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Supplemental Table 1: Primer sequences for MassARRAY assays

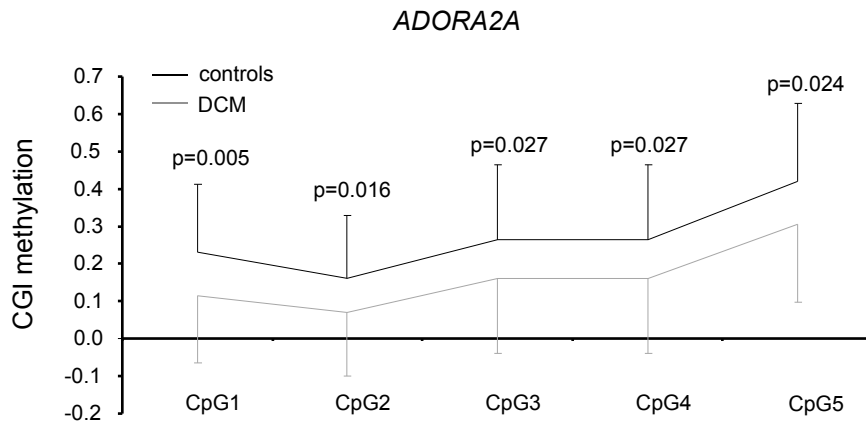
Gene	Primer (forward)	Primer (reverse)	Target Genomic Sequence
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ATP2C1	ATTGGATAAAGGTATAGT TGTTAAAGAAG	AACAATCACAATCTCAAC AAACAAC	ACTGGACAAAGGTACAGCTGCTAAAAGAAGTGTCTGTTTCATTGGCTTCGACAGCTG TACGACTGGTTTCTAATTGCTGTCCAGCCTCTCCCAAGTTCCATATACCACAAACG AATGAAAAGATTAGCTCTCCCTGGAGCTCTCTGAGGCTGAACCTTGCTCTCTCATT ACACATGGTAAGTAAAGCACACCCTTAAAGAATTTGGGAAGTCGCCCGCGATTAC CGGCTCCCCCAAGAACCAAGCAGTCACTGCAGGGTTTTGCAAGTGAGAGTGCAG ACTCGGAGGCTGCTCAGGTGCTCCAGTCCCTGGCAGGAGCATGGACACCTCGC CCCTTCTCCGTGGCCCTCAACGTTGCCTGCTGAGATTGTGACTGCC
CCDC59	TTTTTAGTGAAGTAGAG TGGGAAG	TTAAACAACCTCTTAC ACAATCC	CCCCTAGTGAAGCAGAGTGGGAAGCAGTGGGTGGTGGGGTAGGGCGGGCGGG AAGGGAGGCGGAGGAGAAGGTCCCGCAGACGAAGCGAGCCCTGGTGGGAAGC CAGCAGAACCCAGTGGCTGGCGGGGAGGCGGGCGCCCTGGTGGGAACCGGA GGAGGGTGGGATTAGTTGAGGGGTGGGGTGGGATGTTCTTTGAAATCAGGATC ACTCTTTCTTTGGGTGCTTGTGTATGTCACAATTTAAAGAAAGCAGGAACAGGGC AGGGGAGTTCCTTATCTAGTAATTCATAATAATTGACGCTAGGGAACCTAGGGGA GCAATGCTCTCAGAGTTTATAAATGCCAGCATGTGGTGGAAATTAAGTCAAGCT TAATAAGATAATTTCAAGTGGTGGTAATGAAGTAGAAAAATAAACAGTGAATGTG GTAGGGATTGTGAAGGAGGCTGCCTCAA
CLDN4	GTTTATTATAGTTTTTT TAGATGGTTTG	CATCAAACTAATTTAT CTCCTAATCA	GTTCCATCAGTGGCCCTCCAGATGGTCTGCGAGGTGACAATGTTGCTGCCGATGA AGGCCGTACGCGCCACATGGGCAGCGCAGCACAGCATGACGGCCAGCCAGC CCAGGACGGCCAGCGCATGCCATTACCTGTAGCCCATGGAGGCCATTGTTCA GCGTCCACGGAGTTGAGGACCTGGAAGGCTGAGGGGATCCGGCTGGGGGCGC GTAGGATCCAAGCGCTGGGACGACTTAACGTTGCGAGAGTGCACCTTTGACC GTGAGTCAGGAGATAAAGCCAGTCTGATGC
ERBB3	GGAGATTTTTAGTAGAG AATAGTTTTTTT	TACTACCAAAACCTAC TAATCCC	GGAGATTCTCCAGTAGAGAACAGGCCCTTAGGTTGCATATCAATAGGGAGCATGT TTAAGGAATGTAGCCGGTAGTCTTTGCTAGGTGTGAGGGGTGAAATTTTTCTTTAT CAAGGCTCAACTGTTTTGAAAGTCTTACAGCTTGAAGTTCTGGAGAAAACAATAGG CTCTCCGGGAGATCCCGAATACCAGTTTAAAGGATTTGAAATGCAAGGCCCTCT GGGACTCCACTGCCAGGATGGGCACCAGGCGGCGCCGCTGGATCCGTCGCCG GACTAGCAGGGCTTTGGGCGAGCA
FDX1	TTTGTTTTATAGTGGGA GAATTTATTT	AACCTATAAAAAATTAA CAAAAAAAC	TTTGTTTTACAGTGGGCAAGATTCACTTGTCTAATCTGACTCCAAGATGACACAAT TTCCAGTTTTTTTTTAAACGGCTAGGGGATGGGGGTATGCGGAACAGAACACAGT GGTCTAGCTAACCGATTTCGGCTAGACGCTCCAGCTATCTTCAAAATATTTTTGTTTCT GCACGGCACTTACAGCCGCTAAAAAAGCATCCAGCTTACAACGGAACTGGAGGGT TGTAAGGCCCCCTGCGCTGGCCCGCCCATGGACCGGGCGCGTGGGCGT GAGAGCGGGGCGGGCCGCGCTCTGCTTGCCTAATGTTCTTTATAGGTC GACTCTAAATCTAGTGAAGGGTGAATGGGAGGCTAGAACAGCCCGCCCTCCCT GCAGGAAGCCCCATTGGGTTGGGCTGGGAAAAGGACAGACTGGCTGAGGG GGGAAGGGCCTGGAGCCGGGGTGGTGGGGCAGCGGGGATGTCGGGGTGGC GGGGTGGGGGAAATTTCTAAAATAAGGAAACCGTAGCCCGGGGGTCCCGGTT TCCATATAACAGGCATCTCTGAAGTGCCTGTGCTGTGCCTGGCGTGTGCTAGGGA GACACTTCCATTCATTCTCCACTCCAGTAACTGAGCATCTATTAGGCTCCAGCC CCTATGCTGGGTTCTGAGGATGCAGCGACGAGAATAGAAGACAAGAAATGTTCC TTCTCTGGAGCTTACCTTCTGCTTTGGA
FLJ20701	GATTTTAAATTTAGTGA GGGGTGAA	TCCAAAACAAAAATAAA CTCCAAA	GACTCTAAATCTAGTGAAGGGTGAATGGGAGGCTAGAACAGCCCGCCCTCCCT GCAGGAAGCCCCATTGGGTTGGGCTGGGAAAAGGACAGACTGGCTGAGGG GGGAAGGGCCTGGAGCCGGGGTGGTGGGGCAGCGGGGATGTCGGGGTGGC GGGGTGGGGGAAATTTCTAAAATAAGGAAACCGTAGCCCGGGGGTCCCGGTT TCCATATAACAGGCATCTCTGAAGTGCCTGTGCTGTGCCTGGCGTGTGCTAGGGA GACACTTCCATTCATTCTCCACTCCAGTAACTGAGCATCTATTAGGCTCCAGCC CCTATGCTGGGTTCTGAGGATGCAGCGACGAGAATAGAAGACAAGAAATGTTCC TTCTCTGGAGCTTACCTTCTGCTTTGGA
GF1	TTTATTTAATGAGTAAA GGGTGAGGT	CCTAAAATCATACCCAA CACTAAAT	TCCACTCCAATGAGCAAAGGGTGTAGGCTTTGAGTATACACAGCAGGCCACACACT ATGGGTCATGGCATACAGTCTAGCGTTGGAGGTTGCTGCATTTGTCATGTATCTAT GAGTTAGGTTTTAAGTTTTTCCCCCTGTTCTATTAATAATAATTAAGTAAATTAAC CCCACTATTCATTTACTCAGTCCACAGCCTTTTGTAAAGAGCCCGCTAGGACATA AAGATGAAGATCCAGTGCCTACCCTCATGAAACATAGAATCCGAGCCGAGGAGCT TACTTTGCAATAGTCATCCAAGTGGTCTTTATGGCGCTTACTGCTCCCGCCAAC ACCCAGTGCTGGGTATGACCTCAGG
GSTM5	GGAGGGGGTTTATTGAT TTTAGTTT	TAACCTTCTACACCAA ACCAACC	GGAGGGGCTTATTGATTCAGCCCGGGCGCTGCTCGGGGGCTACAGAATGG CGTGTTCGGGGTTGTGGCGGGCCGAGGGGCGGGGTCGCAGCAAGGCCCGCCT GTCCCTCCTGGGCTCTCAAAGTCTGAGCCCGCTCCGCTGATGCCTGTCTGCAG AATCCGACCAACCAAGCACCATGCCATGACTCTGGGTAAGTGGACATCCGTTG GGTAAGCGAGGCTCTGTTGGTGGGACAGGGGGCGGAGGCGGGATGTGTG GAGTAGTGCAGGACTGGCTCTAGGGACCGTTCCTTTCAGGGCTGCCCGCTCA GAAGGGCCTGTGCATGACGCTGTGTGTGTTTGGGGTGGGGGCGGGTAGAGGA GGCAGCGGTACGTGAGTATAGACTAGGGCTGGCCTGGTGCAGAAAGTAC
HOXB13	GGTAGTTTTGGTTTTGG GTTTT	ACTATCCCTAAATCTAT CTCTCCC	GGCAGCCCTGGCTTTGGGCTGGGTAAGTACTAGCACCCAGTTCACTCCCGGTACCC TTCTGTCCAGATGCTCTGGAATGAGTGTCTCCGGGCCCAAGGAGGTGCCCTG GACGCCCTTACCAGGGACTCGCTACTGCCAGAATGCTCTGGAGGCCCTGATTTG GGTGAGGCTGAGGGAAGAGCGGGAGACACGAACGTAGACGTAGAAGACATCCGTTG GATCTGGATGGAACCCAGGACTCCACTTCCGACCTGAAGGGGAAATGGAGCC TCTAGAGTGGCCTGTGGAAGGGTCTGGATTTCCCTTTAAGTAAAGACATACGGAGG GACGGAGCCACAGGACTTGAAGGAGGGACGGGGAGAGGAGAGATGAGACT AGGGACAGC
ID4	AATGGAGTGTTTTTTTA TTGGTT	AATATCCTAATCACTCC TTC	AATGGAGTGGCCTTCCATTGGCCCGAGCGTCACTCCCGAGGTGGCACTGCCCG CCTGATGGCTGGCCACTCCAGACCCCGCCCACTCTCCACTCGGATAGCCCG ACTCCCGCCCGCCAGCAGCCCGGAGCCCGCCCTCGCTCTCCCTCCGGC CCCGCCCGCCCGCCAGCGGGCTCCGCTCGGCTCGCGCTGCGACCCGGCCCGC CGCTGTCCCGCCCGGGGCGCACGGCTATAA

LY75	GTATTTTGTAGGTTT TTGGGG	AAAAATCATAAATCCCTT TCCAATC	GCACCTCTGTCTAGGCCTCTGGGGGCCCCCGGCCCGCCCGCCCGCCCTCGG CCAATCAGACGTGCGTCTCTCGGCCCGGGGGGAGCGGGCCAGGTGTGGAA ATGAACAGGGCTGGGGCCTAGATACCTGCGTGGGTAGGACCCCGGAGGAAG GTACGTGCGGATCGGTGGGAGAGCCAGGCACAGAGGCTCCTGCAGTGGAGG GTTCCGGTCCCGCTTTCATCAGCCAAGCTGGGAGATCGGCCCTACTGGGA CTTGGCACCGCCCTGGTGGTGGTTCTATCAGTTTAGAACCCTTGGCCTCTGCCTG GCGCACTGTGTCAGGACGACTTCTCCATTCCAGCCTGGACTGGAAGGGACCC ATGATCTCT
NAT1	TTTTTTAGGAAGTAAAA GGAATGTT	TCAAACCTCCATATCTC ACTATCCC	CCTCCTTAGGAAGTAAAGGAATGTAGTGTGGATTTTGCATTGGAGGCTAGTCT GACCCCACTGCAGTGAACACAGCACTGGGCAGAGCCTCCAAGGCCCTTATTCTA GGCTGGAGGCCACAGAGGAGCATTTAGACCCCGCCCGGGTCAAGGAAATC TGCTACCTCAGCAGGAGGAATCCAAGTCCAGTCCACTTCAACAACCACTAACTAAA GTGGCCTTCCGCGAGCCCTAAACAAGATTGCACTCAGGTAGATTATTTGGAAG ATGATTTAAGGACGTACCAGTGCAGGAGTTGTCGCGGGACAGTGAGACCAGGGCA GTTTGAC
PPARGC1A	GATTTTTTAAAGTTTTT GTTTGG	ACAAATACCTTCAATTCA CTCTCAA	GATTCCTTAAAGCTCCTGCTGGACTACTTTCTGGCTCCTCTTTGCCAAGC CCATCCCCCTTACAGGAATAATAGCATCTGAGGGAAGCGTCAGTTGTGGCTGCAG CGCCGAGCCCTGCCAGCTCAGTGTACTCCATACAGACTCAGAGTCCG GTTGCACATGTCCACGCCATCCAGCTCCTGAATGACGCCAGTCAAGCTTTTTCAAC TCCAATCCAGTGACACAGACACTCATGACGCAACCCAGCCCTTACTGA GAGTGAACGAAAGCCCTGT
SLC9A6	GTTTTGATTGGGTAGG GGT	AACTACCATAAATCATA ACCAAACC	GTCTTTGACTGGGCAGGGGCTTCGGACGGCGCGGGAGAGGCTAGAGCCATG GACGAGGAGATCGTGTCCGAGAAGCCGAGGAGGCCACCCGAGGACAGC GCCAACCTGCTCATCTTATCTGCTCACCCTCACCACTTCCACAATCTGGCTC TTAAGCACCCCGGGCCCGCTTCTGACGAAACCCGCTGGCTATGATTTATGG CAAGTTC
SULF2	GAGTTTTGTAAAGTAGA TAAAGAAAAAT	TAACACACAAACAAAAA ACATC	GAGTCTGTGAAAGCAGATAAAAGAAAACATTTATTAACGTGTCATTACGAGGGGAG CGCCCGCCGGGGCTGTGCGACTCCCGCGGAACATTTGGCTCCCTCCAGCTCCG AGAGAGGAGAAGAAGAAGCGAAAAAGGAGGAGTTCAGTCTTTCCAGCAAGT GGACCTGATCGATGGCCCTCCTGAATTTATCACGATTTGATTTATTAGCGATGCC CCCTGGTTTGTGTGTATC
TDG	TGGTTGGTAGTATTTAGA TAGTGGTTG	ATATACACAAACCCCAA AAACAA	TGGCTGGCAGTACCAGACAGTGGCTGGACTAAGCTCCTCCTCCAGGCTTCTACC GTCCCCACGGACCCCTTTCTGTGCTGCACTTCCGCTCCTCGGAGCCAAATCCC ACGCGTACTGGCCGTACGTGATGTAGGACAGCCCAATCACGCTCACCCCTTCTC GTTGGCGCCAGCTCCGCGCTTGGCCTTTCGGGAAGGGTGGAGACCAGAAAGA CGGGACTAGGAGCGCTCTGCCGACGTACGCTTTTGTCTCCAGTATTTTCGGGGGG TGGTGACCGCTGGGGATAGGGTGTCTGCTTGGGGTGTGTATAT
TFF1	AGGTTGTAGAGTTGGTT GTGGTT	AACTTTCTAAATCTCAA TCCCTCAA	AGGCTGCCAGAGTGGCTGTGGCCCCACAGAGCAGGAAGAAGCACGCCCTTACCTG TCTGGGCTCGGCGAGGGTGCAGAGGGCCAGCATGGACACCAGGACAGGGCGC AGATCACCTTGTCTCCATGGTGGCCATTGCCTCCTCTGTCTCAAAGCCAGCC CGAGTCAAGGATGAGAGGCCCGCCGAGCCCGGATTTTATAGGGCAGGCTCTGTT TGCTTAAAGAGCGTTAGATAACATTTGCTAAGGAGCCCGGGGATCCTCTGAGAC AATAATCTCACTGATTTTTATCAAAGGTGTTCTAGACATGGTCAAGCTACATGGA AGGATTTGCTGATAGACAGAGACGACATGTGGTGGAGTCTCTGGCTGAGGGATC TGAGATTCAGAAAGTC
TKT	GGGAAGGTTATTATTATT GTTGTTTT	AAATCCCAAAATCTACA CCCA	GGGAAGGCCACCATTACTGCTGTTCTACAGAACCGGCCCTCTTAAACCTCTCCAC CACCTGGCTGTGTGGCGCCCGGGAGTGTCCCCCTTCCAGATGGGAAACGG AGGCTCCGAGTTAGTACAGTACCAAGTTACACACAGGGAGATCTGATTTGAGCC CCAGCAGTCCGACTCTAGAGACCCTGTTTTAATTCTCTTGCAGGAGACTCGGGG GCCCGGCTTCTCCCACTCAGACTACGCTCCCTACCCTGTCTCTGCCACCC CTGGGTTGGTCCGAGTTTGGAGCAGGGGGCTGCTGAGACGCCAGGACGGCGG GGCTGATTGGGGAAAGGGGAGGAGGGCGGTGGCACGTGGGTGAGAACCCCT GGGATCC
XRCC5	GTTTTTGTAGGTTTGA AAGGGG	AAAAAAATCTAACTCCA AAACTCTAA	GTTTCTGCTAGGCCTGAAAGGGGGCGGGAACCGTGCCCGGAACTCTGAGCAT GCGCAGATCCCGCCGAGCTTGGCAGATCCCGCCGAGCTCGCAGATTTCCGG CCGAGCATGCGCAGATTCTCTCCGAGCATGCGCAGATTCCCGCCGAGCATGCGCA GATTCGGCCGAGCATGCGCAGATTCTCTCCATTCCGCGTGTGCGGAGCGTGTG GTGTTTGGCCGCTGAAACGCTAGTACGACAGATTTACTTAAAGATTCACTTAATC ACTTAAAGATTCAGTCCCTTTTCTCTATTGAGAATAACACCTAAGGCATTTGTGT CAGAGCTCTGGAGTTAGATTTCTTT

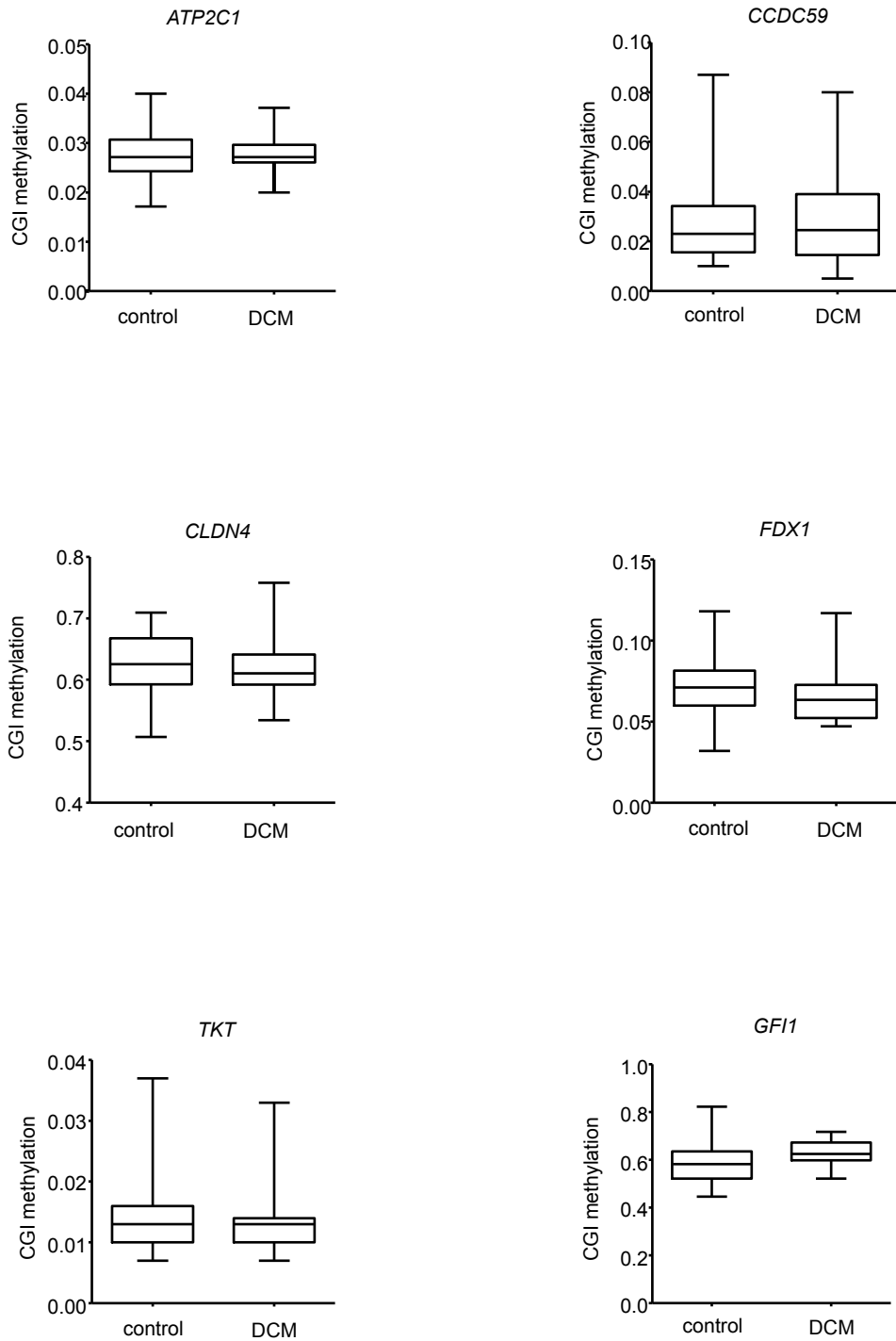
Supplemental Table 2: Primer sequences for promoter luciferase assay

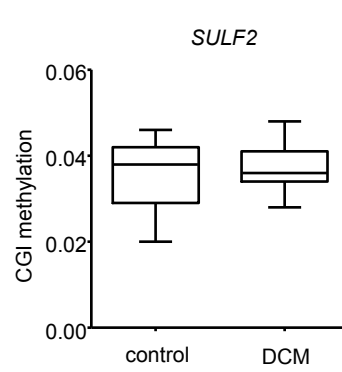
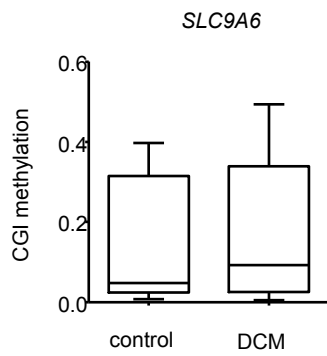
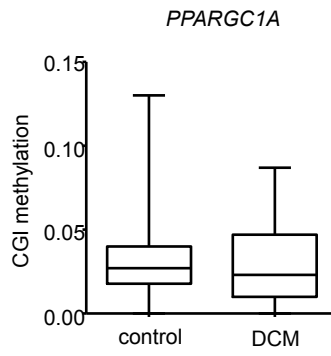
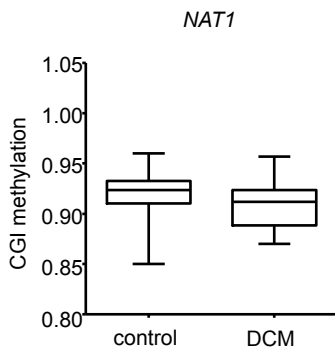
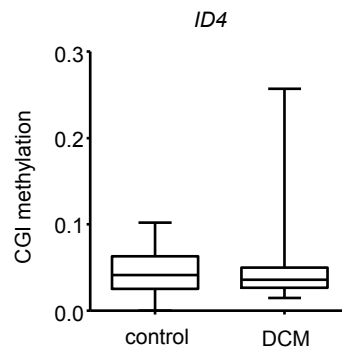
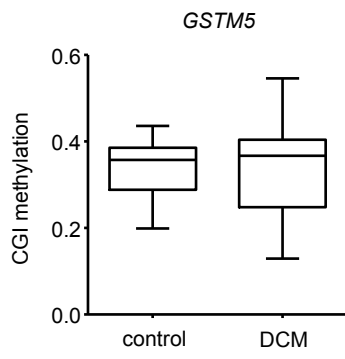
Gene	Primer (forward)	Primer (reverse)	Target Genomic Sequence
LY75	TGGCACTACCCTGAACA TCA	CATGAAATTTCTGGTTCT GCAT	TGGCACTACCCTGAACATCAATGAAGGCTGTCTGTTTCTGGTCTGCTTCCGCAGTG AGAGGCAGCAGGTCCCCAAGCAGGCGACCTGCCCTTACCCTGAGGCTGTCAGCC TTGGGGGAGCGGGTCAATTTGGAGCTGATAAACCAATGAGAAGAAAGTTTGTTC TCTAGGCGGTGGGTGAGGGCATCATAGCTGACTCTTGGTCTTGGTCACTTTCGGAG GAGATGGTTTATTAACCTGACTTCCTTCTGATGCGCACCGTAGGCCAGTGAAT CCGGGAATCGTGGGAATCCTTGGCGCTGTGGGTGGAGGCTCCTCTTGGCCCTGT GGCCAAGGTGACCAAGGGCCGAAGGAAAAGCGAGAACGGGAGGGACGGGACGCA AGAGGGCAGATGGGAACCCATACTCCAGCAACATTATATAAGAGAGGGCAGCAT GGAGCAGCGCACCCGGCCAAAAAGCCTCCGTGCGCCTACTCTACGGTGACCCGC GTCCCTCTGCACCAAGGGCCCTGTCTCCACATCCACCGGCCCTCCTCCG GGCCCCGAGGGCACTGGGGCGCTTCTCTGCCAGACCTCCCTTGCAGTCACTC TTCCGGCTCCAGAGCCCCCGCCCCAACAGCAAAGCAGCCGTGACCTGCCCCAG GGCGCAGCCCTGCCCAAGGCTGGAAGGCAGCAGAGCTGTGGCGTCGAGGCACC CAGCGGACTGCGGGCTGGCGTCCCGCGGTTACCTGCGGGCCAGAGGGCTCC GCGAGATCGAAGAACCAGAAGAGCAGCATGAGGAGCCCCGGCGGGCGGAGGG GTCGCCACGCTGCTCATCTGAGCTGGCGCAAGCCTTCCGGCCGGTCTCCG GGCGCACGGCTCCCGCCCGCTGCTGAGCGCGGCTGCCCGCCCGCACCT CTGTCTAGGCCTCTGGGGCGCCCCGGCCCCCGCCCGCCCTCGGCCAATC AGACGTGCGTCTCCTCGGCCCGGGCGGAGCGGGCCAGGTGTGGGAAATGAAC AGGCTGGGCGCTAGATACCTGCGTGGGTAGGACCCGCGAGGAAGGTACGT GCGGATCGGTGGGAGGCCAGGCACCAGAGGCTCCTGCACTGGAGGGTTCGG TCCCCGCTTTCATCAGCCAAGCTGGGGAGATGCGGCCCTTACTGGGACTTGGCA CCGCCCTGGTGGGTGGTTCTATCAGTTTGAACCTTGGCCTTGCCTGGCGCACT GTGGTCAGGGACGACTTCTCCATTCCAGCCTGGACTGGAAGGGACCCATGATCTC TTCTACCCGGAGGAGGAAGTGAGCACCTGCCCTGTGGGTGGCTGCGGCCAAGCC TAAGAATTCAGTCGTCTTGGCAACGCTTGGGTATTTGACAGTGCAAAACAAGGT GGAATAATGGTACACTGCAGTTCTACCCATAGTTGTTAAAGAATTAAGCAAGAATT ACTAGAATGACCAAACGACACTTCCAAGGATGACTTATGCTTTATAAAAAGTTGACCT TTGCGAGTAAGCTCTTTCCTTAATAATTTAATGATAATAATAATTAGCTGGTAGAAAT GTAGAAGTCTGCATGCAGAACCAGAAATTCATG

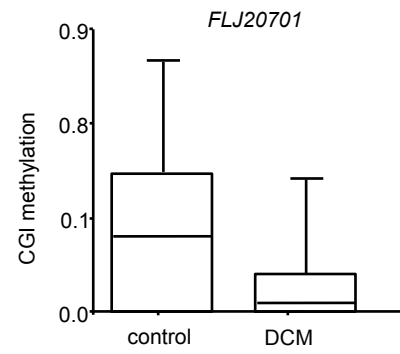
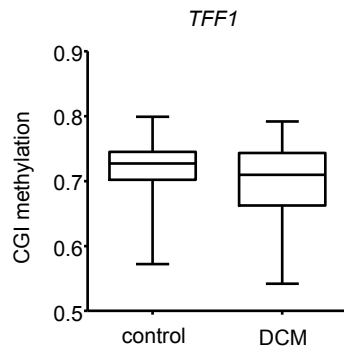
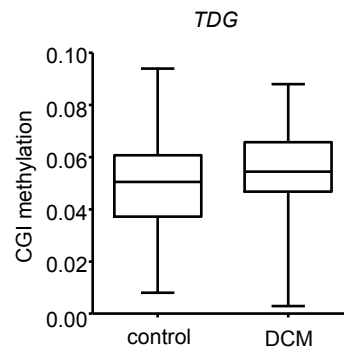
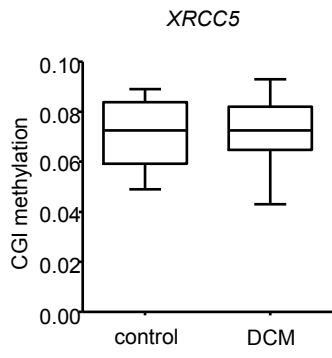
Supplemental Figure 1: MassARRAY-based validation of differential methylation in *ADORA2A*. Graph representing individual CpG methylation in *ADORA2A* measured by MassARRAY in DCM patients and controls.



Supplemental Figure 2: MassARRAY-based validation of genes. Graphs representing the mean CGI methylation of targets included in the replication stage. DCM patients show a statistically not significant reduction in methylation level in *CLDN4*, *FDX1*, *HOXB13*, *ID4*, *NAT1*, *PPARGC1A*, *SULF2*, *TFF1*, *TKT* and a statistically not significant increase of methylation in *ATP2C*, *CCDC59*, *GFI1*, *GSTM5m*, *SLC9A6*, and *TDG*.







Supplemental Figure 3: Protein conservation of LY75. Amino acid sequence alignments of human (h), mouse (m) and zebrafish (z) LY75 demonstrating its cross-species homology. Black boxes indicate amino acid identity, gray boxes indicate amino acids with similar chemical properties.

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hly75  MRTCGRFERRFAGLLILFWFELAEPSRANDEFTIVHNTCKCLFELVGVAVADCEDEEDKLLMKK
mly75  MRTCGRFERRFAGLLILFWFELAEPSRANDEFTIVHNTCKCLFELVGVAVADCEDEENNLWKKK
zly75  --MYGSHQIFSSFLISGGHIGSCASAGNSCLLTKRKLSTCKKLVQNGALKLGNCSSVPAFLWKKK

hly75  VSOHRLFHLESOKCLGLDITRAVDNLRMFSCDSVMLWVKCEHHSLYCAARVRLALDKGCHTALISNNSD
mly75  VSOHRLFHLESOKCLGLDITRAVDNLRMFSCDSVMLWVKCEHHSLYTAAQYRLALDKGCHTALISNNSD
zly75  GSAHRLFHLESMSGLGLEVR--AKTWTIFSCDSTELRWKCYEDVTVFVYEMHLSMGAQESVITAKRDQD

hly75  VWKKGSSBEELGQFVHEIYTRDQNSYGRCEFFPELICTWHHDCIDEDHSGFWCATTILNVEYDFKWC
mly75  VWKKGSSBEELGQFVHEIYTRDQNSYGRCEFFPELICTWHHDCIDEDHSGFWCATTILNVEYDFKWC
zly75  WKKSEGSNLECGQRTARKKHLSCGNSKCAICEFFPELKTQTHHSCGFFTEENLEKCSLRAVYCEQKQG

hly75  ICLXPEACEENWEKNECFSSCYFNNICTALSWKEAYVSCONQAGDILLSASAELAVIKRKEGLAKIFW
mly75  ICLXPEACEENWEKNECFSSCYFNNICTALSWKEAYVSCONQAGDILLSASAELAVITGKEDIARLIVW
zly75  NCLLYVVEGSSSLWEKRFVTKCYCVVTAIVVWWEARDAKRSQCDLLSSEPODIOCFKREKRDPSKLVW

hly75  IGLNQLYSARGWEWSDHPTNPLNWFDRSAPHTGGSSCARMESGLWQSFSCSAQLPYVCRKPLNNT
mly75  IGLNQLYSARGWEWSDHPTNPLNWFDRSAPHTGGSSCARMESGLWQSFSCSAQLPYVCRKPLNNT
zly75  IGLNQLYSARGWEWSDHPTNPLNWFDRSAPHTGGSSCARMESGLWQSFSCSAQLPYVCRKPLNNT

hly75  EPLDVMVYTDHCDACNLNNGFCYLLVNESN--SWDAABKCKAFKASDLISHSGLADVEVVVVKLHNE
mly75  EPLDVMVYTDHCDACNLNNGFCYLLANESS--SWDAABKCKAFKADLISHSGLADVEVVVVKLHNG
zly75  TSSVVRDVKHNSCGWIGWKCICYPHSABSKMSQHEALDLCMKDDKRLASHSIDLEMLHNEH--E

hly75  DLRKEVWIGLKNINIFLQWSDGTEVILTYWDENEENVFNKTPNCVSYLGLGQWVKVQSCERKLYVVC
mly75  DLRKEVWIGLKNINIFLQWSDGTEVILTYWDENEENVFNKTPNCVSYLGLGQWVKVQSCERKLYVVC
zly75  DLRKEVWIGLWNGGSSVFWVWIKAPVFWYVARACVPLLENLNCVYFSGEHTVWVSDCKPRKAVV

hly75  KRKGEKNDASDRKCFPDEGWKRHGETCYKYIEHVEPFGTNCNLTITSRFEQELANLMMKVDKSLRKY
mly75  KRKGEKNDASDRKCFPDEGWKRHGETCYKYIEHVEPFGTNCNLTITSRFEQELANLMMKVDKSLRKY
zly75  MNSQNLNLSAAEFCPPDGNMKRHGCACTWDTNIEFKNSCHLNNRFEQELNLSLKEHISEVLY

hly75  FWTGLRDVDSGEYNWALVGRRAVTFSNWNFLPEASGGCVAMSTGKSLGWKVEKCRSFKALSTICKK
mly75  FWTGLRDVDSGEYNWALVGRRAVTFSNWNFLPEASGGCVAMSTGKSLGWKVEKCRSFKALSTICKK
zly75  FWTGLRDSKSGSGEYVWFODETADCVTWNKRLPEASGGCVVMSGFNGLGWVKNCRSFKAGNICKK

hly75  VSG---LQFEEERKRFDDPCFEGVQSFPSLSCYKVFHADRIVKRNWEAERFQCALGAHLSFSSVU
mly75  VSG---LQFEEERKRFDDPCFEGVQSFPSLSCYKVFHADRIVKRNWEAERFQCALGAHLSFSSVU
zly75  FIKSKVQPIEPFVVENASCAFQWVSRDLNYCYKVFHBEELFKRSWEAERREGALCHLPSFEPVYK

hly75  EIKKFLHLEDOFSGQRLWIGLNKRSFDLQGSWOWSDRTFVSNIMENEFQODDTRDCAAQVBEER
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mly75  WRRQWHLVYDSE--LILRPFACAKLEWVCOIPKGRTPKTPDWYNPDRASIHGFFLITGSEYWFVAL
zly75  WFLFLFLTRASPRFFPSTHSDAKLEWVCOIFSGEKKFVWNEP--GHTSFAHLEKSEWENF

hly75  HLNVEEAVLYCASNHSFLATITSEVGLKAIKKNLANISG--EQKWWVHISEMFIIDHLSR--YFHFH
mly75  HLNVEEAVLYCASNHSFLATITSEVGLKAIKKNLANISG--EQKWWVHISEMFIIDHLSR--YFHFH
zly75  HLNVEEAVLYCASNHSFLAIPDLKALHLEQCESEHSGPHFVWWDARYPGPHVEMESH--MRYV

hly75  FTFGEBCDYSAKTWLIDLKPTDCSKLFFICEKYNVSSLEKYSPE--AAKVQCSQWIFPONKCFKR
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zly75  ESSRGRGFPSPVVE--LDFYSRTGKSGFVGCETVWVSSLEKGFHDFHFVGTGCGGTYHAKKQIQI

hly75  IKPVSFI--FSQASITCHSYGGLTLPVLSQEQDFITSLLEMEAT--LWIGLRWTAYEINWTDNREL
mly75  IKPVSFI--FSQASITCHSYGGLTLPVLSQEQDFITSLLEMEAT--LWIGLRWTAYEINWTDNREL
zly75  ISESYFONKKEANFQQLKCEIITISIQEQDFITSLLEKFPNPRKWIGLKRRPE--TQWVDSPE

hly75  TVSNFHPLLVGRRLTEENFFEESNRHCALILNLOKSEBTGTWNFTSCSERHESLQCKYSEVKSQTL
mly75  TVSNFHPLLVGRRLTEENFFEESNRHCALILNLOKSEBTGTWNFTSCSERHESLQCKYSEVKSQTL
zly75  WLFNFKLHLEQFFRSFNFNPEQLLEICAYINDRHSVMTGTDYFSCTEFCQNSLCCVYAKLEBEFKP

hly75  QNREHVKVLANLYKIKLITLWHSKKECKRNNQVSTIDPYQOAFVQALNNSIHWIGLESODE
mly75  QNREHVKVLANLYKIKLITLWHSKKECKRNNQVSTIDPYQOAFVQALNNSIHWIGLESODE
zly75  ENN--FTVQGHLEKIQODNLWADALQCRSNPLASVFNAYQVLEHVEVSEKFLWIGLFSDD

hly75  ELNFGWSDGKRLHFSRWABENQQLDCCVLDTDGFWKTVDCNDNPGAICYYSNETEKEVEVDSVKCE
mly75  ELNFGWSDGKRLHFSRWABENQQLDCCVLDTDGFWKTVDCNDNPGAICYYSNETEKEVEVDSVKCE
zly75  GEHLEKLNNSHSEENRWT--SETEGSCVFLDTDGFWRATDCSELSGAICHIE--SIKRTLEDKPCHHK

hly75  SEVLTNPWIPFONCYNFTLNKRMATQDEVHRCQKLNKCHLISIRGERENNFVOLLIFYNYMAS
mly75  SEVLTNPWIPFONCYNFTLNKRMATQDEVHRCQKLNKCHLISIRGERENNFVOLLIFYNYMAS
zly75  S--LQGSWHRKKNVTLNMSRWNGDIS--KIKSTLDRHLELIRDEAENNFILQVLRKRLAM

hly75  WMLGITYR--NRLMWFDKTFLSYTHWRAC--RPTKNEKFLAGLSTDGFDWIDCFKVEEENYFHOHSI
mly75  WMLGITYR--NRLMWFDKTFLSYTHWRAC--RPTKNEKFLAGLSTDGFDWIDCFKVEEENYFHOHSI
zly75  FVWLGMSNTKTDQRLWIDCYIQPSNMYGCRBN--N--S--IAGLNLEWFTTIRKHLYV--FICQSI

hly75  IACKIEMVDYREENITLPOFNPYDGCYISVIOKRVTYWYBALNCSQSGGHLASVHNQNGFLLEDIVKR
mly75  IACKIEMVDYREENITLPOFNPYDGCYISVIOKRVTYWYBALNCSQSGGHLASVHNQNGFLLEDIVKR
zly75  WCKLENLKDEMLKGVVDINTPCLISRRKAKLNVWQALSGSNQGLHASTDKTINENALHAKR

hly75  DGFPLWVGLSSHDSSESSFEWSDGTFDYF---KQOTSPCCVLDPKCKWHEKCNVVDGAICYK
mly75  DGFPLWVGLSSHDSSESSFEWSDGTFDYF---KQOTSPCCVLDPKCKWHEKCNVVDGAICYK
zly75  DCFELWGLSKQVSRWSEWSDGAVKERTDGFEDDSDSEERCVFISTGNWAVNCHATQCAICYN

hly75  PTKKKLKSLIYSSRCFAAKNCSRWYKYGHCYKSS--DQALHSFSEAKKCSKHDSATIVSIKDEE
mly75  PTKKKLKSLIYSSRCFAAKNCSRWYKYGHCYKSS--DQALHSFSEAKKCSKHDSATIVSIKDEE
zly75  HLNSTSP--FKSSSSCFKSSGCSWYDEKCYNFNTYNSFEMMDAKNVQCLLSSNLTIRSKPE

hly75  NKFYSLRMRENNTMRVWLGLSOHSVDQSWWLDGSEVTFVKWEN----KSGCFCGCSLIASNET
mly75  NKFYSLRMRENNTMRVWLGLSOHSVDQSWWLDGSEVTFVKWEN----KSGCFCGCSLIASNET
zly75  NFEVSDYLNKPSITRVWIALVDAKQPTGQDQSEIDSSWELSNKAQHSIDGTQLCAVMSISGGS

hly75  WKVKECGLCFGRVVCVFLDCEPSTWVQFQDSCYIFLQEAIKVESIEDVRNQCETHRADMISIHNEEENA
mly75  WKVKECGLCFGRVVCVFLDCEPSTWVQFQDSCYIFLQEAIKVESIEDVRNQCETHRADMISIHNEEENA
zly75  WQASCSNSRSVVCVCHLAEVQF

hly75  FILDTLKKQKCPDDILLGMFYDTDASFKWFDNSNMTFDKWTQDDDELDVDTCAFLHIKTGEWKKGNC
mly75  -----
zly75  -----

hly75  EVSSVEGLTCKTAIPYKRKYLSDNHILSALVIASTVILVIGALWFLYKHSDSRFTVFTAPQSPY
mly75  -----
zly75  -----

hly75  NEDCVLVGGEINEYFVQFD
mly75  NEDCVLVGGEINEYFVQFD
zly75  AASSTSMNDAL-----

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Supplemental Figure 4: Regular molecular chamber definition in *adora2a*-morphants. Molecular chamber definition is not impaired in *adora2a*-morphants compared to the control-injected zebrafish as demonstrated by regular *amhc* and *vmhc* expression.

