatase homolog (S. cerevisiae)	Pptc7	10.37	10.32
protein phosphatase 1A, magnesium dependent, alpha isoform	Ppm1a	10.20	10.66
protein phosphatase 1K (PP2C domain containing)	Ppm1k	10.13	10.67
protein phosphatase 2, epsilon isoform	Ppp2r5e	9.82	10.29
protein phosphatase 2 (formerly 2A), alpha isoform	Ppp2r2a	9.80	10.36
protein phosphatase 2, gamma isoform	Ppp2r5c	9.55	10.18
protein phosphatase 6, catalytic subunit	Ppp6c	9.55	9.76
protein phosphatase 2, regulatory subunit B, delta isoform	Ppp2r2d	9.44	9.41
protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	9.41	9.52
protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma is	Ppm1g	9.37	10.02
protein phosphatase 2 (formerly 2A), beta isoform	Ppp2r1b	9.25	9.58
protein phosphatase 5, catalytic subunit	Ppp5c	9.19	9.30
CTD (carboxy-terminal domain) phosphatase, subunit 1	Ctdp1	9.02	9.52
integrin-linked kinase-associated serine/threonine phosphatase 2C	Ilkap	8.94	9.78
protein phosphatase 3, catalytic subunit, beta isoform	Ppp3cb	8.89	9.20
protein phosphatase 1 (formerly 2C)-like	Ppm1l	8.78	9.20
protein phosphatase 4, regulatory subunit 1	Ppp4r1	8.50	9.01
protein phosphatase 3, regulatory subunit B, (calcineurin B, type I)	Ppp3r1	7.86	8.20
cell division cycle 25 homolog A (S. pombe)	Cdc25a	7.74	8.41
protein phosphatase 2C, magnesium dependent, catalytic subunit	Ppm2c	7.66	8.28
protein phosphatase 4, catalytic subunit	Ppp4c	7.42	8.27
cell division cycle 25 homolog B (S. pombe)	Cdc25b	7.14	6.99
protein phosphatase 3, catalytic subunit, gamma isoform	Ppp3cc	7.11	6.82
protein phosphatase 2, delta isoform	Ppp2r5d	6.74	7.43
protein phosphatase 2 (formerly 2A), beta isoform	Ppp2r2b	6.72	7.74
protein phosphatase 1M	Ppm1m	6.55	6.90
protein phosphatase 2 (formerly 2A), alpha	Ppp2r3a	6.10	7.20
protein phosphatase 2, beta isoform	Ppp2r5b	6.02	6.16
protein phosphatase 1F (PP2C domain containing)	Ppm1f	5.95	6.36
Table 6B. Tyrosine phosphatases			
acid phosphatase 1, soluble	Acp1	12.20	12.28
protein tyrosine phosphatase 4a2	Ptp4a2	11.67	12.30
protein tyrosine phosphatase, receptor type, F	Ptprf	10.74	11.32
protein tyrosine phosphatase, receptor type, J	Ptprj	10.60	11.51
protein tyrosine phosphatase, non-receptor type 11	Ptpn11	10.44	10.73
protein tyrosine phosphatase, receptor type, S	Ptprs	10.26	10.29
protein tyrosine phosphatase, non-receptor type 1	Ptpn1	9.40	9.53
protein tyrosine phosphatase, non-receptor type 2	Ptpn2	9.26	9.67
protein tyrosine phosphatase, receptor type, K	Ptprk	9.11	9.22
protein tyrosine phosphatase, receptor type, A	Ptpra	8.96	9.64
protein tyrosine phosphatase, non-receptor type 9	Ptpn9	8.95	9.38
protein tyrosine phosphatase, mitochondrial 1	Ptpmt1	8.88	8.98

protein tyrosine phosphatase, non-receptor type 13	Ptpn13	8.83	9.61
protein tyrosine phosphatase, non-receptor type 14	Ptpn14	8.75	9.59
similar to protein tyrosine phosphatase, receptor type, G	Ptprg	8.53	7.55
protein tyrosine phosphatase, receptor type, D	Ptprd	8.48	8.11
protein tyrosine phosphatase, receptor type, C	Ptprc	8.36	8.46
protein tyrosine phosphatase, receptor type, M	Ptprm	8.36	8.97
protein tyrosine phosphatase, non-receptor type 21	Ptpn21	8.13	8.83
protein tyrosine phosphatase, receptor type, G	Ptprg	7.91	8.01
protein tyrosine phosphatase, non-receptor type 18	Ptpn18	7.86	8.59
protein tyrosine phosphatase, non-receptor type 23	Ptpn23	7.62	8.04
protein tyrosine phosphatase, non-receptor type 12	Ptpn12	7.35	7.75
protein tyrosine phosphatase, non-receptor type 6	Ptpn6	7.28	7.21
protein tyrosine phosphatase, receptor type, U	Ptpru	6.86	6.92
protein tyrosine phosphatase domain containing 1	Ptpdc1	6.73	6.97
protein tyrosine phosphatase 4a3	Ptp4a3	6.10	6.19
protein tyrosine phosphatase, receptor type, E	Ptpre	5.90	6.32

Table 6C. Dual-specificity phosphatases

dual specificity phosphatase 1	Dusp1	11.46	11.73
dual specificity phosphatase 3	Dusp3	10.47	10.92
slingshot homolog 1 (Drosophila)	Ssh1	9.19	9.73
dual specificity phosphatase 16	Dusp16	8.91	9.64
CDC14 cell division cycle 14 homolog A (S. cerevisiae)	Cdc14a	8.68	9.04
dual specificity phosphatase 19	Dusp19	8.40	9.32
dual specificity phosphatase 22	Dusp22	8.02	8.08
dual specificity phosphatase 6	Dusp6	7.69	7.86
dual specificity phosphatase 7	Dusp7	7.49	8.11
CDC14 cell division cycle 14 homolog B (S. cerevisiae)	Cdc14b	7.41	8.17
dual specificity phosphatase 23	Dusp23	7.40	7.18
dual specificity phosphatase 26 (putative)	Dusp26	7.30	6.08
dual specificity phosphatase 12	Dusp12	7.28	7.84
slingshot homolog 2 (Drosophila)	Ssh2	7.06	7.57
dual specificity phosphatase 28	Dusp28	7.04	7.04
dual specificity phosphatase 18	Dusp18	6.92	6.69
slingshot homolog 2 (Drosophila)	Ssh2	6.58	7.73
dual specificity phosphatase 8	Dusp8	6.41	6.54
slingshot homolog 3 (Drosophila)	Ssh3	6.39	6.72
dual specificity phosphatase 4	Dusp4	6.28	5.61*
epilepsy, progressive myoclonic epilepsy, type 2 gene alpha	Epm2a	6.04	6.16
dual specificity phosphatase 10	Dusp10	5.88	6.40

* - the A-value is below the cut-off level

Supplemental Table 4. Small GTPases

Gene Name	Gene Symbol	DCT/CNT A_Value	CCD A_Value
Table 9A. Rab small GTP-binding proteins			
RAB1, member RAS oncogene family	Rab1	12.58	12.82
RAB14, member RAS oncogene family	Rab14	11.96	12.08
RAB7, member RAS oncogene family	Rab7	11.69	12.07
RAB10, member RAS oncogene family	Rab10	11.68	11.85
RAB2A, member RAS oncogene family	Rab2a	11.67	11.90
RAB21, member RAS oncogene family	Rab21	11.29	11.53
RAB18, member RAS oncogene family	Rab18	10.68	11.30
RAB11a, member RAS oncogene family	Rab11a	10.44	10.77
RAB28, member RAS oncogene family	Rab28	10.41	11.10
RAB22A, member RAS oncogene family	Rab22a	10.23	10.42
RAB9, member RAS oncogene family	Rab9	9.98	10.24
RAB4A, member RAS oncogene family	Rab4a	9.94	10.23
RAB11B, member RAS oncogene family	Rab11b	9.83	10.88
RAB17, member RAS oncogene family	Rab17	9.74	10.19
RAB6B, member RAS oncogene family	Rab6b	9.73	10.27
RAB25, member RAS oncogene family	Rab25	9.61	10.31
RAB6, member RAS oncogene family	Rab6	9.60	9.96
RAB20, member RAS oncogene family	Rab20	9.54	10.82
RAB5A, member RAS oncogene family	Rab5a	9.48	10.06
RAB5B, member RAS oncogene family	Rab5b	9.46	10.01
RAB15, member RAS oncogene family	Rab15	9.35	10.12
RAB3A, member RAS oncogene family	Rab3a	9.16	8.83
RAB8A, member RAS oncogene family	Rab8a	9.14	9.39
RAB33B, member of RAS oncogene family	Rab33b	9.05	9.66
RAB35, member RAS oncogene family	Rab35	9.01	9.42
RAB24, member RAS oncogene family	Rab24	8.88	9.37
RAB, member of RAS oncogene family-like 3	Rabl3	8.83	8.94
RAB8B, member RAS oncogene family	Rab8b	8.80	9.40
RAB27A, member RAS oncogene family	Rab27a	8.70	7.01
RAB12, member RAS oncogene family	Rab12	8.58	9.09
RAB, member of RAS oncogene family-like 2A	Rabl2a	8.33	8.47
Rab40c, member RAS oncogene family	Rab40c	8.28	8.38
RAB5C, member RAS oncogene family	Rab5c	8.23	8.05
RAB, member of RAS oncogene family-like 4	Rabl4	8.08	8.41
RAB31, member RAS oncogene family	Rab31	8.02	8.04
RAB39B, member RAS oncogene family	Rab39b	7.87	8.02
RAB34, member of RAS oncogene family	Rab34	7.85	7.66
RAB1B, member RAS oncogene family	Rab1b	7.79	8.09
RAB23, member RAS oncogene family	Rab23	7.67	8.04
RAB13, member RAS oncogene family	Rab13	7.66	8.08
RAB7, member RAS oncogene family-like 1	Rab7l1	7.46	8.09
RAB3D, member RAS oncogene family	Rab3d	7.41	8.46
RAB4B, member RAS oncogene family	Rab4b	7.38	7.85
RAB27b, member RAS oncogene family	Rab27b	7.35	7.86
RAB19, member RAS oncogene family	Rab19	7.13	7.69
RAB43, member RAS oncogene family	Rab43	6.79	7.17
RAB2B, member RAS oncogene family	Rab2b	6.63	7.24
RAB32, member RAS oncogene family	Rab32	6.55	7.45
RAB38, member of RAS oncogene family	Rab38	6.38	6.71
Rab40b, member RAS oncogene family	Rab40b	6.33	6.98
TBC1 domain family, member 7	Tbc1d7	6.30	6.73

RAB36, member RAS oncogene family	Rab36	5.87	6.21

Table 9B. Arf small GTP-binding proteins

ADP-ribosylation factor 6	Arf6	12.58	13.00
ADP-ribosylation factor 1	Arf1	11.89	11.93
ADP-ribosylation factor 3	Arf3	11.64	12.25
ADP-ribosylation factor-like 1	Arl1	11.61	11.94
ADP-ribosylation factor-like 3	Arl3	11.46	11.73
SAR1 gene homolog A (S. cerevisiae)	Sar1a	11.46	12.09
SAR1 gene homolog B (S. cerevisiae)	Sar1b	10.69	11.12
ADP-ribosylation factor 4	Arf4	10.48	10.99
ADP-ribosylation factor-like 4C	Arl4c	10.07	9.25
ADP-ribosylation factor-like 5A	Arl5a	9.72	10.22
ADP-ribosylation factor-like 8B	Arl8b	9.53	10.18
ADP-ribosylation factor-like 4A	Arl4a	9.18	9.27
ADP-ribosylation factor related protein 1	Arfrp1	9.05	9.73
ADP-ribosylation factor-like 6	Arl6	8.90	9.54
ADP-ribosylation factor-like 8A	Arl8a	8.87	9.33
ADP-ribosylation factor 2	Arf2	8.52	9.15
ADP-ribosylation factor-like 2	Arl2	7.85	8.20
ADP-ribosylation factor-like 4D	Arl4d	7.38	9.24
ADP-ribosylation factor-like 5B	Arl5b	7.17	7.52
tripartite motif-containing 23	Trim23	6.07	6.90
ADP-ribosylation factor-like 10	Arl10	5.49*	6.61

Table 9C. Rho small GTP-binding proteins

cell division cycle 42 homolog (S. cerevisiae)	Cdc42	12.89	12.74
ras homolog gene family, member A	Rhoa	11.66	11.84
RAS-related C3 botulinum substrate 1	Rac1	11.32	11.81
ras homolog gene family, member B	Rhob	9.80	10.14
ras homolog gene family, member U	Rhou	9.77	10.58
ras homolog gene family, member Q	Rhoq	8.74	9.34
Rho family GTPase 3	Rnd3	8.16	9.13
ras homolog gene family, member T2	Rhot2	8.06	8.88
ras homolog gene family, member T1	Rhot1	8.05	8.84
Rho-related BTB domain containing 1	Rhobtb1	7.44	8.02
Rho-related BTB domain containing 2	Rhobtb2	7.39	7.54
ras homolog gene family, member C	Rhoc	7.35	8.05
Rho family GTPase 2	Rnd2	7.18	7.67
ras homolog gene family, member D	Rhod	6.74	7.87
ras homolog gene family, member J	Rhoj	6.70	6.50
Rho-related BTB domain containing 3	Rhobtb3	6.63	7.56
ras homolog gene family, member G	Rhog	5.83	6.67
RAS-related C3 botulinum substrate 3	Rac3	5.71*	6.03

Table 9D. Ras and Ras-related small GTP-binding proteins

Ras-related GTP binding D	Rragd	12.40	12.60
RAS related protein 1b	Rap1b	10.75	11.28
RAS-related protein-1a	Rap1a	10.33	10.80
v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	Kras	10.32	10.57
RAN, member RAS oncogene family	Ran	9.81	10.39
v-ral simian leukemia viral oncogene homolog A (ras related)	Rala	9.34	9.79
Harvey rat sarcoma virus oncogene 1	Hras1	9.18	9.21
Ras-related GTP binding C	Rragc	9.14	9.67
v-ral simian leukemia viral oncogene homolog B (ras related)	Ralb	9.08	10.30
neuroblastoma ras oncogene	Nras	9.02	9.38

NFKB inhibitor interacting Ras-like protein 1	Nkiras1	8.78	9.10
Ras-related GTP binding A	Rraga	8.50	8.68
RAS related protein 2a	Rap2a	8.24	8.82
RAP2B, member of RAS oncogene family	Rap2b	8.20	9.23
Harvey rat sarcoma oncogene, subgroup R	Rras	8.04	8.51
Ras-like without CAAX 1	Rit1	7.79	8.31
RAS-like, family 11, member B	Rasl11b	7.73	9.02
muscle and microspikes RAS	Mras	7.64	7.79
NFKB inhibitor interacting Ras-like protein 2	Nkiras2	7.60	7.79
RAS, dexamethasone-induced 1	Rasd1	7.40	7.76
related RAS viral (r-ras) oncogene homolog 2	Rras2	7.40	8.50
Ras-related associated with diabetes	Rrad	6.87	8.55
RASD family, member 2	Rasd2	6.59	7.38
RAS and EF hand domain containing	Rasef	6.04	6.66
GTP binding protein (gene overexpressed in skeletal muscle)	Gem	5.96	6.32
RAS-like, family 2, locus 9	Rasl2-9	5.69*	6.29
RAS-like, family 11, member A	Rasl11a	5.09*	7.22

* - the A-value is below the cut-off level

Supplemental Table 4. Small GTPases

Gene Name	Gene Symbol	DCT/CNT A_Value	CCD A_Value
Table 9A. Rab small GTP-binding proteins			
RAB1, member RAS oncogene family	Rab1	12.58	12.82
RAB14, member RAS oncogene family	Rab14	11.96	12.08
RAB7, member RAS oncogene family	Rab7	11.69	12.07
RAB10, member RAS oncogene family	Rab10	11.68	11.85
RAB2A, member RAS oncogene family	Rab2a	11.67	11.90
RAB21, member RAS oncogene family	Rab21	11.29	11.53
RAB18, member RAS oncogene family	Rab18	10.68	11.30
RAB11a, member RAS oncogene family	Rab11a	10.44	10.77
RAB28, member RAS oncogene family	Rab28	10.41	11.10
RAB22A, member RAS oncogene family	Rab22a	10.23	10.42
RAB9, member RAS oncogene family	Rab9	9.98	10.24
RAB4A, member RAS oncogene family	Rab4a	9.94	10.23
RAB11B, member RAS oncogene family	Rab11b	9.83	10.88
RAB17, member RAS oncogene family	Rab17	9.74	10.19
RAB6B, member RAS oncogene family	Rab6b	9.73	10.27
RAB25, member RAS oncogene family	Rab25	9.61	10.31
RAB6, member RAS oncogene family	Rab6	9.60	9.96
RAB20, member RAS oncogene family	Rab20	9.54	10.82
RAB5A, member RAS oncogene family	Rab5a	9.48	10.06
RAB5B, member RAS oncogene family	Rab5b	9.46	10.01
RAB15, member RAS oncogene family	Rab15	9.35	10.12
RAB3A, member RAS oncogene family	Rab3a	9.16	8.83
RAB8A, member RAS oncogene family	Rab8a	9.14	9.39
RAB33B, member of RAS oncogene family	Rab33b	9.05	9.66
RAB35, member RAS oncogene family	Rab35	9.01	9.42
RAB24, member RAS oncogene family	Rab24	8.88	9.37
RAB, member of RAS oncogene family-like 3	Rabl3	8.83	8.94
RAB8B, member RAS oncogene family	Rab8b	8.80	9.40
RAB27A, member RAS oncogene family	Rab27a	8.70	7.01
RAB12, member RAS oncogene family	Rab12	8.58	9.09
RAB, member of RAS oncogene family-like 2A	Rabl2a	8.33	8.47
Rab40c, member RAS oncogene family	Rab40c	8.28	8.38
RAB5C, member RAS oncogene family	Rab5c	8.23	8.05
RAB, member of RAS oncogene family-like 4	Rabl4	8.08	8.41
RAB31, member RAS oncogene family	Rab31	8.02	8.04
RAB39B, member RAS oncogene family	Rab39b	7.87	8.02
RAB34, member of RAS oncogene family	Rab34	7.85	7.66
RAB1B, member RAS oncogene family	Rab1b	7.79	8.09
RAB23, member RAS oncogene family	Rab23	7.67	8.04
RAB13, member RAS oncogene family	Rab13	7.66	8.08
RAB7, member RAS oncogene family-like 1	Rab7l1	7.46	8.09
RAB3D, member RAS oncogene family	Rab3d	7.41	8.46
RAB4B, member RAS oncogene family	Rab4b	7.38	7.85
RAB27b, member RAS oncogene family	Rab27b	7.35	7.86
RAB19, member RAS oncogene family	Rab19	7.13	7.69
RAB43, member RAS oncogene family	Rab43	6.79	7.17
RAB2B, member RAS oncogene family	Rab2b	6.63	7.24
RAB32, member RAS oncogene family	Rab32	6.55	7.45
RAB38, member of RAS oncogene family	Rab38	6.38	6.71
Rab40b, member RAS oncogene family	Rab40b	6.33	6.98
TBC1 domain family, member 7	Tbc1d7	6.30	6.73

RAB36, member RAS oncogene family	Rab36	5.87	6.21

Table 9B. Arf small GTP-binding proteins

ADP-ribosylation factor 6	Arf6	12.58	13.00
ADP-ribosylation factor 1	Arf1	11.89	11.93
ADP-ribosylation factor 3	Arf3	11.64	12.25
ADP-ribosylation factor-like 1	Arl1	11.61	11.94
ADP-ribosylation factor-like 3	Arl3	11.46	11.73
SAR1 gene homolog A (S. cerevisiae)	Sar1a	11.46	12.09
SAR1 gene homolog B (S. cerevisiae)	Sar1b	10.69	11.12
ADP-ribosylation factor 4	Arf4	10.48	10.99
ADP-ribosylation factor-like 4C	Arl4c	10.07	9.25
ADP-ribosylation factor-like 5A	Arl5a	9.72	10.22
ADP-ribosylation factor-like 8B	Arl8b	9.53	10.18
ADP-ribosylation factor-like 4A	Arl4a	9.18	9.27
ADP-ribosylation factor related protein 1	Arfrp1	9.05	9.73
ADP-ribosylation factor-like 6	Arl6	8.90	9.54
ADP-ribosylation factor-like 8A	Arl8a	8.87	9.33
ADP-ribosylation factor 2	Arf2	8.52	9.15
ADP-ribosylation factor-like 2	Arl2	7.85	8.20
ADP-ribosylation factor-like 4D	Arl4d	7.38	9.24
ADP-ribosylation factor-like 5B	Arl5b	7.17	7.52
tripartite motif-containing 23	Trim23	6.07	6.90
ADP-ribosylation factor-like 10	Arl10	5.49*	6.61

Table 9C. Rho small GTP-binding proteins

cell division cycle 42 homolog (S. cerevisiae)	Cdc42	12.89	12.74
ras homolog gene family, member A	Rhoa	11.66	11.84
RAS-related C3 botulinum substrate 1	Rac1	11.32	11.81
ras homolog gene family, member B	Rhob	9.80	10.14
ras homolog gene family, member U	Rhou	9.77	10.58
ras homolog gene family, member Q	Rhoq	8.74	9.34
Rho family GTPase 3	Rnd3	8.16	9.13
ras homolog gene family, member T2	Rhot2	8.06	8.88
ras homolog gene family, member T1	Rhot1	8.05	8.84
Rho-related BTB domain containing 1	Rhobtb1	7.44	8.02
Rho-related BTB domain containing 2	Rhobtb2	7.39	7.54
ras homolog gene family, member C	Rhoc	7.35	8.05
Rho family GTPase 2	Rnd2	7.18	7.67
ras homolog gene family, member D	Rhod	6.74	7.87
ras homolog gene family, member J	Rhoj	6.70	6.50
Rho-related BTB domain containing 3	Rhobtb3	6.63	7.56
ras homolog gene family, member G	Rhog	5.83	6.67
RAS-related C3 botulinum substrate 3	Rac3	5.71*	6.03

Table 9D. Ras and Ras-related small GTP-binding proteins

Ras-related GTP binding D	Rragd	12.40	12.60
RAS related protein 1b	Rap1b	10.75	11.28
RAS-related protein-1a	Rap1a	10.33	10.80
v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	Kras	10.32	10.57
RAN, member RAS oncogene family	Ran	9.81	10.39
v-ral simian leukemia viral oncogene homolog A (ras related)	Rala	9.34	9.79
Harvey rat sarcoma virus oncogene 1	Hras1	9.18	9.21
Ras-related GTP binding C	Rragc	9.14	9.67
v-ral simian leukemia viral oncogene homolog B (ras related)	Ralb	9.08	10.30
neuroblastoma ras oncogene	Nras	9.02	9.38

NFKB inhibitor interacting Ras-like protein 1	Nkiras1	8.78	9.10
Ras-related GTP binding A	Rraga	8.50	8.68
RAS related protein 2a	Rap2a	8.24	8.82
RAP2B, member of RAS oncogene family	Rap2b	8.20	9.23
Harvey rat sarcoma oncogene, subgroup R	Rras	8.04	8.51
Ras-like without CAAX 1	Rit1	7.79	8.31
RAS-like, family 11, member B	Rasl11b	7.73	9.02
muscle and microspikes RAS	Mras	7.64	7.79
NFKB inhibitor interacting Ras-like protein 2	Nkiras2	7.60	7.79
RAS, dexamethasone-induced 1	Rasd1	7.40	7.76
related RAS viral (r-ras) oncogene homolog 2	Rras2	7.40	8.50
Ras-related associated with diabetes	Rrad	6.87	8.55
RASD family, member 2	Rasd2	6.59	7.38
RAS and EF hand domain containing	Rasef	6.04	6.66
GTP binding protein (gene overexpressed in skeletal muscle)	Gem	5.96	6.32
RAS-like, family 2, locus 9	Rasl2-9	5.69*	6.29
RAS-like, family 11, member A	Rasl11a	5.09*	7.22

* - the A-value is below the cut-off level

Supplemental Table 5. SNAREs

Gene Name	Gene Symbol	DCT/CNT A_Value	CCD A_Value
vesicle-associated membrane protein 2	Vamp2	11.74	11.38
vesicle-associated membrane protein 8	Vamp8	11.66	12.03
synaptosomal-associated protein 23	Snap23	11.50	11.72
synaptosomal-associated protein, 47	Snap47	11.19	11.51
vesicle transport through interaction with t-SNAREs 1B homolog	Vti1b	10.68	10.94
syntaxin 7	Stx7	10.64	11.30
vesicle-associated membrane protein 3	Vamp3	10.55	10.89
syntaxin 8	Stx8	10.40	11.16
SNAP-associated protein	Snapap	10.18	10.61
YKT6 homolog (S. Cerevisiae)	Ykt6	9.73	10.37
syntaxin 3	Stx3	9.60	10.30
syntaxin 4A (placental)	Stx4a	9.49	9.99
syntaxin 12	Stx12	9.47	10.30
blocked early in transport 1 homolog (S. cerevisiae)-like	Bet1l	9.38	9.35
golgi SNAP receptor complex member 1	Gosr1	9.37	9.75
SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	Sec22b	9.35	9.73
syntaxin 16	Stx16	9.04	9.23
blocked early in transport 1 homolog (S. cerevisiae)	Bet1	9.02	9.64
golgi SNAP receptor complex member 2	Gosr2	8.85	8.65
vesicle-associated membrane protein 4	Vamp4	8.63	8.80
syntaxin 17	Stx17	8.56	9.00
vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	Vti1a	8.43	8.76
syntaxin 5A	Stx5a	8.39	9.16
vesicle-associated membrane protein 7	Vamp7	8.11	9.09
syntaxin 6	Stx6	7.77	8.33
syntaxin 18	Stx18	7.72	8.17
syntaxin 6	Stx6	7.69	8.65
SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	Sec22c	7.55	8.30
synaptosomal-associated protein 29	Snap29	7.47	8.08
vesicle-associated membrane protein 1	Vamp1	6.75	6.64

Supplemental Table 6. Cytoskeleton and cytoskeleton-related proteins

Gene Name	Gene Symbol	DCT/CNT A_Value	CCD A_Value
Table 12A. Actin and actin-binding proteins			
actin, beta	Actb	13.35	13.80
cofilin 1, non-muscle	Cfl1	12.96	12.98
actin, gamma, cytoplasmic 1	Actg1	12.93	13.06
catenin (cadherin associated protein), beta 1	Ctnnb1	12.74	13.26
syndecan 4	Sdc4	12.61	12.99
catenin (cadherin associated protein), alpha 1	Ctnna1	12.59	13.02
tropomyosin 1, alpha	Tpm1	12.30	12.87
Wiskott-Aldrich syndrome-like (human)	Wasl	11.90	12.81
spectrin beta 2	Spnb2	11.76	12.23
LIM and SH3 protein 1	Lasp1	11.67	11.83
cingulin-like 1	Cgnl1	11.56	12.13
ARP2 actin-related protein 2 homolog (yeast)	Actr2	11.49	12.01
tensin 1	Tns1	11.47	11.85
gelsolin	Gsn	11.37	12.06
cortactin	Cttn	11.33	12.17
cysteine and glycine-rich protein 1	Csrp1	11.18	11.75
cofilin 2, muscle	Cfl2	11.13	11.49
utrophin	Utrn	11.12	12.18
radixin	Rdx	11.11	11.24
tensin 3	Tns3	11.03	11.71
actin related protein 2/3 complex, subunit 3	Arpc3	10.96	11.35
adducin 1 (alpha)	Add1	10.85	11.48
ARP3 actin-related protein 3 homolog (yeast)	Actr3	10.84	11.50
tropomodulin 1	Tmod1	10.80	10.99
shroom family member 3	Shroom3	10.80	11.08
ezrin	Ezr	10.69	11.19
capping protein (actin filament) muscle Z-line, beta	Capzb	10.68	11.15
junction plakoglobin	Jup	10.65	10.97
formin binding protein 1-like	Fnbp1l	10.64	11.61
filamin, beta	Flnb	10.62	10.73
cysteine and glycine-rich protein 2	Csrp2	10.55	11.02
LIM domain and actin binding 1	Lima1	10.51	10.67
Coronin, actin binding protein 1C, mRNA	Coro1c	10.49	10.96
spire homolog 1 (Drosophila)	Spire1	10.48	10.34
actin-binding LIM protein 1	Ablim1	10.35	10.93
kelch domain containing 8A	Klhdc8a	10.34	11.75
PDZ and LIM domain 5	Pdlim5	10.30	10.26
LIM domain containing preferred translocation partner in lipoma	Lpp	10.27	11.27
huntingtin interacting protein 1 related	Hip1r	10.22	10.43
tropomyosin 3, gamma	Tpm3	10.19	10.92
capping protein (actin filament) muscle Z-line, alpha 2	Capza2	10.16	10.53
paxillin	Pxn	10.16	11.18
actin related protein 2/3 complex, subunit 5-like	Arpc5l	10.15	10.56
enabled homolog (Drosophila)	Enah	10.11	11.08
microtubule-actin crosslinking factor 1	Macf1	10.00	10.86
actin related protein 2/3 complex, subunit 5	Arpc5	9.96	10.56
ankyrin 3, epithelial	Ank3	9.92	9.74
sorbin and SH3 domain containing 2	Sorbs2	9.91	10.94
dystrophin, muscular dystrophy	Dmd	9.90	10.53
twinfilin, actin-binding protein, homolog 1 (Drosophila)	Twf1	9.89	10.93
ARP10 actin-related protein 10 homolog (S. cerevisiae)	Actr10	9.81	10.22

actin related protein 2/3 complex, subunit 4	Arpc4	9.81	10.97
actin related protein 2/3 complex, subunit 1B	Arpc1b	9.75	10.80
kelch-like 2, Mayven (Drosophila)	Klhl2	9.70	10.26
ectodermal-neural cortex 1	Enc1	9.69	10.20
syndecan 2	Sdc2	9.68	10.36
parvin, alpha	Parva	9.58	10.30
ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	Actr1a	9.57	10.16
vinculin	Vcl	9.51	9.87
myeloid/lymphoid or mixed-lineage leukemia, translocated to, 4	Mllt4	9.51	10.07
capping protein (actin filament) muscle Z-line, alpha 1	Capza1	9.48	9.87
talin 1	Tln1	9.48	10.01
adducin 3 (gamma)	Add3	9.46	9.19
septin 10	sept.10	9.41	9.60
actinin alpha 4	Actn4	9.38	10.09
syndecan 1	Sdc1	9.36	9.47
ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	Actr1b	9.30	9.45
stomatin (Epb7.2)-like 2	Stoml2	9.23	9.55
twinfilin, actin-binding protein, homolog 2 (Drosophila)	Twf2	9.16	9.13
septin 7	07.sept	9.15	9.67
catenin (cadherin associated protein), alpha-like 1	Ctnnal1	9.11	9.79
ARP8 actin-related protein 8 homolog (S. cerevisiae)	Actr8	9.09	9.58
septin 9	septin 9	9.08	9.74
tropomyosin 4	Tpm4	9.07	9.80
erythrocyte protein band 4.9	Epb4.9	8.99	9.10
actin related protein 2/3 complex, subunit 1A	Arpc1a	8.92	10.23
drebrin-like	Dbnl	8.89	9.21
synaptopodin	Synpo	8.84	9.01
actinin, alpha 1	Actn1	8.81	9.52
spectrin beta 3	Spnb3	8.79	10.27
coronin, actin binding protein 2A	Coro2a	8.75	8.91
WAS protein family, member 2	Wasf2	8.71	9.64
plectin 1	Plec1	8.71	9.47
moesin	Msn	8.64	8.03
caldesmon 1	Cald1	8.60	9.18
tropomodulin 3	Tmod3	8.55	9.06
septin 2	septin 2	8.53	9.58
spire homolog 2 (Drosophila)	Spire2	8.41	8.88
PDZ and LIM domain 3	Pdlim3	8.34	8.33
coronin, actin binding protein 1B	Coro1b	8.30	9.52
transgelin 2	Tagln2	8.22	8.76
septin 4	septin 4	8.16	8.42
fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	Fscn1	8.06	8.45
tropomyosin 2, beta	Tpm2	7.99	6.42
formin binding protein 1	Fnbp1	7.96	8.58
huntingtin interacting protein 1	Hip1	7.87	8.31
coronin 7	Coro7	7.86	8.58
septin 11	septin 11	7.82	8.63
formin binding protein 4	Fnbp4	7.77	8.38
calponin 2	Cnn2	7.77	9.10
talin 2	Tln2	7.76	7.78
actin-like 6A	Actl6a	7.75	8.10
sorbin and SH3 domain containing 1	Sorbs1	7.69	7.77
kelch-like 12 (Drosophila)	Klhl12	7.66	7.92
filamin, alpha	Flna	7.62	8.41
actin, alpha 2, smooth muscle, aorta	Acta2	7.59	6.16
drebrin 1	Dbn1	7.51	7.58

actin-binding LIM protein 2	Ablim2	7.48	7.16
septin 6	septin 6	7.47	6.87
kelch-like 17 (Drosophila)	Klhl17	7.43	7.62
kelch-like 18 (Drosophila)	Klhl18	7.38	7.17
transgelin	Tagln	7.36	6.92
nebulin-related anchoring protein	Nrap	7.32	6.81
septin 8	septin 8	7.29	8.11
formin-like 2	Fmnl2	7.22	8.48
synaptopodin 2-like	Synpo2l	7.18	7.11
coronin, actin binding protein 1A	Coro1a	7.16	7.30
espin	Espn	7.12	7.11
kelch-like 20 (Drosophila)	Klhl20	7.10	7.60
kelch-like 25 (Drosophila)	Klhl25	7.10	7.54
syntrophin, acidic 1	Snta1	7.08	7.62
zyxin	Zyx	6.97	7.90
actinin alpha 2	Actn2	6.96	7.30
kelch-like 7 (Drosophila)	Klhl7	6.96	8.00
sorbin and SH3 domain containing 3	Sorbs3	6.95	7.58
capping protein (actin filament), gelsolin-like	Capg	6.91	9.04
whirlin	Whrn	6.89	6.36
villin-like	Vill	6.86	6.46
kelch-like 8 (Drosophila)	Klhl8	6.82	7.42
palladin, cytoskeletal associated protein	Palld	6.73	6.35
stomatin	Stom	6.71	6.53
WAS protein family, member 3 (Wasf3), mRNA	Wasf3	6.71	7.48
PDZ domain containing 2	Pdzd2	6.70	6.95
stomatin-like 1	Stoml1	6.69	7.17
syntrophin, basic 2	Sntb2	6.68	6.84
Rho GTPase activating protein 6	Arhgap6	6.60	7.16
giant axonal neuropathy	Gan	6.51	6.49
septin 1	septin 1	6.34	5.94
multiple PDZ domain protein	Mpdz	6.23	7.01
PDZ and LIM domain 7	Pdlim7	6.22	6.06
formin-like 3	Fmnl3	6.17	8.22
syndecan 3	Sdc3	6.15	5.98
spectrin beta 1	Spnb1	5.75*	5.86
ARP6 actin-related protein 6 homolog (yeast)	Actr6	5.73*	5.32*
septin 3	septin 3	5.53*	6.32
actinin alpha 3	Actn3	5.41*	6.19
villin 1	Vil1	5.40*	6.07
filamin binding LIM protein 1	Fblim1	5.24*	6.16

Table 12B. Myosin and myosin-like proteins

myosin, heavy polypeptide 9, non-muscle	Myh9	12.12	12.56
myosin, light chain 12B, regulatory	Myl12b	11.80	12.55
myosin X	Myo10	10.70	10.60
myosin IC	Myo1c	10.64	10.58
myosin VI	Myo6	10.21	10.93
myosin, heavy polypeptide 10, non-muscle	Myh10	10.14	11.43
myosin 1H	Myo1h	9.23	10.17
myosin XVIIIA	Myo18a	9.14	9.71
myosin VB	Myo5b	8.56	9.06
myosin IXb	Myo9b	8.52	9.12
myosin IE	Myo1e	8.32	8.95
myosin, light polypeptide 9, regulatory	Myl9	8.26	6.85
myosin ID	Myo1d	7.95	8.73

myosin IXa	Myo9a	7.89	8.72
myosin VA	Myo5a	7.87	7.97
myosin VC	Myo5c	7.64	8.70
myosin, heavy polypeptide 11, smooth muscle	Myh11	7.43	5.61
myosin, heavy polypeptide 6, cardiac muscle, alpha	Myh6	6.85	6.53
myosin, heavy polypeptide 7, cardiac muscle, beta	Myh7	6.84	6.57
myosin VIIB	Myo7b	6.75	6.47
myosin, light polypeptide 6B	Myl6b	6.72	6.77
myosin, light polypeptide 4	Myl4	6.68	6.99
myosin IB	Myo1b	6.51	7.07
myosin VIIA	Myo7a	6.49	6.65
myosin IB	Myo1b	6.43	7.64
myosin, heavy polypeptide 14	Myh14	6.36	6.21
myosin light chain, phosphorylatable, fast skeletal muscle	Mylpf	6.31	6.85
myosin VIIA and Rab interacting protein	Myrip	6.14	4.94*
myomesin 1	Myom1	5.87	5.66*
myosin IIIB	Myo3b	5.46*	6.08

Table 12C. Microtubule and microtubule-related proteins

tubulin, alpha 4A	Tuba4a	13.63	13.51
tubulin, alpha 1B	Tuba1b	12.88	13.17
tubulin, alpha 1A	Tuba1a	12.61	12.89
tubulin, beta 2A	Tubb2a	12.32	12.64
gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	Gabarapl1	12.28	12.39
microtubule-associated protein 1 light chain 3 beta	Map1lc3b	11.89	12.01
dynein light chain roadblock-type 1	Dynlrb1	11.87	11.89
dynein light chain LC8-type 1	Dynll1	11.86	12.45
dynein light chain LC8-type 1 /// predicted gene, EG627788	Dynll1 /// E	11.75	12.50
gamma-aminobutyric acid receptor associated protein	Gabarap	11.50	11.62
dynein light chain Tctex-type 3	Dynlt3	11.49	11.85
dynein light chain LC8-type 2	Dynll2	11.17	11.69
tubulin, beta 2B	Tubb2b	11.03	11.27
kinesin family member 5B	Kif5b	11.00	11.06
microtubule-associated protein, RP/EB family, member 1	Mapre1	10.77	11.28
dynactin 6	Dctn6	10.76	11.35
tubulin folding cofactor B	Tbcb	10.62	11.38
dynactin 4	Dctn4	10.58	11.20
kinesin family member 13B	Kif13b	10.53	10.89
dynein cytoplasmic 1 intermediate chain 2	Dync1i2	10.36	10.55
microtubule-associated protein 1 light chain 3 alpha	Map1lc3a	10.26	10.35
microtubule-associated protein, RP/EB family, member 2	Mapre2	10.26	10.24
destrin	Dstn	10.25	10.99
kinesin family member 21A	Kif21a	10.23	10.07
neurofilament, light polypeptide	Nefl	10.21	8.28
kinesin family member 1C	Kif1c	10.19	10.94
dynactin 5	Dctn5	10.15	11.03
kinesin family member 26B	Kif26b	10.13	10.96
kinesin family member 1B	Kif1b	10.12	10.97
tubulin, beta 5	Tubb5	10.01	10.60
dynein, cytoplasmic 1 light intermediate chain 2	Dync1li2	9.97	10.63
dynein cytoplasmic 1 heavy chain 1	Dync1h1	9.91	10.72
WD repeat domain 1	Wdr1	9.87	9.62
dynein, axonemal, light chain 1	Dnalc1	9.71	10.19
kinesin-associated protein 3	Kifap3	9.68	10.03
MAP/microtubule affinity-regulating kinase 2	Mark2	9.68	10.50
CAP-GLY domain containing linker protein 1	Clip1	9.38	9.94

tubulin, gamma complex associated protein 4	Tubgcp4	9.32	9.83
microtubule-associated protein 4	Mtap4	9.27	9.51
microtubule-associated protein 7	Mtap7	9.26	9.29
formin 1	Fmn1	9.19	9.45
tubulin, beta 2C	Tubb2c	9.04	10.03
kinesin family member 16B	Kif16b	9.02	9.28
dynactin 2	Dctn2	8.92	10.25
kinesin light chain 4	Klc4	8.88	9.82
microtubule-associated protein 2	Mtap2	8.84	9.77
katanin p60 (ATPase-containing) subunit A1	Katna1	8.77	9.22
tubulin tyrosine ligase	Ttl	8.72	8.75
KIF13A	Kif13a	8.68	9.77
kinesin family member 3A	Kif3a	8.52	8.47
kinesin family member C3	Kifc3	8.29	9.22
kinesin family member 2A	Kif2a	8.23	8.91
kinectin 1	Ktn1	8.21	8.76
tubulin tyrosine ligase-like family, member 4	Ttll4	8.15	8.41
microtubule-associated protein 7 domain containing 1	Mtap7d1	8.13	8.14
tubulin tyrosine ligase-like family, member 5	Ttll5	8.02	8.56
kinesin family member 3B	Kif3b	7.99	8.38
kinesin family member 12	Kif12	7.91	8.72
kinesin family member 3C	Kif3c	7.85	8.29
kinesin family member 22	Kif22	7.82	7.02
Dynein light chain Tctex-type 1 (Dynlt1), mRNA	Dynlt1	7.79	7.98
dynactin 1	Dctn1	7.74	8.27
Tubulin, beta 6, mRNA (cDNA clone MGC:6469 IMAGE:2631779)	Tubb6	7.70	8.44
tubulin tyrosine ligase-like 1	Ttll1	7.56	8.12
kinesin family member 23	Kif23	7.54	7.66
kinesin family member 20A	Kif20a	7.48	7.39
kinesin light chain 2	Klc2	7.44	7.45
dynein, axonemal, light chain 4	Dnalc4	7.36	8.05
WD repeat domain 78	Wdr78	7.35	7.74
kinesin light chain 3	Klc3	7.34	7.35
MAP/microtubule affinity-regulating kinase 4	Mark4	7.34	7.79
CAP-GLY domain containing linker protein 2	Clip2	7.32	7.50
microtubule-associated protein, RP/EB family, member 3	Mapre3	7.30	7.07
microtubule-associated protein tau	Mapt	7.12	8.73
tubulin tyrosine ligase-like family, member 10	Ttll10	7.03	7.58
dynein, axonemal, heavy chain 11	Dnahc11	6.92	7.54
dynein cytoplasmic 1 light intermediate chain 1	Dync1li1	6.89	7.16
kinesin light chain 1	Klc1	6.87	7.23
dynein, axonemal, heavy chain 7B	Dnahc7b	6.79	7.47
WD repeat domain 34	Wdr34	6.73	8.05
kinesin family member 5C	Kif5c	6.64	6.89
tubulin, gamma complex associated protein 5	Tubgcp5	6.56	7.09
tubulin, gamma 1	Tubg1	6.55	7.20
tubulin, gamma complex associated protein 2	Tubgcp2	6.54	6.93
WD repeat domain 60	Wdr60	6.50	7.04
tubulin polymerization-promoting protein family member 3	Tppp3	6.48	6.60
microtubule-associated protein 1 A	Mtap1a	6.40	6.54
kinesin family member C2	Kifc2	6.37	6.61
CAP-GLY domain containing linker protein family, member 4	Clip4	6.37	5.92
tubulin, gamma complex associated protein 3	Tubgcp3	6.14	6.43
tubulin, beta 4	Tubb4	6.11	5.55*
tubulin tyrosine ligase-like family, member 11	Ttll11	5.99	6.14
kinesin family member 11	Kif11	5.97	6.02

midline 2	Mid2	5.85	6.57
kinesin family member 20B	Kif20b	5.75*	5.86
midline 1	Mid1	5.75*	5.86
dynein cytoplasmic 2 heavy chain 1	Dync2h1	5.00*	6.21
dynein light chain roadblock-type 2	Dynlrb2	4.90*	5.91
MAP/microtubule affinity-regulating kinase 1	Mark1	4.90*	6.41

Table 12D. Intermediate filaments and related proteins

keratin 7	Krt7	12.42	12.89
plakophilin 4	Pkp4	11.75	11.73
keratin 18	Krt18	11.13	12.45
keratin 8	Krt8	10.92	11.84
lamin A	Lmna	10.68	10.75
plastin 3 (T-isoform)	Pls3	10.38	11.37
plakophilin 2	Pkp2	9.51	10.12
keratin 10	Krt10	9.39	9.68
keratin 80	Krt80	8.25	8.54
vimentin	Vim	8.17	7.54
keratin 23	Krt23	7.98	9.95
lamin B2	Lmnb2	7.07	7.40
keratin 24	Krt24	6.95	6.00
lamin B1	Lmnb1	6.95	7.02
keratin 34	Krt34	6.72	6.52
keratin 19	Krt19	6.64	7.51
plakophilin 3	Pkp3	6.36	6.71
plastin 1 (I-isoform)	Pls1	6.10	6.00

* - the A-value is below the cut-off level

Supplemental Table 7. Transporters and channels.

Gene Name	Gene Symbol	DCT/CNT A_value	CCD A_Value
Table 13A. Water channels			
aquaporin 3	Aqp3	13.11	13.45
aquaporin 6	Aqp6	11.53	12.84
aquaporin 4	Aqp4	8.16	11.63
aquaporin 11	Aqp11	8.11	6.90
aquaporin 2	Aqp2	7.95	10.25
aquaporin 5	Aqp5	6.51	6.20
aquaporin 1	Aqp1	6.09	6.57
Table 13B. Ion channels and transporters excluding SLC proteins.			
ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	13.86	13.87
voltage-dependent anion channel 1	Vdac1	13.73	13.74
ATPase, H+ transporting, lysosomal V1 subunit A	Atp6v1a	13.11	13.10
ATPase, H+ transporting, lysosomal V0 subunit C	Atp6v0c	12.99	12.66
ATPase, H+ transporting, lysosomal V1 subunit D	Atp6v1d	12.99	13.17
ATPase, Na+/K+ transporting, alpha 1 polypeptide	Atp1a1	12.76	12.12
VATPase, H+ transporting, lysosomal V1 subunit E1	Atp6v1e1	12.71	12.61
ATPase, H+ transporting, lysosomal V0 subunit D2	Atp6v0d2	12.58	12.78
voltage-dependent anion channel 2	Vdac2	12.54	12.63
potassium inwardly-rectifying channel, subfamily J, member 16	Kcnj16	12.44	12.63
potassium inwardly-rectifying channel, subfamily J, member 1	Kcnj1	12.41	12.69
FXYD domain-containing ion transport regulator 2	Fxyd2	12.40	11.11
ATPase, H+ transporting, lysosomal V1 subunit F	Atp6v1f	12.25	12.36
ATPase, H+ transporting, lysosomal V0 subunit B	Atp6v0b	12.01	11.93
ATPase, H+ transporting, lysosomal V0 subunit E	Atp6v0e	11.90	11.97
sodium channel, nonvoltage-gated 1 gamma	Scnn1g	11.54	11.88
potassium voltage-gated channel, subfamily Q, member 1	Kcnq1	11.51	11.68
potassium voltage-gated channel, Isk-related subfamily, member 1	Kcne1	11.47	11.68
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Atp2a2	11.45	11.61
chloride channel Kb	Clcnkb	11.33	11.70
ATPase, H+ transporting, lysosomal V1 subunit H	Atp6v1h	11.32	11.64
ATPase, H+ transporting, lysosomal V1 subunit C1	Atp6v1c1	11.27	11.48
ATPase, H+ transporting, lysosomal accessory protein 1	Atp6ap1	11.14	11.33
FXYD domain-containing ion transport regulator 4	Fxyd4	11.09	13.27
expressed sequence BF642829	BF642829	11.09	11.73
chloride channel 5	Clcn5	11.06	10.81
vacuolar protein sorting 25 (yeast)	Vps25	10.97	11.32
sodium channel, type IV, beta	Scn4b	10.92	8.47
transmembrane protein 16F	Tmem16f	10.91	11.18
potassium inwardly-rectifying channel, subfamily J, member 10	Kcnj10	10.85	10.68
sodium channel, nonvoltage-gated 1 beta	Scnn1b	10.84	11.39
ATPase, H+ transporting, lysosomal V0 subunit D1	Atp6v0d1	10.80	11.52
voltage-dependent anion channel 3	Vdac3	10.78	11.15
ATPase, Na+/K+ transporting, beta 3 polypeptide	Atp1b3	10.60	11.51
ATPase, H+ transporting, lysosomal V1 subunit G1	Atp6v1g1	10.59	11.16
polycystic kidney disease 2	Pkd2	10.43	11.00
ATPase, H+ transporting, lysosomal V1 subunit B1	Atp6v1b1	10.43	10.16
inositol 1,4,5-triphosphate receptor 2	Itpr2	10.40	10.98
chloride channel 3	Clcn3	10.40	10.75
two pore channel 1	Tpcn1	10.22	10.39
ATPase, H+/K+ exchanging, gastric, alpha polypeptide	Atp4a	10.15	10.33
inositol 1,4,5-triphosphate receptor 1	Itpr1	10.02	10.62

ATPase, H+ transporting, lysosomal V1 subunit B2	Atp6v1b2	9.97	10.36
ATPase, Ca++ transporting, plasma membrane 2	Atp2b2	9.83	10.17
calcium channel, voltage-dependent, L type, alpha 1D subunit	Cacna1d	9.77	10.66
ATPase, Cu++ transporting, alpha polypeptide	Atp7a	9.75	10.49
chloride intracellular channel 1	Clic1	9.64	10.71
chloride intracellular channel 4 (mitochondrial)	Clic4	9.62	9.55
potassium channel, subfamily K, member 1 (TWIK-1)	Kcnk1	9.45	10.45
ATPase, Ca++-sequestering	Atp2c1	9.38	10.25
sodium channel, nonvoltage-gated, type I, alpha	Scnn1a	9.37	9.54
ATPase, H+ transporting, lysosomal V0 subunit A4	Atp6v0a4	9.27	9.03
purinergic receptor P2X, ligand-gated ion channel 4	P2rx4	9.19	9.29
ATX1 (antioxidant protein 1) homolog 1 (yeast)	Atox1	9.09	9.82
transient receptor potential cation channel, subfamily M, member 6	Trpm6	9.09	7.39
chloride channel 4-2	Clcn4-2	8.97	9.67
transient receptor potential cation channel, subfamily C, member 2	Trpc2	8.91	9.87
ATPase, H+ transporting, lysosomal V1 subunit C2	Atp6v1c2	8.82	8.91
transient receptor potential cation channel, subfamily M, member 7	Trpm7	8.75	9.29
ATPase, H+ transporting, lysosomal V0 subunit A1	Atp6v0a1	8.69	9.13
ATPase, H+ transporting, lysosomal V0 subunit A2	Atp6v0a2	8.41	8.49
chloride channel 7	Clcn7	8.41	9.02
transient receptor potential cation channel, subfamily M, member 4	Trpm4	8.36	9.32
calcium channel, voltage-dependent, beta 4 subunit	Cacnb4	8.23	7.89
potassium inwardly rectifying channel, subfamily J, member 11	Kcnj11	8.16	8.44
transmembrane protein 37	Tmem37	8.10	7.69
chloride channel 6	Clcn6	8.04	8.29
mucolipin 1	Mcoln1	7.90	8.66
MRS2-like, magnesium homeostasis factor (S. cerevisiae)	Mrs2l	7.88	8.34
transient receptor potential cation channel, subfamily V, member 6	Trpv6	7.86	8.90
ATP-binding cassette, sub-family C (CFTR/MRP), member 4	Abcc4	7.80	8.56
transient receptor potential cation channel, subfamily V, member 5	Trpv5	7.68	5.58*
transmembrane and coiled-coil domains 3	Tmco3	7.66	8.32
stromal interaction molecule 1	Stim1	7.65	7.83
cholinergic receptor, nicotinic, alpha polypeptide 4	Chrna4	7.58	5.12*
potassium voltage-gated channel, subfamily H (eag-related), member 3	Kcnh3	7.57	7.17
calcium channel, voltage-dependent, alpha2/delta subunit 1	Cacna2d1	7.55	6.24
B-box and SPRY domain containing	Bspry	7.44	8.37
potassium voltage gated channel, Shaw-related subfamily, member 2	Kcnc2	7.43	8.08
glutamate receptor, ionotropic, NMDA3B	Grin3b	7.40	7.25
RIKEN cDNA 2010001E11 gene /// expressed sequence AI317395	2010001E	7.32	6.92
calcium channel, voltage-dependent, gamma subunit 8	Cacng8	7.31	6.72
polycystic kidney disease 2-like 2	Pkd2l2	7.24	7.78
stromal interaction molecule 2	Stim2	7.20	8.06
potassium voltage-gated channel, subfamily Q, member 2	Kcnq2	7.13	6.87
potassium voltage gated channel, Shaw-related subfamily, member 3	Kcnc3	7.12	7.50
calcium channel, voltage-dependent, beta 3 subunit	Cacnb3	7.10	7.52
chloride intracellular channel 5	Clic5	7.06	6.39
transient receptor potential cation channel, subfamily V, member 4	Trpv4	6.91	7.55
gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 1	Gabrg1	6.77	9.07
calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	Cacna1a	6.74	6.61
potassium voltage gated channel, Shaw-related subfamily, member 4	Kcnc4	6.72	6.43
potassium intermediate/small conductance calcium-activated channel subfamily N, member 3	Kcnn3	6.69	7.36
ATPase, H+/K+ exchanging, beta polypeptide	Atp4b	6.67	6.22
transmembrane protein 142A	Tmem142	6.66	6.81
calcium channel, voltage-dependent, gamma subunit 2	Cacng2	6.63	6.00
FXYD domain-containing ion transport regulator 1	Fxyd1	6.62	5.88

potassium intermediate/small conductance calcium-activated channel subfamily N, member 1	Kcnn1	6.60	6.47
transient receptor potential cation channel, subfamily C, member 5	Trpc5	6.60	6.40
potassium channel, subfamily K, member 3	Kcnk3	6.60	6.15
FXYD domain-containing ion transport regulator 5	Fxyd5	6.59	6.96
glutamate receptor, ionotropic, kainate 4	Grik4	6.59	6.65
expressed sequence AI317395	AI317395	6.59	5.64*
chloride channel Ka	Clcnka	6.59	6.28
cholinergic receptor, nicotinic, gamma polypeptide	Chrng	6.56	6.20
claudin 16	Cldn16	6.52	5.79*
glutamate receptor, ionotropic, kainate 5 (gamma 2)	Grik5	6.52	6.61
transient receptor potential cation channel, subfamily C, member 4	Trpc4	6.45	5.23*
antigen p97 (melanoma associated)	Mfi2	6.43	5.91
sodium channel, voltage-gated, type VIII, alpha	Scn8a	6.40	6.01
two pore segment channel 2	Tpcn2	6.36	6.71
transient receptor potential cation channel, subfamily C, member 7	Trpc7	6.36	5.78*
ATPase, H+ transporting, lysosomal V1 subunit G2	Atp6v1g2	6.33	6.33
potassium inwardly-rectifying channel, subfamily J, member 4	Kcnj4	6.33	6.45
potassium channel, subfamily T, member 1	Kcnt1	6.32	6.17
potassium inwardly-rectifying channel, subfamily J, member 15	Kcnj15	6.29	6.37
expressed sequence AI118078	AI118078	6.29	6.23
sodium channel, voltage-gated, type I, beta	Scn1b	6.24	5.69*
calcium channel, voltage-dependent, beta 1 subunit	Cacnb1	6.23	6.72
sodium channel, voltage-gated, type II, beta	Scn2b	6.20	5.80
ATPase, Na+/K+ transporting, beta 2 polypeptide	Atp1b2	6.19	5.43*
amiloride-sensitive cation channel 5, intestinal	Accn5	6.19	5.84
potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	Kcns3	6.19	7.58
purinergic receptor P2X, ligand-gated ion channel, 5	P2rx5	6.15	6.13
calcium channel, voltage-dependent, beta 2 subunit	Cacnb2	6.13	6.96
purinergic receptor P2X-like 1, orphan receptor	P2rxl1	6.11	5.70*
transient receptor potential cation channel, subfamily V, member 2	Trpv2	6.08	5.49*
amiloride-sensitive cation channel 4, pituitary	Accn4	6.07	5.93
transient receptor potential cation channel, subfamily M, member 3	Trpm3	6.07	5.93
ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	Atp2a1	6.05	6.20
chloride intracellular channel 3	Clic3	6.05	5.69*
potassium voltage-gated channel, subfamily G, member 2	Kcng2	6.03	5.98
potassium voltage gated channel, Shab-related subfamily, member 1	Kcnb1	6.00	5.74*
transient receptor potential cation channel, subfamily M, member 2	Trpm2	5.97	5.50*
bestrophin 1	Best1	5.96	6.06
potassium voltage gated channel, Shaw-related subfamily, member 1	Kcnc1	5.93	5.47*
cation channel, sperm associated 2	Catsper2	5.93	5.89
calcium channel, voltage-dependent, gamma subunit 4	Cacng4	5.93	5.21*
Kv channel-interacting protein 1	Kcnip1	5.90	5.74*
gamma-aminobutyric acid (GABA-A) receptor, pi	Gabrp	5.88	4.75*
calcium channel, voltage-dependent, gamma subunit 1	Cacng1	5.88	4.94*
glutamate receptor, ionotropic, NMDA2B (epsilon 2)	Grin2b	5.82	5.54*
potassium voltage-gated channel, shaker-related subfamily, member 7	Kcna7	5.81	5.59*
hydrogen voltage-gated channel 1	Hvcn1	5.75*	6.39
cholinergic receptor, nicotinic, beta polypeptide 4	Chrnb4	5.69*	6.86
amiloride-sensitive cation channel 2, neuronal	Accn2	5.47*	5.82
ATPase, H+/K+ transporting, nongastric, alpha polypeptide	Atp12a	5.41*	5.89
purinergic receptor P2X, ligand-gated ion channel, 7	P2rx7	5.30*	5.82
cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)	Chrnb1	5.01*	6.93
FXYD domain-containing ion transport regulator 3	Fxyd3	4.97*	6.55
gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon	Gabre	4.68*	6.27

Table 13C. Solute carrier proteins (SLC).

solute carrier family 26, member 4 (pendrin)	Slc26a4	13.43	13.45
solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	Slc25a5	12.88	12.94
solute carrier family 2 (urate transporter), member 9	Slc2a9	12.42	10.74
solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4	Slc25a4	12.42	12.54
solute carrier family 16 (monocarboxylic acid transporters), member 7	Slc16a7	12.12	11.52
solute carrier family 2 (facilitated glucose transporter), member 1 (GLUT1)	Slc2a1	12.10	12.73
solute carrier family 12, member 3 (NCC)	Slc12a3	10.77	5.28*
solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11	Slc25a11	10.13	10.66
solute carrier family 27 (fatty acid transporter), member 1	Slc27a1	10.12	10.46
solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	Slc25a20	10.07	10.59
solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	Slc25a23	9.76	9.59
solute carrier family 25 (mitochondrial carrier, Aralar), member 12	Slc25a12	9.48	9.66
solute carrier family 5 (sodium/glucose cotransporter), member 2 (SGLT2)	Slc5a2	9.48	9.52
solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	Slc25a19	9.48	9.66
solute carrier family 40 (iron-regulated transporter), member 1	Slc40a1	9.46	9.10
solute carrier family 2 (facilitated glucose transporter), member 4 (GLUT4)	Slc2a4	9.32	8.67
solute carrier family 25 (mitochondrial carrier ornithine transporter), member 15	Slc25a15	9.25	9.27
solute carrier family 25, member 36	Slc25a36	9.16	9.84
solute carrier family 25, member 30	Slc25a30	9.10	8.66
solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	Slc11a2	8.97	9.46
solute carrier family 25 (mitochondrial carrier, brain), member 14	Slc25a14	8.95	9.60
solute carrier family 16 (monocarboxylic acid transporters), member 10	Slc16a10	8.85	9.08
solute carrier family 5 (inositol transporters), member 3	Slc5a3	8.72	9.03
solute carrier family 25, member 32	Slc25a32	8.69	9.14
solute carrier family 12, member 7 (KCC4)	Slc12a7	8.61	8.97
solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	Slc25a25	8.52	9.07
solute carrier organic anion transporter family, member 4a1	Slco4a1	8.44	9.03
solute carrier family 15 (H+/peptide transporter), member 2 (PEPT2)	Slc15a2	8.43	8.65
solute carrier family 22 (organic cation transporter), member 5	Slc22a5	8.42	8.77
solute carrier family 22 (organic anion/cation transporter), member 12	Slc22a12	8.33	7.89
solute carrier family 25, member 44	Slc25a44	8.30	8.56
solute carrier family 12, member 2 (NKCC1)	Slc12a2	8.28	8.96
solute carrier organic anion transporter family, member 3a1	Slco3a1	8.24	9.10
solute carrier family 37 (glucose-6-phosphate transporter), member 4	Slc37a4	8.20	8.05
solute carrier family 37 (glycerol-3-phosphate transporter), member 3	Slc37a3	8.19	8.81
solute carrier family 2 (facilitated glucose transporter), member 12	Slc2a12	8.13	7.88
solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13	Slc25a13	8.09	8.76
solute carrier family 16 (monocarboxylic acid transporters), member 9	Slc16a9	7.98	8.37
solute carrier family 16 (monocarboxylic acid transporters), member 13	Slc16a13	7.95	8.06
solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1	Slc25a1	7.91	8.49
solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	Slc13a3	7.78	7.54
solute carrier family 16 (monocarboxylic acid transporters), member 11	Slc16a11	7.71	7.30
solute carrier family 18 (vesicular monoamine), member 1	Slc18a1	7.71	7.84

solute carrier family 27 (fatty acid transporter), member 4	Slc27a4	7.71	8.17
solute carrier family 34 (sodium phosphate), member 1	Slc34a1	7.68	7.72
solute carrier family 2, (facilitated glucose transporter), member 8	Slc2a8	7.64	8.29
solute carrier family 12, member 1 (NKCC2)	Slc12a1	7.64	6.83
solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17	Slc25a17	7.50	8.11
solute carrier family 15, member 4	Slc15a4	7.46	8.45
solute carrier family 25, member 34	Slc25a34	7.36	7.62
solute carrier family 23 (nucleobase transporters), member 2	Slc23a2	7.34	7.72
solute carrier family 46, member 1	Slc46a1	7.28	7.79
solute carrier family 17 (anion/sugar transporter), member 5	Slc17a5	7.25	7.79
solute carrier family 22 (organic anion transporter), member 6	Slc22a6	7.21	7.72
solute carrier family 16 (monocarboxylic acid transporters), member 8	Slc16a8	7.08	7.01
solute carrier family 12, member 6 (KCC3)	Slc12a6	7.07	7.75
solute carrier family 5 (sodium/glucose cotransporter), member 1 (SGLT1)	Slc5a1	6.94	6.42
solute carrier family 17 (sodium phosphate), member 1 (NPT1)	Slc17a1	6.90	7.08
solute carrier family 17 (sodium phosphate), member 3 (NPT4)	Slc17a3	6.90	7.47
solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	Slc25a29	6.86	7.47
solute carrier family 22 (organic cation transporter), member 17	Slc22a17	6.84	8.13
solute carrier family 15 (oligopeptide transporter), member 1	Slc15a1	6.81	4.73*
solute carrier family 26 (sulfate transporter), member 2	Slc26a2	6.81	8.09
solute carrier family 16 (monocarboxylic acid transporters), member 6	Slc16a6	6.73	7.52
solute carrier family 16 (monocarboxylic acid transporters), member 14	Slc16a14	6.71	6.16
solute carrier organic anion transporter family, member 1a1	Slco1a1	6.70	6.74
solute carrier family 18 (vesicular monoamine), member 2	Slc18a2	6.67	6.64
solute carrier family 25, member 45	Slc25a45	6.59	7.21
solute carrier family 37 (glycerol-3-phosphate transporter), member 1	Slc37a1	6.59	7.00
solute carrier family 22 (organic anion transporter), member 8	Slc22a8	6.56	6.43
solute carrier family 22 (organic cation transporter), member 13	Slc22a13	6.50	6.60
solute carrier family 6 (neurotransmitter transporter), member 18	Slc6a18	6.49	6.63
solute carrier organic anion transporter family, member 2b1	Slco2b1	6.41	6.49
solute carrier organic anion transporter family, member 4C1	Slco4c1	6.40	7.78
solute carrier family 22 (organic cation transporter), member 2	Slc22a2	6.39	6.47
solute carrier family 5 (sodium/glucose cotransporter), member 10	Slc5a10	6.30	6.42
solute carrier family 37 (glycerol-3-phosphate transporter), member 2	Slc37a2	6.25	5.98
solute carrier family 22 (organic cation transporter), member 18	Slc22a18	6.24	6.34
solute carrier family 16 (monocarboxylic acid transporters), member 2	Slc16a2	6.24	6.41
solute carrier family 22 (organic cation transporter), member 3	Slc22a3	6.24	5.14
solute carrier family 22 (organic cation transporter), member 1	Slc22a1	6.21	6.31
solute carrier family 22 (organic anion transporter), member 7	Slc22a7	6.20	6.40
solute carrier family 26, member 11	Slc26a11	6.16	6.30
solute carrier family 22 (organic anion/cation transporter), member 15	Slc22a15	6.13	6.16
solute carrier family 2 (facilitated glucose transporter), member 5	Slc2a5	6.10	5.56*
solute carrier family 15, member 3	Slc15a3	6.06	5.30*
solute carrier family 25 (mitochondrial carrier, glutamate), member 22	Slc25a22	6.06	5.85
solute carrier family 12, member 4	Slc12a4	5.91	6.32
solute carrier family 25, member 27	Slc25a27	5.91	6.09
solute carrier family 16 (monocarboxylic acid transporters), member 4	Slc16a4	5.89	6.79
solute carrier organic anion transporter family, member 2a1	Slco2a1	5.88	5.28*
solute carrier family 23 (nucleobase transporters), member 1	Slc23a1	5.88	6.31
solute carrier family 5 (sodium-dependent vitamin transporter), member 6	Slc5a6	5.84	6.05
solute carrier family 22 (organic cation transporter), member 4	Slc22a4	5.72*	5.88
solute carrier family 16 (monocarboxylic acid transporters), member 12	Slc16a12	5.63*	5.92
solute carrier family 6 (neurotransmitter transporter), member 20	Slc6a20	5.59*	6.33
solute carrier family 26, member 7	Slc26a7	5.29*	7.77

solute carrier family 5 (iodide transporter), member 8	Slc5a8	5.10*	5.82

* - the A-value is below the cut-off level

Supplemental Table 8. Transcription factors

Gene Name	Gene Symbol	DCT/CNT A_Value	CCD A_Value
zinc finger protein 526	Zfp526	13.23	13.31
ring-box 1	Rbx1	13.04	13.19
pituitary tumor-transforming gene 1	Pttg1	12.79	12.76
mortality factor 4 like 1	Morf4l1	12.76	13.05
Jun proto-oncogene related gene d	Jund	12.74	12.75
homeo box D8	Hoxd8	12.66	12.80
early growth response 1	Egr1	12.64	13.46
TSC22 domain family, member 1	Tsc22d1	12.38	12.51
homeo box D9	Hoxd9	12.37	12.50
Jun oncogene	Jun	12.28	12.83
FBJ osteosarcoma oncogene	Fos	12.25	12.85
nascent polypeptide-associated complex alpha polypeptide	Naca	12.17	12.64
endothelial differentiation-related factor 1	Edf1	12.14	12.37
SUB1 homolog (S. cerevisiae)	Sub1	11.81	12.28
ring finger protein 7	Rnf7	11.67	12.20
ecotropic viral integration site 1	Evi1	11.64	12.07
pleiomorphic adenoma gene-like 1	Plagl1	11.62	11.83
MPN domain containing	Mpnd	11.57	11.89
peroxisome proliferative activated receptor, gamma, coactivator 1 a	Ppargc1a	11.55	11.37
Kruppel-like factor 9	Klf9	11.52	11.44
cAMP responsive element binding protein 3	Creb3	11.45	11.92
fusion, derived from t(12;16) malignant liposarcoma (human)	Fus	11.43	11.79
eukaryotic translation initiation factor 3, subunit H	Eif3h	11.42	11.79
transcription factor CP2-like 1	Tcfcp2l1	11.41	11.91
thyroid hormone receptor associated protein 3	Thrap3	11.40	11.56
mortality factor 4 like 2	Morf4l2	11.35	11.61
transcriptional regulator, SIN3B (yeast)	Sin3b	11.32	11.44
vitamin D receptor	Vdr	11.31	9.46
proliferation-associated 2G4	Pa2g4	11.31	11.85
hypoxia inducible factor 1, alpha subunit	Hif1a	11.30	11.95
PR domain containing 16	Prdm16	11.29	11.71
POU domain, class 3, transcription factor 3	Pou3f3	11.27	12.11
zinc finger, HIT domain containing 1	Znhit1	11.22	11.52
nuclear receptor co-repressor 1	Ncor1	11.21	11.55
amino-terminal enhancer of split	Aes	11.13	11.49
transformation related protein 53 binding protein 1	Trp53bp1	11.13	11.76
zinc finger, matrin type 2	Zmat2	11.11	11.42
leucine rich repeat (in FLII) interacting protein 1	Lrrfip1	11.11	11.66
BUD31 homolog (yeast)	Bud31	11.09	10.85
GATA binding protein 2	Gata2	11.08	12.22
estrogen-related receptor gamma	Esrrg	11.08	11.05
transcription elongation factor A (SII) 1	Tcea1	11.07	11.37
zinc finger, MYND domain containing 11	Zmynd11	11.06	11.35
zinc finger CCCH-type containing 15	Zc3h15	11.04	10.95
endothelial PAS domain protein 1	Epas1	11.02	11.08
jagged 1	Jag1	11.01	11.47
Cbp/p300-interacting transactivator	Cited2	10.95	11.44
LPS-induced TN factor	Litaf	10.91	11.85
forkhead box I1	Foxi1	10.89	11.54
ring finger protein 11	Rnf11	10.89	11.22
nuclear factor, erythroid derived 2, like 2	Nfe2l2	10.88	11.28
AF4/FMR2 family, member 1	Aff1	10.88	11.58

Kruppel-like factor 6	Klf6	10.88	11.73
GATA zinc finger domain containing 1	Gatad1	10.84	11.01
AT rich interactive domain 4B (RBP1-like)	Arid4b	10.84	11.22
WW domain binding protein 5	Wbp5	10.84	11.84
replication initiator 1	Repin1	10.81	10.87
BCL2-associated transcription factor 1	Bclaf1	10.80	10.99
activating transcription factor 4	Atf4	10.78	10.78
ets homologous factor	Ehf	10.78	11.84
serum deprivation response	Sdpr	10.73	10.56
forkhead box O3	Foxo3	10.73	10.93
leucine rich repeat (in FLII) interacting protein 2	Lrrfip2	10.73	10.83
SNW domain containing 1	Snw1	10.72	10.81
PHD finger protein 17	Phf17	10.71	10.70
purine rich element binding protein B	Purb	10.70	11.04
forkhead box J3	Foxj3	10.68	11.23
TAF13 RNA polymerase II	Taf13	10.67	10.69
general transcription factor II I	Gtf2i	10.65	11.14
male-specific lethal 3 homolog (Drosophila)	Msl3	10.63	11.01
TAR DNA binding protein	Tardbp	10.62	11.03
homeo box D10	Hoxd10	10.59	7.40
CCAAT/enhancer binding protein zeta	Cebpz	10.58	11.12
biogenesis of lysosome-related organelles complex-1, subunit 1	Bloc1s1	10.57	10.74
yes-associated protein 1	Yap1	10.55	10.63
nuclear receptor subfamily 2, group F, member 6	Nr2f6	10.54	10.72
homeo box A9	Hoxa9	10.53	6.80
E26 avian leukemia oncogene 2, 3' domain	Ets2	10.43	11.01
cold shock domain protein A	Csda	10.43	10.78
praja 2, RING-H2 motif containing	Pja2	10.42	10.72
general transcription factor IIF, polypeptide 1	Gtf2f1	10.37	10.92
CCCTC-binding factor	Ctcf	10.36	10.59
ELK4, member of ETS oncogene family	Elk4	10.34	11.04
forkhead box N3	Foxn3	10.33	10.85
YY1 transcription factor	Yy1	10.32	10.67
activating transcription factor 2	Atf2	10.32	11.15
forkhead box K1	Foxk1	10.32	10.93
leucine-zipper-like transcriptional regulator, 1	Lztr1	10.32	10.36
basic helix-loop-helix family, member e40	Bhlhe40	10.29	11.37
nuclear factor, erythroid derived 2,-like 1	Nfe2l1	10.28	10.77
MAD homolog 1 (Drosophila)	Smad1	10.28	10.99
TAF10 RNA polymerase II	Taf10	10.28	10.76
zinc finger, CCHC domain containing 3	Zcchc3	10.27	11.21
nuclear factor I/C	Nfic	10.27	10.17
interferon-induced protein 35	Ifi35	10.27	10.94
c-myc binding protein	Mycbp	10.26	10.36
D site albumin promoter binding protein	Dbp	10.25	10.62
prefoldin 1	Pfdn1	10.23	10.70
cAMP responsive element binding protein 3-like 2	Creb3l2	10.23	10.88
Ring finger protein 185 (Rnf185), mRNA	Rnf185	10.22	10.68
AF4/FMR2 family, member 4	Aff4	10.21	11.04
zinc finger protein 422	Zfp422	10.21	10.65
PHD finger protein 14	Phf14	10.21	10.87
GA repeat binding protein, alpha	Gabpa	10.18	10.32
homeo box D11	Hoxd11	10.16	6.59
forkhead box P1	Foxp1	10.15	10.79
zinc finger and BTB domain containing 7a	Zbtb7a	10.15	10.81
nuclear receptor coactivator 2	Ncoa2	10.14	10.69

forkhead box O1	Foxo1	10.13	10.01
polyglutamine binding protein 1	Pqbp1	10.13	10.60
HLA-B associated transcript 2	Bat2	10.13	10.81
RIKEN cDNA 9030612M13 gene	9030612M13Rik	10.13	10.45
CREB binding protein	Crebbp	10.13	11.11
transcription elongation factor B (SIII), polypeptide 2	Tceb2	10.12	10.70
COP9 (constitutive photomorphogenic) homolog, subunit 5	Cops5	10.12	10.77
inhibitor of DNA binding 2	Id2	10.11	10.77
zinc finger protein 238	Zfp238	10.10	10.62
aryl hydrocarbon receptor nuclear translocator	Arnt	10.10	10.61
FBJ osteosarcoma oncogene B	Fosb	10.08	10.24
nuclear receptor coactivator 4	Ncoa4	10.08	10.74
signal transducer and activator of transcription 3	Stat3	10.06	10.75
ring finger protein 114	Rnf114	10.06	10.99
zinc finger and BTB domain containing 4	Zbtb4	10.06	10.39
scaffold attachment factor B	Safb	10.05	10.52
zinc finger and BTB domain containing 20	Zbtb20	10.03	10.66
homeo box B7 /// homeo box B8	Hoxb7 /// Hoxb8	10.03	10.29
zinc finger homeobox 3	Zfhx3	10.03	10.52
Ngfi-A binding protein 1	Nab1	10.02	10.49
CCR4-NOT transcription complex, subunit 4	Cnot4	9.99	10.46
zinc finger protein 251	Zfp251	9.98	10.64
GLIS family zinc finger 2	Glis2	9.97	10.74
retinoblastoma binding protein 8	Rbbp8	9.96	10.23
MAD homolog 4 (Drosophila)	Smad4	9.95	10.54
zinc finger protein 809	Zfp809	9.95	10.43
chromatin modifying protein 4B /// similar to zinc finger protein 341	Chmp4b /// LOC	9.95	10.55
GLIS family zinc finger 3	Glis3	9.94	10.57
forkhead box Q1	Foxq1	9.93	9.48
AE binding protein 2	Aebp2	9.93	10.67
zinc finger CCCH type containing 11A	Zc3h11a	9.91	10.49
RIKEN cDNA 2010315B03 gene	2010315B03Rik	9.91	10.05
THO complex 2	Thoc2	9.91	10.49
CCAAT/enhancer binding protein (C/EBP), gamma	Cebpg	9.90	10.42
zinc finger protein 664	Zfp664	9.90	10.68
homeo box C10	Hoxc10	9.89	5.53*
microphthalmia-associated transcription factor	Mitf	9.89	10.30
trans-acting transcription factor 1	Sp1	9.88	10.99
RIKEN cDNA 0610009B22 gene	0610009B22Rik	9.87	10.38
nuclear factor I/X	Nfix	9.87	11.35
methyltransferase like 14	Mettl14	9.87	10.46
ring finger protein 4	Rnf4	9.86	10.39
polymerase (RNA) II (DNA directed) polypeptide G	Polr2g	9.84	10.08
expressed sequence C80913	C80913	9.84	9.92
suppressor of Ty 16 homolog (S. cerevisiae)	Supt16h	9.84	10.35
zinc fingers and homeoboxes 3	Zhx3	9.84	10.48
Zinc finger protein 358 (Zfp358), mRNA	Zfp358	9.83	10.18
Shwachman-Bodian-Diamond syndrome homolog (human)	Sbds	9.82	10.12
zinc finger protein 161	Zfp161	9.82	10.28
RUN and FYVE domain containing 3	Rufy3	9.81	9.98
structure specific recognition protein 1	Ssrp1	9.81	10.40
SAP domain containing ribonucleoprotein	Sarnp	9.81	9.61
nuclear receptor subfamily 2, group F, member 2	Nr2f2	9.79	10.14
ring finger protein 14	Rnf14	9.79	10.10
AT rich interactive domain 4A (RBP1-like)	Arid4a	9.79	9.84
YEATS domain containing 4	Yeats4	9.77	10.04

cell division cycle 5-like (S. pombe)	Cdc5l	9.77	10.05
nuclear transcription factor, X-box binding 1	Nfx1	9.77	9.87
zinc finger with KRAB and SCAN domains 1	Zkscan1	9.77	10.28
signal transducer and activator of transcription 6	Stat6	9.75	10.03
C1D nuclear receptor co-repressor	C1d	9.75	9.91
activating transcription factor 6	Atf6	9.75	9.82
TEA domain family member 1	Tead1	9.73	10.79
zinc finger protein 219	Zfp219	9.70	10.13
high mobility group box transcription factor 1	Hbp1	9.69	10.34
BAT2 domain containing 1	Bat2d	9.68	10.49
activating transcription factor 1	Atf1	9.66	10.76
XPA binding protein 2	Xab2	9.66	10.17
TAF15 RNA polymerase II	Taf15	9.65	9.52
family with sequence similarity 48, member A	Fam48a	9.64	10.05
speckle-type POZ protein	Spop	9.61	10.10
interferon regulatory factor 6	Irf6	9.59	10.84
cAMP responsive element binding protein 1	Creb1	9.59	10.32
CCR4-NOT transcription complex, subunit 1	Cnot1	9.59	10.63
LIM domain binding 1	Ldb1	9.59	9.93
CCR4-NOT transcription complex, subunit 2	Cnot2	9.57	10.40
nuclear receptor subfamily 2, group C, member 2	Nr2c2	9.57	10.35
C-terminal binding protein 2	Ctbp2	9.55	9.86
Max interacting protein 1	Mxi1	9.54	9.80
purine rich element binding protein A	Pura	9.53	10.03
enhancer of rudimentary homolog (Drosophila)	Erh	9.53	10.28
zinc finger protein 329	Zfp329	9.51	9.44
Jumonji domain containing 3, mRNA (cDNA clone IMAGE:1378940)	Kdm6b	9.50	10.39
myeloid/lymphoid or mixed-lineage leukemia 3	Mll3	9.50	9.88
ZXD family zinc finger C	Zxdc	9.48	10.01
nuclear factor I/B	Nfib	9.48	10.86
E74-like factor 2	Elf2	9.47	9.88
bromodomain containing 1	Brd1	9.47	10.04
myoneurin	Mynn	9.46	10.14
transcription factor 20	Tcf20	9.45	10.55
similar to Zinc finger BED domain containing protein 4	LOC667118	9.45	9.97
kelch-like ECH-associated protein 1	Keap1	9.44	9.83
upstream binding transcription factor, RNA polymerase I	Ubtf	9.44	10.51
suppressor of Ty 5 homolog (S. cerevisiae)	Supt5h	9.43	9.69
Max dimerization protein 3	Mxd3	9.43	9.35
RAR-related orphan receptor gamma	Rorc	9.42	9.93
empty spiracles homolog 2 (Drosophila)	Emx2	9.42	10.90
transcriptional regulator, SIN3A (yeast)	Sin3a	9.41	9.78
core binding factor beta	Cbfb	9.41	9.66
RIKEN cDNA 5830417I10 gene	5830417I10Rik	9.40	9.48
UTP6, small subunit (SSU) processome component, homolog	Utp6	9.40	10.31
interleukin enhancer binding factor 2	Ilf2	9.39	10.20
zinc finger and SCAN domain containing 21	Zscan21	9.39	10.46
transducin-like enhancer of split 3, homolog of Drosophila E(spl)	Tle3	9.38	9.78
MYST histone acetyltransferase (monocytic leukemia) 3	Myst3	9.38	9.97
zinc finger protein 217	Zfp217	9.37	10.13
homeo box B4	Hoxb4	9.37	9.98
inhibitor of DNA binding 3	Id3	9.36	10.15
nuclear receptor subfamily 1, group D, member 2	Nr1d2	9.35	9.39
zinc finger protein 187	Zfp187	9.35	10.41
zinc finger protein 191	Zfp191	9.34	10.18
dachshund 1 (Drosophila)	Dach1	9.34	9.08

transcription factor AP-2 beta	Tcfap2b	9.34	9.48
RE1-silencing transcription factor	Rest	9.33	10.27
predicted gene, EG382639	EG382639	9.33	10.01
TAF9 RNA polymerase II	Taf9	9.32	9.44
GATA binding protein 3	Gata3	9.32	10.52
scaffold attachment factor B2	Safb2	9.32	9.95
homeo box B5	Hoxb5	9.31	9.97
family with sequence similarity 164, member A	Fam164a	9.31	10.23
cyclin L1	Ccnl1	9.30	9.89
TSC22 domain family, member 2	Tsc22d2	9.30	9.24
ring finger protein 1	Ring1	9.29	9.38
zinc finger, ZZ domain containing 3	Zzz3	9.29	9.52
anaphase promoting complex subunit 11	Anapc11	9.28	9.12
SERTA domain containing 1	Sertad1	9.27	9.69
remodeling and spacing factor 1	Rsf1	9.27	9.85
zinc finger protein 553	Zfp553	9.26	9.53
zinc finger protein 644	Zfp644	9.26	9.78
paternally expressed 3	Peg3	9.24	8.40
grainyhead-like 2 (Drosophila)	Grhl2	9.24	9.94
general transcription factor II A, 1	Gtf2a1	9.24	9.81
LIM domains containing 1	Limd1	9.23	10.09
transcription factor Dp 2	Tfdp2	9.23	9.23
zinc finger protein 263	Zfp263	9.23	9.58
zinc and ring finger 2	Znrf2	9.23	9.83
ras responsive element binding protein 1	Rreb1	9.22	9.87
sprouty homolog 2 (Drosophila)	Spry2	9.22	10.59
MAD homolog 5 (Drosophila)	Smad5	9.21	9.49
transcription factor Dp 1	Tfdp1	9.20	9.70
ets variant gene 3	Etv3	9.19	9.43
forkhead box K2	Foxk2	9.18	9.70
PHD finger protein 10	Phf10	9.18	9.77
Dr1 associated protein 1 (negative cofactor 2 alpha)	Drap1	9.18	9.38
CCAAT/enhancer binding protein (C/EBP), alpha	Cebpa	9.17	9.53
ataxin 3	Atxn3	9.17	9.62
zinc finger protein 260	Zfp260	9.17	9.61
zinc finger protein 629	Zfp629	9.16	9.03
zinc finger protein 408	Zfp408	9.16	9.52
SRY-box containing gene 4	Sox4	9.15	10.65
fos-like antigen 2 /// similar to fos-like antigen 2	Fosl2	9.15	10.18
zinc finger and BTB domain containing 1	Zbtb1	9.13	10.17
programmed cell death 2-like	Pdcd2l	9.13	9.53
vascular endothelial zinc finger 1	Vezf1	9.13	9.87
paired box gene 8	Pax8	9.12	10.14
myeloid/lymphoid or mixed-lineage leukemia	Mllt3	9.12	9.33
X-box binding protein 1, mRNA	Xbp1	9.11	10.03
thyrotroph embryonic factor	Tef	9.11	9.63
zinc finger, MYND-type containing 8	Zmynd8	9.11	9.71
nucleus accumbens associated 2	Nacc2	9.11	9.65
D4, zinc and double PHD fingers family 2	Dpf2	9.10	9.30
ski sarcoma viral oncogene homolog (avian)	Ski	9.10	9.68
serum response factor	Srf	9.09	9.83
ring finger protein, LIM domain interacting	Rlim	9.09	9.66
polycomb group ring finger 2	Pcgf2	9.08	9.40
down-regulator of transcription 1	Dr1	9.07	9.76
pre B-cell leukemia transcription factor 2	Pbx2	9.07	9.77
cut-like homeobox 1	Cux1	9.07	9.48

zinc finger and BTB domain containing 43	Zbtb43	9.06	9.65
MAD homolog 3 (Drosophila)	Smad3	9.06	9.07
RIKEN cDNA 1810007M14 gene	1810007M14Rik	9.04	10.02
ring finger protein 2	Rnf2	9.04	9.62
zinc finger protein 768	Zfp768	9.03	8.57
nuclear receptor subfamily 3, group C, member 2	Nr3c2	9.03	9.53
delta-like 1 (Drosophila)	Dll1	9.02	9.92
zinc finger protein 397	Zfp397	9.00	9.31
RING1 and YY1 binding protein	Rybp	8.99	9.13
RIKEN cDNA 5730601F06 gene	5730601F06Rik	8.99	9.60
CCR4-NOT transcription complex, subunit 7	Cnot7	8.97	9.46
cyclin T2	Ccnt2	8.97	9.58
sal-like 1 (Drosophila)	Sall1	8.97	5.57*
zinc finger protein 740	Zfp740	8.95	9.27
tripartite motif-containing 28	Trim28	8.93	9.75
ring finger protein 5	Rnf5	8.93	9.69
zinc finger and BTB domain containing 6	Zbtb6	8.93	9.47
MAF1 homolog (S. cerevisiae) (Maf1), mRNA	Maf1	8.92	9.87
jumonji, AT rich interactive domain 2	Jarid2	8.92	9.50
lysine (K)-specific demethylase 5D	Kdm5d	8.92	9.25
MAD homolog 2 (Drosophila)	Smad2	8.91	9.84
nuclear transcription factor-Y beta	Nfyb	8.90	9.50
circadian locomoter output cycles kaput	Clock	8.89	9.48
serum response factor binding protein 1	Srfbp1	8.89	9.08
zinc finger protein 516	Zfp516	8.89	9.31
HLA-B associated transcript 2-like	Bat2l	8.88	9.64
SKI-like	Skil	8.88	9.71
prostate tumor over expressed gene 1	Ptov1	8.87	9.17
transcription factor 12	Tcf12	8.87	9.56
inhibitor of growth family, member 2	Ing2	8.86	9.36
myeloid/lymphoid or mixed-lineage leukemia	Mllt6	8.86	9.67
nuclear receptor interacting protein 1	Nrip1	8.86	9.42
transcription factor 4	Tcf4	8.85	9.34
RIKEN cDNA 1700023B02 gene	1700023B02Rik	8.85	8.75
zinc finger protein 617	Zfp617	8.85	9.42
bromodomain and PHD finger containing, 3	Brpf3	8.85	8.61
RAR-related orphan receptor alpha	Rora	8.83	9.69
general transcription factor IIB	Gtf2b	8.83	9.47
T-box 2	Tbx2	8.82	9.07
hairy and enhancer of split 6 (Drosophila)	Hes6	8.82	9.30
upstream binding protein 1	Ubp1	8.82	9.24
lysine (K)-specific demethylase 5B	Kdm5b	8.81	9.41
zinc finger protein 398	Zfp398	8.81	9.51
nuclear factor of activated T-cells 5	Nfat5	8.81	9.76
nuclear receptor coactivator 3	Ncoa3	8.80	9.67
zinc finger, RAN-binding domain containing 2	Zranb2	8.80	9.14
zinc finger protein 445	Zfp445	8.80	9.23
ELK3, member of ETS oncogene family	Elk3	8.79	8.83
thyroid hormone receptor alpha	Thra	8.79	9.62
AS42 oncogene homolog	Maf	8.79	9.02
nuclear factor of activated T-cells, cytoplasmic	Nfatc3	8.77	9.16
Kruppel-like factor 10	Klf10	8.76	9.63
homeodomain leucine zipper-encoding gene	Homez	8.76	8.86
zinc finger protein 281	Zfp281	8.75	8.70
TAF1 RNA polymerase II	Taf1	8.75	9.37
zinc finger protein 687	Zfp687	8.74	8.26

RIKEN cDNA 4930529C04 gene	4930529C04Rik	8.74	8.59
polyhomeotic-like 1 (Drosophila)	Phc1	8.73	9.25
expressed sequence AI987944 /// expressed sequence AW146154	AI987944	8.73	9.40
SRY-box containing gene 6	Sox6	8.72	9.66
inhibitor of growth family, member 1	Ing1	8.72	9.15
zinc finger protein 606	Zfp606	8.71	9.00
zinc finger and BTB domain containing 2	Zbtb2	8.70	9.39
TOX high mobility group box family member 4	Tox4	8.69	9.02
HNF1 homeobox B	Hnf1b	8.68	9.56
homeo box A10	Hoxa10	8.67	6.66
zinc finger protein 3	Zfp3	8.67	9.11
interferon regulatory factor 1	Irf1	8.67	9.37
zinc finger protein 292	Zfp292	8.66	9.05
myocyte enhancer factor 2A	Mef2a	8.65	9.50
cullin associated and neddylation disassociated 1	Cand1	8.65	9.63
zinc finger protein 507	Zfp507	8.65	8.88
regulatory factor X, 1 (influences HLA class II expression)	Rfx1	8.65	9.66
general transcription factor II A, 2	Gtf2a2	8.64	9.66
single-minded homolog 1 (Drosophila)	Sim1	8.64	9.56
Scm-like with four mbt domains 1	Sfmbt1	8.64	8.77
AT hook containing transcription factor 1	Ahctf1	8.62	8.67
RIKEN cDNA 5730507C01 gene	5730507C01Rik	8.62	8.27
ash2 (absent, small, or homeotic)-like (Drosophila)	Ash2l	8.61	9.14
retinoblastoma-like 2	Rbl2	8.61	9.16
TOX high mobility group box family member 3	Tox3	8.61	9.20
zinc finger protein 467	Zfp467	8.61	8.57
suppressor of Ty 6 homolog (S. cerevisiae)	Supt6h	8.60	9.54
retinoid X receptor alpha	Rxra	8.60	8.84
regulatory factor X, 5 (influences HLA class II expression)	Rfx5	8.59	9.00
nuclear receptor coactivator 1	Ncoa1	8.59	9.08
mediator complex subunit 14	Med14	8.59	9.50
zinc finger protein 707	Zfp707	8.59	9.28
SAP30 binding protein	Sap30bp	8.59	9.03
SRY-box containing gene 12	Sox12	8.58	8.81
4lysine (K)-specific demethylase 6A	Kdm6a	8.57	9.30
transcription factor E3	Tcfe3	8.57	8.75
zinc finger and BTB domain containing 38	Zbtb38	8.57	8.77
nuclear factor I/A	Nfia	8.56	10.65
human immunodeficiency virus type I enhancer binding protein 2	Hivep2	8.55	9.37
mediator of RNA polymerase II transcription, subunit 4 homolog	Med4	8.54	8.72
hepatoma-derived growth factor, related protein 2	Hdgfrp2	8.53	9.20
retinoid X receptor beta	Rxrb	8.53	8.65
activating transcription factor 3	Atf3	8.53	8.87
transcription factor AP-2, alpha	Tcfap2a	8.52	9.18
N-myc (and STAT) interactor	Nmi	8.52	9.31
activating transcription factor 5	Atf5	8.52	9.13
general transcription factor III A	Gtf3a	8.52	8.97
RIKEN cDNA 1300003B13 gene	1300003B13Rik	8.52	8.39
inhibitor of growth family, member 5	Ing5	8.52	8.74
N-acetylglucosamine-1-phosphate transferase, alpha and beta	Gnptab	8.52	9.14
castor homolog 1, zinc finger (Drosophila)	Casz1	8.52	8.56
cyclin T1	Ccnt1	8.50	9.43
zinc finger protein 821	Zfp821	8.49	9.08
GA repeat binding protein, beta 2	Gabpb2	8.49	8.57
RB1-inducible coiled-coil 1	Rb1cc1	8.49	9.12
chromobox homolog 4 (Drosophila Pc class)	Cbx4	8.48	9.61

zinc finger protein 672	Zfp672	8.48	8.84
empty spiracles homolog 1 (Drosophila)	Emx1	8.48	6.85
homeo box A3	Hoxa3	8.48	7.05
apoptosis antagonizing transcription factor	Aatf	8.47	9.29
zinc finger protein 384	Zfp384	8.47	8.64
deltex 2 homolog (Drosophila)	Dtx2	8.47	8.43
PHD finger protein 12	Phf12	8.47	8.87
zinc finger protein 775	Zfp775	8.47	8.40
BTB and CNC homology 1	Bach1	8.46	8.98
RIKEN cDNA 6720457D02 gene	6720457D02Rik	8.45	8.25
zinc finger protein 763	Zfp763	8.44	9.01
K(lysine) acetyltransferase 5	Kat5	8.43	8.93
transducin-like enhancer of split 4, homolog of Drosophila E(spl)	Tle4	8.43	9.19
neural proliferation, differentiation and control gene 1	Npdc1	8.42	8.53
TAF2 RNA polymerase II	Taf2	8.41	9.14
forkhead box J2	Foxj2	8.39	8.74
staphylococcal nuclease and tudor domain containing 1	Snd1	8.38	9.24
lysine (K)-specific demethylase 5C	Kdm5c	8.38	8.95
nuclear receptor subfamily 3, group C, member 1	Nr3c1	8.38	8.33
PWP1 homolog (S. cerevisiae)	Pwp1	8.37	9.03
transcription factor EB	Tcfeb	8.37	8.61
MAX gene associated	Mga	8.37	9.01
zinc finger protein 62	Zfp62	8.37	8.85
mastermind like 1 (Drosophila)	Maml1	8.36	8.89
zinc finger protein 560	Zfp560	8.36	9.18
Kruppel-like factor 15	Klf15	8.36	8.27
Pbx/knotted 1 homeobox	Pknox1	8.36	8.58
thyroid hormone receptor interactor 4	Trip4	8.35	8.32
zinc fingers and homeoboxes 1	Zhx1	8.35	9.21
zinc finger protein 787	Zfp787	8.34	8.85
zinc finger protein 827	Zfp827	8.33	9.14
zinc finger protein 148	Zfp148	8.33	9.31
Bmi1 polycomb ring finger oncogene	Bmi1	8.32	8.92
WW domain containing transcription regulator 1	Wwtr1	8.32	8.83
MYST histone acetyltransferase 2	Myst2	8.32	8.41
regulatory factor X, 7	Rfx7	8.32	8.55
general transcription factor IIF, polypeptide 2	Gtf2f2	8.31	8.74
zinc finger protein 369	Zfp369	8.31	8.60
E2F transcription factor 3	E2f3	8.31	8.88
RIKEN cDNA 9130019O22 gene	9130019O22Rik	8.31	8.50
transcription elongation factor A (SII)-like 1	Tceal1	8.29	9.12
signal transducer and activator of transcription 1	Stat1	8.29	9.16
lysine (K)-specific demethylase 5A	Kdm5a	8.29	8.91
RIKEN cDNA D330038O06 gene	D330038O06Rik	8.29	8.75
zinc finger, BED domain containing 4	Zbed4	8.27	8.97
ets variant gene 6 (TEL oncogene)	Etv6	8.27	9.35
CREB/ATF bZIP transcription factor	Crebzf	8.27	8.83
cyclin D binding myb-like transcription factor 1	Dmtf1	8.26	9.12
mediator complex subunit 21	Med21	8.26	8.95
cDNA sequence BC049349	BC049349	8.26	8.49
core-binding factor, runt domain, alpha subunit 2, translocated to, 2	Cbfa2t2	8.26	8.81
period homolog 1 (Drosophila)	Per1	8.26	9.09
zinc finger and BTB domain containing 41 homolog	Zbtb41	8.25	8.76
transcription elongation factor A (SII)-like 3	Tceal3	8.25	9.44
zinc and ring finger 1	Znrf1	8.24	8.98
cAMP responsive element modulator	Crem	8.22	8.65

nuclear transcription factor-Y alpha	Nfya	8.22	8.43
zinc finger and BTB domain containing 40	Zbtb40	8.22	8.65
interferon regulatory factor 3	Irf3	8.21	8.85
zinc finger and SCAN domain containing 12	Zscan12	8.21	9.00
period homolog 2 (Drosophila)	Per2	8.20	8.27
zinc finger protein 362	Zfp362	8.19	8.54
mbt domain containing 1	Mbtd1	8.19	8.61
general transcription factor II E, polypeptide 2 (beta subunit)	Gtf2e2	8.19	8.61
RuvB-like protein 2	Ruvbl2	8.18	9.23
jumonji domain containing 1C	Jmjd1c	8.18	8.76
zinc finger protein 612	Zfp612	8.18	8.64
hepatic leukemia factor	Hlf	8.18	7.14
CCR4-NOT transcription complex, subunit 3	Cnot3	8.18	8.64
RIKEN cDNA 5730403B10 gene	5730403B10Rik	8.18	8.65
human immunodeficiency virus type I enhancer binding protein 1	Hivep1	8.17	8.67
PHD finger protein 20-like 1	Phf20l1	8.17	8.82
heat shock factor 1	Hsf1	8.16	8.49
v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G	Mafg	8.16	8.32
zinc finger protein 46	Zfp46	8.15	8.81
YY1 associated factor 2	Yaf2	8.15	8.60
menage a trois 1	Mnat1	8.15	8.86
Sp2 transcription factor	Sp2	8.14	7.96
zinc finger protein 655	Zfp655	8.14	8.57
TAF5-like RNA polymerase II	Taf5l	8.14	8.18
homeo box C9	Hoxc9	8.14	6.70
estrogen related receptor, alpha	Esrra	8.14	8.59
recombination signal binding protein for immunoglobulin kappa J	Rbpj	8.13	8.19
PHD finger protein 20	Phf20	8.13	8.78
TAF11 RNA polymerase II	Taf11	8.13	8.75
expressed sequence AW146020	AW146020	8.12	8.29
peroxisome proliferative activated receptor, gamma coactivator 1 beta	Ppargc1b	8.12	8.61
POU domain, class 6, transcription factor 1	Pou6f1	8.12	8.59
zinc finger protein 367	Zfp367	8.11	9.00
programmed cell death 2	Pdcd2	8.10	7.97
zinc finger with KRAB and SCAN domains 6	Zkscan6	8.10	8.62
zinc finger protein 746	Zfp746	8.09	8.83
zinc finger protein 592	Zfp592	8.09	8.53
zinc finger protein 704	Zfp704	8.08	8.29
RIKEN cDNA 2310001H12 gene	2310001H12Rik	8.08	8.46
metal response element binding transcription factor 2	Mtf2	8.07	8.76
zinc finger protein 764	Zfp764	8.07	8.43
transcription elongation factor B (SIII), polypeptide 3	Tceb3	8.07	8.69
Zinc finger protein 212	Zfp212	8.07	8.58
myocyte enhancer factor 2D	Mef2d	8.06	8.25
nuclear receptor subfamily 4, group A, member 1	Nr4a1	8.05	9.19
pleckstrin homology domain containing, family F member 2	Plekhf2	8.05	8.79
transcription elongation regulator 1 (CA150)	Tcerg1	8.05	8.78
v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K	Mafk	8.04	8.56
zinc finger protein 111	Zfp111	8.04	8.64
zinc finger protein 84	Zfp84	8.04	8.34
MYC-associated zinc finger protein	Maz	8.04	8.66
zinc finger protein 661	Zfp661	8.04	7.69
activating transcription factor 7	Atf7	8.04	8.53
TSC22 domain family, member 3	Tsc22d3	8.01	8.79
glucocorticoid modulatory element binding protein 1	Gmeb1	8.01	8.78

l(3)mbt-like 2 (Drosophila)	L3mbtl2	8.01	8.74
trichorhinophalangeal syndrome I (human)	Trps1	8.01	7.68
zinc fingerprotein 618	Zfp618	8.01	8.57
zinc finger protein 651	Zfp651	8.00	8.21
PC4 and SFRS1 interacting protein 1	Psip1	7.99	8.60
tripartite motif-containing 33	Trim33	7.99	8.11
E74-like factor 3	Elf3	7.97	8.92
nuclear receptor co-repressor 2	Ncor2	7.97	8.58
RuvB-like protein 1	Ruvbl1	7.96	8.78
Max dimerization protein 4	Mxd4	7.96	8.45
predicted gene, EG631624	EG631624	7.95	8.11
zinc finger matrin type 3	Zmat3	7.95	7.95
zinc finger protein 688	Zfp688	7.95	7.79
RRN3 RNA polymerase I transcription factor homolog (yeast)	Rrn3	7.94	8.56
Zinc finger protein 498, mRNA	Zfp498	7.94	8.12
retinoblastoma 1	Rb1	7.93	8.10
upstream transcription factor 2	Usf2	7.93	8.35
CCAAT/enhancer binding protein (C/EBP), beta	Cebpb	7.93	8.34
nuclear factor of kappa light polypeptide gene enhancer in B-cells 2	Nfkb2	7.93	7.80
zinc fingers and homeoboxes 2	Zhx2	7.92	9.01
signal transducer and activator of transcription 5B	Stat5b	7.91	7.82
RUN and FYVE domain containing 1	Rufy1	7.91	8.16
IKAROS family zinc finger 5	Ikzf5	7.91	8.14
v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B	Mafb	7.91	7.89
homeo box B6	Hoxb6	7.90	9.07
RIKEN cDNA 2810021G02 gene	2810021G02Rik	7.89	8.38
metal response element binding transcription factor 1	Mtf1	7.89	8.46
zinc finger protein 7	Zfp7	7.89	8.74
sterol regulatory element binding factor 2	Srebf2	7.89	8.15
deformed epidermal autoregulatory factor 1 (Drosophila)	Deaf1	7.88	8.44
deoxynucleotidyltransferase, terminal, interacting protein 1	Dnttip1	7.87	8.24
zinc finger and BTB domain containing 24	Zbtb24	7.87	7.91
cDNA sequence BC018101 /// zinc finger protein 97	BC018101	7.87	8.48
zinc finger protein 236	Zfp236	7.87	8.09
Kruppel-like factor 4 (gut)	Klf4	7.86	7.60
v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F	Maff	7.86	8.65
AT rich interactive domain 5B (MRF1-like)	Arid5b	7.86	8.47
zinc finger protein 639	Zfp639	7.86	7.91
membrane-bound transcription factor peptidase, site 2	Mbtps2	7.86	7.89
POU domain, class 2, transcription factor 1	Pou2f1	7.85	7.89
cut-like homeobox 2	Cux2	7.85	8.10
general transcription factor II I repeat domain-containing 1	Gtf2ird1	7.85	8.14
H6 homeo box 2	Hmx2	7.84	8.47
nuclear factor related to kappa B binding protein	Nfrkb	7.84	8.11
zinc finger protein 192	Zfp192	7.84	8.49
zinc finger with KRAB and SCAN domains 3	Zkscan3	7.83	8.36
teashirt zinc finger family member 1	Tshz1	7.83	7.96
PR domain containing 4	Prdm4	7.83	8.86
zinc finger and BTB domain containing 17	Zbtb17	7.81	7.66
zinc finger protein 146	Zfp146	7.81	8.26
elongation factor RNA polymerase II 2	Ell2	7.81	8.52
RUN and FYVE domain-containing 2	Rufy2	7.81	8.11
timeless interacting protein	Tipin	7.80	8.32
zinc finger and BTB domain containing 33	Zbtb33	7.80	8.73
zinc finger protein 317	Zfp317	7.80	8.61
polymerase I and transcript release factor	Ptrf	7.78	8.88

nuclear receptor subfamily 1, group D, member 1	Nr1d1	7.78	8.80
zinc finger protein 322A	Zfp322a	7.78	7.87
sex determining region of Chr Y	Sry	7.77	7.48
KDM3B lysine (K)-specific demethylase 3B	Kdm3b	7.76	8.18
E2F transcription factor 6	E2f6	7.76	7.75
zinc finger protein 512	Zfp512	7.76	8.64
cyclin C	Ccnc	7.76	8.04
transcriptional adaptor 3 (NGG1 homolog, yeast)-like	Tada3l	7.75	8.38
purine-rich element binding protein G	Purg	7.75	7.40
E74-like factor 1	Elf1	7.74	8.68
zinc finger protein 26	Zfp26	7.74	8.48
Homeo box B2 (Hoxb2), mRNA	Hoxb2	7.74	7.61
zinc finger protein 810	Zfp810	7.74	8.52
gene trap locus 3	Gtl3	7.74	8.19
transcription factor CP2	Tcfcp2	7.73	8.75
suppressor of Ty 3 homolog (S. cerevisiae)	Supt3h	7.73	7.76
zinc fingr protein 551	Zfp551	7.73	8.35
LIM domain only 4	Lmo4	7.72	9.44
retinoblastoma binding protein 5	Rbbp5	7.71	7.79
SERTA domain containing 2	Sertad2	7.70	8.36
GTF2I repeat domain containing 2	Gtf2ird2	7.70	7.91
CCAAT/enhancer binding protein (C/EBP), delta	Cebpd	7.70	7.67
avian erythroblastosis virus E-26 (v-ets) oncogene related	Erg	7.70	7.64
YEATS domain containing 2	Yeats2	7.70	7.74
TSC22 domain family, member 4	Tsc22d4	7.70	8.33
RIKEN cDNA 2810021J22 gene	2810021J22Rik	7.70	7.93
sterol regulatory element binding transcription factor 1	Srebf1	7.69	8.00
zinc finger, ZZ-type with EF hand domain 1	Zzef1	7.69	7.72
nuclear respiratory factor 1	Nrf1	7.68	9.22
activating transcription factor 6 beta	Atf6b	7.66	8.12
zinc finger protein (C2H2 type) 276	Zfp276	7.66	7.50
mediator of RNA polymerase II transcription, subunit 25 homolog	Med25	7.66	8.62
RIKEN cDNA C920016K16 gene	C920016K16Rik	7.66	7.80
four and a half LIM domains 1	Fhl1	7.65	7.63
trans-acting transcription factor 3	Sp3	7.65	8.13
B-cell leukemia/lymphoma 6	Bcl6	7.64	8.54
zinc finger protein 410	Zfp410	7.64	8.16
E26 avian leukemia oncogene 1, 5' domain	Ets1	7.63	7.80
expressed sequence AI854703	AI854703	7.63	7.27
putative homeodomain transcription factor 1	Phtf1	7.63	7.94
PR domain containing 2, with ZNF domain	Prdm2	7.63	7.90
trans-acting transcription factor 4	Sp4	7.62	8.45
zinc finger protein 68	Zfp68	7.62	8.31
upstream transcription factor 1	Usf1	7.62	7.83
MyoD family inhibitor domain containing	Mdfic	7.61	9.09
ring finger protein 25	Rnf25	7.61	8.22
zinc finger protein 30	Zfp30	7.61	7.42
zinc finger, HIT domain containing 2	Znhit2	7.60	8.26
zinc finger protein 710	Zfp710	7.60	7.96
ring finger protein 138	Rnf138	7.60	8.05
LIM domain only 2	Lmo2	7.59	7.97
RB-associated KRAB repressor	Rbak	7.59	8.03
transducin-like enhancer of split 1, homolog of Drosophila E(spl)	Tle1	7.58	8.13
MLX interacting protein	Mlxip	7.58	8.02
zinc finger and BTB domain containing 7C	Zbtb7c	7.58	7.79
zinc finger and BTB domain containing 16	Zbtb16	7.58	8.36

lin-9 homolog (C. elegans)	Lin9	7.57	7.72
nuclear receptor binding factor 2	Nrbf2	7.57	7.40
interferon activated gene 203	Ifi203	7.57	7.34
ELK1, member of ETS oncogene family	Elk1	7.54	7.86
transcriptional adaptor 2 (ADA2 homolog, yeast)-like	Tada2l	7.54	7.66
nuclear receptor subfamily 1, group H, member 2	Nr1h2	7.53	7.94
zinc finger protein 715	Zfp715	7.53	7.59
zinc finger, FYVE domain containing 19	Zfyve19	7.53	8.05
zinc finger protein 652	Zfp652	7.53	8.31
Melanin concentrating hormone receptor interacting zinc finger protein	Zmynd19	7.51	7.36
sal-like 2 (Drosophila)	Sall2	7.50	7.48
polymerase (RNA) II (DNA directed) polypeptide D	Polr2d	7.50	8.27
zinc finger protein 59	Zfp59	7.50	7.67
peroxisome proliferator activated receptor alpha	Ppara	7.50	7.97
MAD homolog 7 (Drosophila)	Smad7	7.49	8.67
general transcription factor II H, polypeptide 4	Gtf2h4	7.49	7.98
MMS19 (MET18 S. cerevisiae)	Mms19	7.48	8.03
Zinc finger protein 458 (Zfp458), mRNA	Zfp458	7.48	8.39
RIKEN cDNA 6720487G11 gene	6720487G11Rik	7.47	7.79
transcription factor E2a	Tcfe2a	7.47	7.53
core-binding factor, runt domain, alpha subunit 2, translocated to, 3	Cbfa2t3	7.47	7.69
zinc finger protein 1	Zfp1	7.46	7.96
BRF2, subunit of RNA polymerase III transcription initiation factor	Brf2	7.46	7.26
RIKEN cDNA C330011K17 gene	C330011K17Rik	7.46	8.28
zinc finger with KRAB and SCAN domains 14	Zkscan14	7.45	7.62
RIKEN cDNA 5830417I10 gene /// similar to Dingo protein isoform 2	5830417I10Rik	7.45	8.00
ankyrin repeat, family A (RFXANK-like), 2	Ankra2	7.45	7.34
tumor suppressor candidate 4	Tusc4	7.43	8.03
mediator complex subunit 17	Med17	7.43	8.07
early growth response 2	Egr2	7.43	8.31
zinc finger protein 574	Zfp574	7.43	8.04
zinc finger protein 386 (Kruppel-like)	Zfp386	7.43	8.38
myeloid/lymphoid or mixed-lineage leukemia 1	Mll1	7.41	8.73
zinc finger protein 784	Zfp784	7.41	7.64
snail homolog 2 (Drosophila)	Snai2	7.41	6.90
SCAN domain-containing 1	Scand1	7.41	7.58
zinc finger protein 35	Zfp35	7.40	7.67
transformation related protein 53	Trp53	7.40	7.63
ring finger protein 166	Rnf166	7.40	7.05
hairy/enhancer-of-split related with YRPW motif-like	Heyl	7.39	8.23
zinc finger protein 277	Zfp277	7.38	8.12
TAF5 RNA polymerase II	Taf5	7.38	7.90
zinc finger protein 235	Zfp235	7.37	8.07
zinc finger protein 110	Zfp110	7.37	8.00
TAF6 RNA polymerase II	Taf6	7.36	8.07
predicted gene, EG240038	EG240038	7.36	7.67
DCP1 decapping enzyme homolog A (S. cerevisiae)	Dcp1a	7.35	7.69
zinc finger protein 12	Zfp12	7.35	6.95
RIKEN cDNA 4933403O03 gene /// predicted gene, EG245263	4933403O03Rik	7.35	6.17
regulatory factor X-associated ankyrin-containing protein	Rfxank	7.34	7.51
signal transducer and activator of transcription 5A	Stat5a	7.34	8.35
LIM homeobox protein 1	Lhx1	7.34	7.81
TGFB-induced factor homeobox 1	Tgif1	7.34	7.81
zinc finger protein X-linked	Zfx	7.34	8.07
sine oculis-related homeobox 4 homolog (Drosophila)	Six4	7.33	7.98
mediator complex subunit 27	Med27	7.33	7.76

peroxisome proliferative activated receptor, gamma	Pprc1	7.32	7.45
rearranged L-myc fusion sequence	Rlf	7.32	7.64
RIKEN cDNA 1200003I07 gene	1200003I07Rik	7.32	7.94
homeo box A7	Hoxa7	7.32	6.59
zinc finger protein 426	Zfp426	7.31	7.98
BRF1 homolog, subunit of RNA polymerase III transcription initiation fa	Brf1	7.30	7.56
special AT-rich sequence binding protein 1	Satb1	7.29	8.05
zinc finger protein 87	Zfp87	7.29	7.64
TAF9B RNA polymerase II	Taf9b	7.29	7.84
estrogen receptor 1 (alpha)	Esr1	7.29	5.63*
zinc finger protein 383	Zfp383	7.29	7.39
polymerase (DNA directed), epsilon 3 (p17 subunit)	Pole3	7.28	7.68
POZ (BTB) and AT hook containing zinc finger 1	Patz1	7.28	8.39
TGFB-induced factor homeobox 2	Tgif2	7.28	7.51
transducin-like enhancer of split 2, homolog of Drosophila E(spl)	Tle2	7.28	7.83
homeo box B9	Hoxb9	7.28	8.73
SET and MYND domain containing 2	Smyd2	7.27	8.19
speckle-type POZ protein-like	Spopl	7.27	8.05
myeloid/lymphoid or mixed-lineage leukemia	Mllt10	7.26	7.96
zinc finger protein 280C	Zfp280c	7.26	7.74
myeloid/lymphoid or mixed-lineage leukemia	Mllt1	7.25	8.32
RIKEN cDNA 9430025M13 gene	9430025M13Rik	7.25	7.43
HNF1 homeobox A	Hnf1a	7.24	6.94
zinc finger protein 790	Zfp790	7.24	8.11
homeo box C6	Hoxc6	7.24	6.12
zinc finger protein, autosomal /// zinc finger protein X-linked	Zfa /// Zfx	7.24	7.64
B-cell CLL/lymphoma 6, member B	Bcl6b	7.23	7.39
sine oculis-related homeobox 5 homolog (Drosophila)	Six5	7.23	7.94
mediator of RNA polymerase II transcription, subunit 12 homolog	Med12	7.22	8.14
zinc finger protein 579	Zfp579	7.22	7.56
zinc finger protein 799	Zfp799	7.22	7.96
MAX dimerization protein 1	Mxd1	7.22	7.75
zinc finger protein 454	Zfp454	7.22	7.72
bromodomain and PHD finger containing, 1	Brpf1	7.22	7.86
hairy and enhancer of split 1 (Drosophila)	Hes1	7.21	8.44
zinc finger protein 90	Zfp90	7.21	7.28
zinc finger protein 282	Zfp282	7.20	7.46
CCR4-NOT transcription complex, subunit 8	Cnot8	7.20	8.22
RIKEN cDNA 1700049G17 gene	1700049G17Rik	7.19	7.87
suppressor of hairy wing homolog 4 (Drosophila)	Suhw4	7.18	8.04
RIKEN cDNA 6430526N21 gene	6430526N21Rik	7.18	7.69
zinc finger protein 646	Zfp646	7.18	7.38
RIKEN cDNA 9630025I21 gene	9630025I21Rik	7.18	7.49
l(3)mbt-like 3 (Drosophila)	L3mbtl3	7.17	7.48
mediator complex subunit 26	Med26	7.17	7.08
ubiquitin-like, containing PHD and RING finger domains, 1	Uhrf1	7.16	7.49
zinc finger protein 385B	Zfp385b	7.16	7.24
tripartite motif-containing 24	Trim24	7.15	7.74
zinc finger protein 316	Zfp316	7.15	7.23
general transcription factor II H, polypeptide 1	Gtf2h1	7.15	7.44
mediator of RNA polymerase II transcription, subunit 6 homolog	Med6	7.13	7.86
zinc finger protein 39	Zfp39	7.13	7.87
zinc finger with KRAB and SCAN domains 17	Zkscan17	7.13	6.99
SET and MYND domain containing 3	Smyd3	7.13	8.00
zinc finger protein 788	Zfp788	7.12	7.71
RIKEN cDNA 2810047C21 gene 1 /// predicted gene, EG665577	2810047C21Rik1	7.12	6.99

IKAROS family zinc finger 4	Ikzf4	7.12	7.62
zinc finger protein 2	Zfp2	7.11	8.02
peroxisome proliferator activator receptor delta	Ppard	7.09	7.55
zinc finger and BTB domain containing 26	Zbtb26	7.09	7.40
zinc finger protein 512B	Znf512b	7.09	7.77
forkhead box N2	Foxn2	7.08	7.70
zinc finger protein 93	Zfp93	7.07	7.28
expressed sequence AI894139	AI894139	7.07	7.21
PHD finger protein 15	Phf15	7.07	7.28
WT1-interacting protein	Wtip	7.06	7.71
zinc finger protein 319	Zfp319	7.06	7.49
zinc finger protein 691	Zfp691	7.06	7.35
zinc finger protein 182	Zfp182	7.05	7.90
zinc finger protein 113	Zfp113	7.04	7.21
ubiquitin-like, containing PHD and RING finger domains 2	Uhrf2	7.04	7.90
AT rich interactive domain 3A (BRIGHT-like)	Arid3a	7.04	6.93
zinc finger protein 64	Zfp64	7.03	7.35
polycomb group ring finger 6	Pcgf6	7.03	7.27
CREB regulated transcription coactivator 2	Crtc2	7.03	7.38
Jun-B oncogene	Junb	7.02	8.13
transcription elongation factor A (SII), 3	Tcea3	7.02	6.84
zinc finger protein 532	Zfp532	7.02	6.44
Kruppel-like factor 13	Klf13	7.02	7.79
cDNA sequence D10627	D10627	7.01	7.22
Inhibitor of DNA binding 4 (Id4), mRNA	Id4	7.01	8.44
zinc finger like protein 1	Zfpl1	7.00	7.52
interferon regulatory factor 9	Irf9	7.00	8.02
homeo box C4	Hoxc4	7.00	3.34*
lysine (K)-specific demethylase 3A	Kdm3a	7.00	7.36
RIKEN cDNA 2810047C21 gene 1	2810047C21Rik	7.00	6.75
zinc finger protein 451	Zfp451	7.00	7.43
zinc finger, HIT type 3	Znhit3	6.99	7.40
expressed sequence AA987161	AA987161	6.99	7.88
MAX-like protein X	Mlx	6.98	7.15
zinc finger protein 623	Zfp623	6.98	7.59
RIKEN cDNA 2610008E11 gene	2610008E11Rik	6.97	7.19
aryl-hydrocarbon receptor	Ahr	6.97	7.48
zinc finger protein 637	Zfp637	6.96	7.44
general transcription factor IIH, polypeptide 3	Gtf2h3	6.96	7.08
GDNF-inducible zinc finger protein 1	Gzf1	6.94	7.40
predicted gene, OTTMUSG00000010657	OTTMUSG0000	6.94	7.42
zinc finger protein 462	Zfp462	6.93	8.10
putative homeodomain transcription factor 2	Phtf2	6.92	7.11
MYST histone acetyltransferase 1	Myst1	6.91	7.51
interferon regulatory factor 2	Irf2	6.90	8.09
period homolog 3 (Drosophila)	Per3	6.90	7.74
RIKEN cDNA 4930422I07 gene	4930422I07Rik	6.90	7.23
neuronal PAS domain protein 2	Npas2	6.89	6.43
nuclear factor of activated T-cells, cytoplasmic	Nfatc4	6.89	7.03
zinc finger protein 180	Zfp180	6.89	7.06
zinc finger, FYVE domain containing 1	Zfyve1	6.89	7.30
predicted gene, EG330503	EG330503	6.89	6.79
SRY-box containing gene 18	Sox18	6.88	6.88
Flt3 interacting zinc finger protein 1	Fiz1	6.87	7.64
forkhead box P4	Foxp4	6.87	6.77
Ets2 repressor factor	Erf	6.87	7.44

zinc finger protein 395	Zfp395	6.87	7.80
RIKEN cDNA 4930422I07 gene	4930422I07Rik	6.87	7.47
RIKEN cDNA 4933426I21 gene	4933426I21Rik	6.86	6.58
MKL (megakaryoblastic leukemia)/myocardin-like 1	Mkl1	6.86	7.18
pleiomorphic adenoma gene-like 2	Plagl2	6.85	7.46
cDNA sequence BC023179	BC023179	6.84	7.18
forkhead box P3	Foxp3	6.84	6.52
zinc finger protein 518B	Zfp518b	6.83	7.10
E4F transcription factor 1	E4f1	6.83	7.12
zinc finger protein 518	Zfp518	6.82	7.27
general transcription factor II H, polypeptide 2	Gtf2h2	6.82	7.47
RIKEN cDNA 6330416L07 gene	6330416L07Rik	6.81	7.21
calmodulin binding transcription activator 2	Camta2	6.81	6.97
SET and MYND domain containing 5	Smyd5	6.81	7.27
ubiquitously transcribed tetratricopeptide repeat gene	Uty	6.79	6.33
progesterone receptor	Pgr	6.79	8.06
cell division cycle associated 4	Cdca4	6.78	7.44
Kruppel-like factor 11	Klf11	6.78	7.59
homeo box D3	Hoxd3	6.78	8.09
zinc finger protein 668	Zfp668	6.78	7.16
nuclear receptor subfamily 5, group A, member 1	Nr5a1	6.76	5.94
candidate tumor suppressor in ovarian cancer 2	RP23-143A14.5	6.76	7.62
cDNA sequence BC066028	BC066028	6.76	5.93
zinc finger protein 74	Zfp74	6.76	6.44
zinc finger E-box binding homeobox 1	Zeb1	6.75	6.88
thyroid hormone receptor beta	Thrb	6.75	6.86
DCP1 decapping enzyme homolog b (S. cerevisiae)	Dcp1b	6.75	7.00
mesenchyme homeobox 1	Meox1	6.74	6.34
NK6 homeobox 2	Nkx6-2	6.73	6.45
ring finger protein 125	Rnf125	6.73	6.40
POU domain, class 4, transcription factor 1	Pou4f1	6.73	6.20
inhibitor of growth family, member 4	Ing4	6.73	6.99
brain expressed myelocytomatosis oncogene	Bmyc	6.72	6.59
zinc finger protein 667	Zfp667	6.71	7.53
IKAROS family zinc finger 2	Ikzf2	6.70	7.84
human immunodeficiency virus type I enhancer binding protein 3	Hivep3	6.70	6.16
calmodulin binding transcription activator 1	Camta1	6.70	6.61
CREB regulated transcription coactivator 1	Crtc1	6.70	7.24
RIKEN cDNA 5730403M16 gene	5730403M16Rik	6.69	7.03
zinc finger protein 563	Zfp563	6.69	7.45
retinoic acid induced 1	Rai1	6.69	6.69
nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	Nfkb1	6.68	7.54
SRY-box containing gene 5	Sox5	6.68	6.77
zinc finger protein 41	Zfp41	6.67	6.57
heat shock factor 2	Hsf2	6.66	6.31
v-rel reticuloendotheliosis viral oncogene homolog A (avian)	Rela	6.65	7.23
MKL/myocardin-like 2	Mkl2	6.63	8.18
E1A binding protein p300	Ep300	6.63	7.49
RIKEN cDNA A530054K11 gene	A530054K11Rik	6.62	6.62
zinc finger protein 692	Zfp692	6.61	7.90
homeo box D4	Hoxd4	6.61	6.94
zinc finger protein 109	Zfp109	6.60	6.73
polycomb group ring finger 3	Pcgf3	6.60	7.38
zinc finger protein 748	Zfp748	6.60	7.05
nuclear receptor subfamily 4, group A, member 2	Nr4a2	6.60	6.61
trafficking protein particle complex 2	Trappc2	6.59	7.22

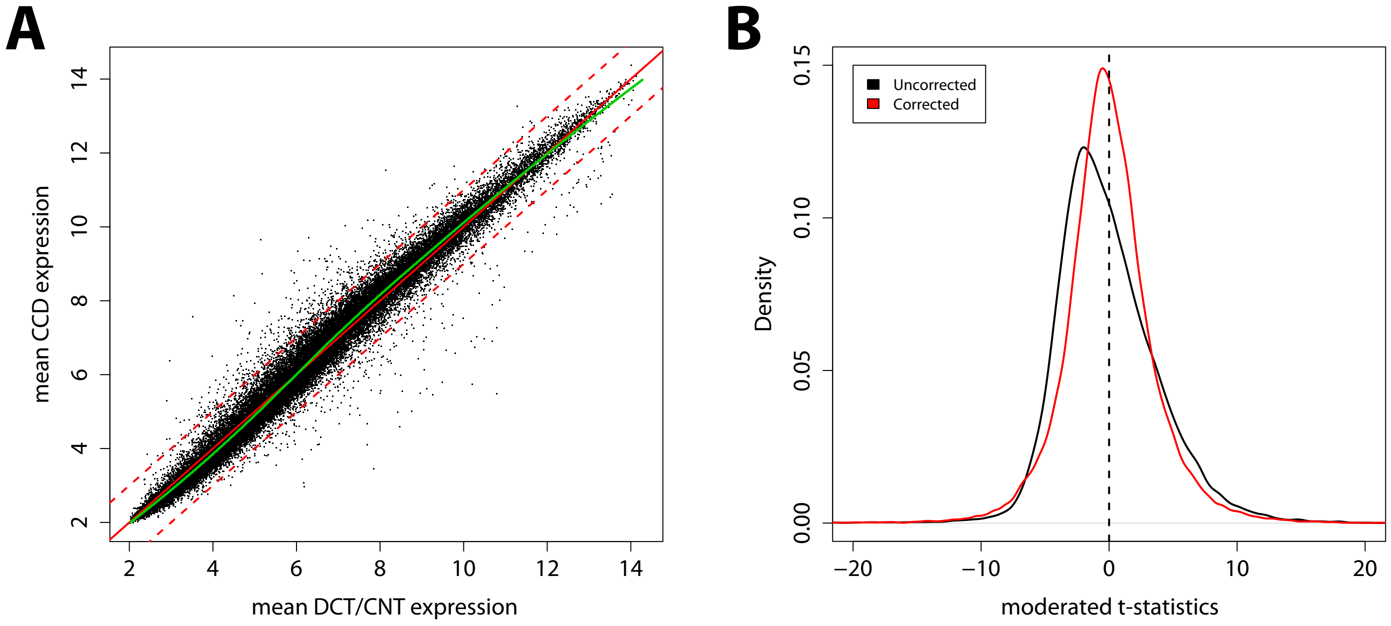
zinc finger protein 213	Zfp213	6.59	6.70
zinc finger protein 128	Zfp128	6.59	6.81
RIKEN cDNA A630033E08 gene	A630033E08Rik	6.59	6.47
zinc finger protein 157	Zfp157	6.59	6.83
polycomb group ring finger 5	Pcgf5	6.59	7.08
zinc finger protein 94	Zfp94	6.59	6.82
RIKEN cDNA 9230108I15 gene	9230108I15Rik	6.58	6.11
heart and neural crest derivatives expressed transcript 1	Hand1	6.58	6.41
PR domain containing 15	Prdm15	6.58	7.50
zinc finger E-box binding homeobox 2	Zeb2	6.57	6.18
zinc finger protein 142	Zfp142	6.57	6.69
mastermind like 2 (Drosophila)	Maml2	6.57	6.68
zinc finger protein 825	Zfp825	6.57	7.07
transformation related protein 63	Trp63	6.57	7.45
Zinc finger protein 120, mRNA (cDNA clone IMAGE:4222737)	Zfp844	6.57	6.59
nuclear receptor subfamily 2, group C, member 1	Nr2c1	6.56	7.38
nuclear factor of activated T-cells, cytoplasmic	Nfatc2	6.56	6.29
GA repeat binding protein, beta 1	Gabpb1	6.56	7.50
zinc finger protein 760	Zfp760	6.56	6.79
SRY-box containing gene 13	Sox13	6.56	6.68
zinc finger protein 143	Zfp143	6.55	6.93
TAF7 RNA polymerase II	Taf7	6.55	6.62
homeo box A5	Hoxa5	6.55	5.14*
four and a half LIM domains 2	Fhl2	6.53	6.31
teashirt zinc finger family member 2	Tshz2	6.53	6.17
zinc finger protein 295	Zfp295	6.52	7.30
zinc finger protein 324	Zfp324	6.52	6.88
Kruppel-like factor 16	Klf16	6.50	7.24
retinoic acid receptor, gamma	Rarg	6.49	7.36
zinc finger protein 628	Zfp628	6.49	7.02
RIKEN cDNA E430024I08 gene	E430024I08Rik	6.47	6.84
Kruppel-like factor 2 (lung)	Klf2	6.47	6.84
interferon activated gene 205	Ifi205 /// Mnda	6.46	5.74*
glucocorticoid modulatory element binding protein 2	Gmeb2	6.46	6.84
Jun dimerization protein 2	Jdp2	6.44	6.99
RIKEN cDNA 4930452B06 gene	4930452B06Rik	6.43	6.94
expressed sequence AU041133	AU041133	6.43	7.00
transcription elongation factor A (SII), 2	Tcea2	6.42	7.13
predicted gene, ENSMUSG00000053512	ENSMUSG0000	6.42	6.40
general transcription factor II E, polypeptide 1 (alpha subunit)	Gtf2e1	6.42	6.92
myocyte enhancer factor 2C	Mef2c	6.42	6.31
RNA binding motif protein 38	Rbm38	6.42	6.12
zinc finger protein 346	Zfp346	6.41	6.65
zinc finger protein 697	Zfp697	6.40	6.61
zinc finger protein 280B	Zfp280b	6.40	7.13
RIKEN cDNA A630033E08 gene	A630033E08Rik	6.40	6.88
transducin-like enhancer of split 6, homolog of Drosophila E(spl)	Tle6	6.39	6.40
sex comb on midleg homolog 1	Scmh1	6.38	7.14
zinc finger and BTB domain containing 39	Zbtb39	6.38	7.35
zinc finger protein 273 /// zinc finger protein 85, related sequence 1	Zfp273	6.38	6.88
zinc finger protein 334	Zfp334	6.37	6.35
zinc finger protein 169	Zfp169	6.36	6.90
basonuclin 2	Bnc2	6.35	6.35
zinc finger protein 28	Zfp28	6.35	6.87
small nuclear RNA activating complex, polypeptide 4	Snapc4	6.34	7.06
hairy/enhancer-of-split related with YRPW motif 2	Hey2	6.33	6.32

E2F transcription factor 5	E2f5	6.33	6.96
zinc finger protein 444	Zfp444	6.32	6.24
zinc finger and BTB domain containing 3	Zbtb3	6.32	6.17
zinc finger protein 37	Zfp37	6.32	7.21
AT rich interactive domain 3B (BRIGHT-like)	Arid3b	6.32	6.25
zinc finger protein 653	Zfp653	6.32	6.65
Ngfi-A binding protein 2	Nab2	6.31	7.38
teashirt zinc finger family member 3	Tshz3	6.31	7.28
MYST histone acetyltransferase monocytic leukemia 4	Myst4	6.30	6.86
inhibitor of DNA binding 1	Id1	6.30	7.77
atonal homolog 7 (Drosophila)	Atoh7	6.30	6.53
NK2 transcription factor related, locus 6 (Drosophila)	Nkx2-6	6.30	5.88
RIKEN cDNA 4930432O21 gene	4930432O21Rik	6.28	6.23
RAR-related orphan receptor beta	Rorb	6.28	8.23
Meis homeobox 3	Meis3	6.26	6.54
zinc finger protein 418	Zfp418	6.25	6.68
zinc finger protein	Zfp229	6.25	6.62
scratch homolog 2, zinc finger protein (Drosophila)	Scrt2	6.25	6.30
T-box 3	Tbx3	6.25	8.29
zinc finger protein 108	Zfp108	6.25	6.54
zinc finger and BTB domain containing 48	Zbtb48	6.23	6.26
RIKEN cDNA 6720489N17 gene, mRNA	6720489N17Rik	6.23	7.27
RIKEN cDNA A430033K04 gene	A430033K04Rik	6.23	6.90
basic helix-loop-helix family, member e22	Bhlhe22	6.22	8.22
elongation factor RNA polymerase II	Ell	6.22	6.59
SRY-box containing gene 11	Sox11	6.21	5.41
zinc finger protein 101	Zfp101	6.21	6.56
regulatory factor X, 2 (influences HLA class II expression)	Rfx2	6.20	6.06
zinc finger and SCAN domain containing 4F	Zscan4f	6.20	4.24*
occludin/ELL domain containing 1	Ocel1	6.20	6.54
zinc finger protein 341	Zfp341	6.20	6.61
transcription factor AP4	Tcfap4	6.19	6.15
Friend leukemia integration 1	Fli1	6.18	5.84
retinoblastoma-like 1 (p107)	Rbl1	6.18	7.17
zinc finger protein 689	Zfp689	6.18	6.49
CDNA sequence BC038328, mRNA (cDNA clone IMAGE:1531884)	Zfp708	6.18	6.87
predicted gene, OTTMUSG00000003825	OTTMUSG	6.18	6.11
delta-like 4 (Drosophila)	Dll4	6.17	6.89
nuclear factor of activated T-cells, cytoplasmic	Nfatc1	6.17	6.55
zinc finger protein 120	Zfp120	6.14	6.60
pleckstrin homology domain containing, family F member 1	Plekhf1	6.13	6.69
zinc finger protein 446	Zfp446	6.13	6.24
LIM domain binding 2	Ldb2	6.12	5.89
nuclear receptor subfamily 1, group H, member 4	Nr1h4	6.11	6.10
forkhead box P2	Foxp2	6.11	4.96*
Kruppel-like factor 7 (ubiquitous)	Klf7	6.10	8.52
caspase 8 associated protein 2	Casp8ap2	6.10	7.20
ets variant gene 5	Etv5	6.10	4.90*
zinc finger protein 597	Zfp597	6.09	6.34
zinc finger and BTB domain containing 5	Zbtb5	6.09	6.33
nuclear receptor interacting protein 2	Nrip2	6.09	5.09*
zinc finger protein 287	Zfp287	6.08	6.67
SET and MYND domain containing 4	Smyd4	6.08	6.53
zinc finger protein 709	Zfp709	6.08	7.37
PHD finger protein 1	Phf1	6.05	6.16
Meis homeobox 2	Meis2	6.05	6.25

ethanol induced 1	Etohi1	6.05	6.33
E2F transcription factor 2	E2f2	6.05	7.65
zinc finger protein 248	Zfp248	6.05	6.67
cDNA sequence AB182283	AB182283	6.05	6.05
zinc finger protein 354C	Zfp354c	6.04	6.86
transcription factor EC	Tcfec	6.03	5.59*
zinc finger and BTB domain containing 7B	Zbtb7b	6.03	6.51
transcription elongation factor A (SII)	Tceanc	5.99	6.31
CREB regulated transcription coactivator 3	Crtc3	5.99	6.09
ets variant gene 4 (E1A enhancer binding protein, E1AF)	Etv4	5.97	5.00*
zinc finger and AT hook domain containing	Zfat	5.96	6.11
jagged 2	Jag2	5.94	5.76*
transcription factor 15	Tcf15	5.94	5.73*
zinc finger protein 60	Zfp60	5.93	5.95
zinc finger protein 493	Zfp493	5.93	6.29
nucleus accumbens associated 1	Nacc1	5.92	5.76*
E74-like factor 5	Elf5	5.91	9.57
SERTA domain containing 3	Sertad3	5.90	6.75
nuclear receptor subfamily 6, group A, member 1	Nr6a1	5.90	6.84
zinc finger protein 654	Zfp654	5.90	6.49
zinc finger protein 595	Zfp595	5.90	6.67
zinc finger protein 160	Zfp160	5.89	6.34
zinc finger protein 407	Zfp407	5.89	6.88
runt related transcription factor 1	Runx1	5.87	5.81
zinc finger protein 52	Zfp52	5.87	6.18
H6 homeo box 3	Hmx3	5.86	7.50
RIKEN cDNA A830023I12 gene	A830023I12Rik	5.86	5.85
Zinc finger protein 40 (Zfp40), mRNA	Zfp40	5.86	6.20
interferon regulatory factor 5	Irf5	5.86	5.87
aryl hydrocarbon receptor nuclear translocator-like	Arntl	5.85	6.17
zinc finger protein 385C	Zfp385c	5.84	5.44*
nuclear receptor subfamily 0, group B, member 2	Nr0b2	5.84	6.25
ovo-like 2 (Drosophila)	Ovol2	5.83	6.43
hypermethylated in cancer 2	Hic2	5.81	5.50*
zinc finger protein 275	Zfp275	5.80	5.92
zinc finger protein 568	Zfp568	5.79*	6.25
RIKEN cDNA 1700029I01 gene	1700029I01Rik	5.79*	6.69
expressed sequence AI987944	AI987944	5.78*	6.71
zinc finger, FYVE domain containing 26	Zfyve26	5.75*	6.79
zinc finger with KRAB and SCAN domains 5	Zkscan5	5.70*	6.42
zinc finger protein 711	Zfp711	5.70*	7.66
similar to SRF-dependent transcription regulation associated protein	LOC636713	5.68*	6.31
TEA domain family member 3	Tead3	5.63*	5.92
signal transducer and activator of transcription 2	Stat2	5.63*	6.06
zinc finger and SCAN domain containing 22	Zscan22	5.62*	5.90
CDNA sequence BC062115, mRNA	BC062115	5.62*	5.84
zinc finger protein 53	Zfp53	5.6*	6.77
avian reticuloendotheliosis viral (v-rel) oncogene related B	Relb	5.59*	6.10
E2F transcription factor 1	E2f1	5.59*	6.22
zinc finger protein 11	Zfp11	5.55*	5.82
MAD homolog 6 (Drosophila)	Smad6	5.54*	6.26
ets variant gene 1	Etv1	5.53*	5.99
interferon regulatory factor 8	Irf8	5.49*	5.91
predicted gene, 380850	380850	5.48*	6.05
zinc finger protein 61	Zfp61	5.46*	6.06
zinc finger protein 758	Zfp758	5.46*	6.19

RIKEN cDNA 3110052M02 gene	3110052M02Rik	5.45*	6.69
zinc finger protein 472	Zfp472	5.44*	6.07
zinc finger protein 202	Zfp202	5.44*	5.93
OVO homolog-like 1 (Drosophila)	Ovol1	5.40*	6.24
myelocytomatosis oncogene	Myc	5.36*	6.92
zinc finger protein 51	Zfp51	5.35*	6.32
zinc finger protein 719	Zfp719	5.33*	6.20
zinc finger protein 513	Zfp513	5.33*	6.17
zinc finger protein 429	Zfp429	5.31*	6.41
zinc finger protein 239	Zfp239	5.30*	5.91
cAMP responsive element binding protein 3-like 4	Creb3l4	5.30*	5.82
general transcription factor IIIC, polypeptide 3	Gtf3c3	5.30*	5.96
zinc finger and BTB domain containing 34	Zbtb34	5.29*	6.67
scleraxis	Scx	5.25*	6.79
v-myc myelocytomatosis viral related oncogene	Mycn	5.24*	6.53
filamin binding LIM protein 1	Fblim1	5.24*	6.16
predicted gene, EG434179	EG434179	5.23*	6.00
zinc finger protein 335	Zfp335	5.19*	6.36
pre B-cell leukemia transcription factor 3	Pbx3	5.15*	7.30
cDNA sequence BC066107	BC066107	5.13*	5.90
zinc finger protein 438	Zfp438	5.13*	5.89
twist homolog 1 (Drosophila)	Twist1	5.07*	6.34
cullin-associated and neddylation-dissociated 2 (putative)	Cand2	4.92*	6.44
RIKEN cDNA 2210010B09 gene	2210010B09Rik	4.89*	5.84
expressed sequence AI449175	AI449175	4.86*	6.17
Kruppel-like factor 5	Klf5	4.6*	6.46

* - the A_value is below the cut-off level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