# Impulsivity is a heritable trait in rodents and associated with a novel quantitative trait locus on chromosome 1

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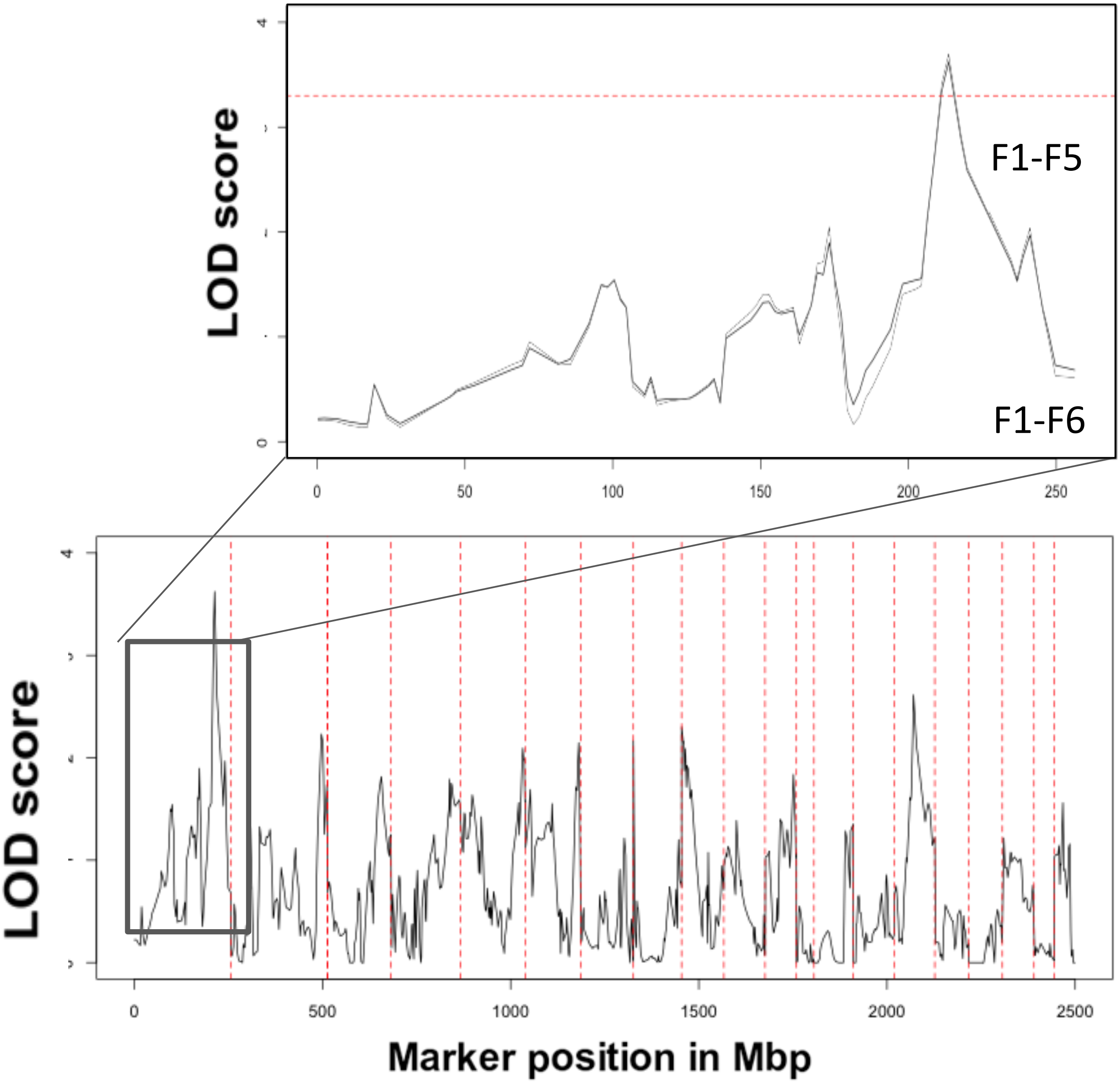

**Supplementary Figure 1: Genome-wide linkage for average total premature responses.** Genome-wide linkage results (F1-F5 generations) on 20 autosomal chromosomes. Dashed red lines indicate chromosomal limits. The impulsivity trait was defined by the average total number of premature responses on the 5CSRTT (non-parametric linkage). **(Inset)** Significant linkage results are observed on chromosome 1 (F1- F5 black line; F1-F6 grey line). The horizontal red line depicts the genome-wide significant LOD score threshold of 3.3. Note no significant difference in LOD scores on chromosome 1 after the addition of data from the F6 generation.

| **Gene symbol** | **Gene description** | **Gene location (Mbp)** |
|---|---|---|
| ***Rgma*** | repulsive guidance molecule A | 128.547399 |
| ***Chd2*** | chromodomain-helicase-DNA-binding protein 2 | 128.609727 |
| ***St8sia2*** | Alpha-2,8-sialyltransferase 8B | 129.158714 |
| ***snoU109*** | Small nucleolar RNA U109 | 129.245228 |
| ***Sv2b*** | Synaptic vesicle glycoprotein 2B | 130.683153 |
| ***Akap13*** | A kinase (PRKA) anchor protein 13 | 131.224569 |
| ***U3*** | Small nucleolar RNA U3 | 131.537652 |
| ***Klhl25*** | Ectoderm-neural cortex protein 2 | 131.540949 |
| ***Agbl1*** | Uncharacterized protein | 131.756899 |
| ***U1*** | U1 spliceosomal RNA | 133.650066 |
| ***Ntrk3*** | NT-3 growth factor receptor | 133.92553 |
| ***Mrpl46*** | 39S ribosomal protein L46, mitochondrial | 134.498792 |
| ***Mrps11*** | 28S ribosomal protein S11, mitochondrial | 134.507836 |
| ***Det1*** | DET1 homolog | 134.549457 |
| ***rno-mir-7a-2*** | rno-mir-7a-2 | 134.607264 |
| ***Aen*** | Apoptosis-enhancing nuclease | 134.615998 |
| ***Isg20*** | interferon-stimulated gene 20 kDa protein | 134.631524 |
| ***Acan*** | Aggrecan core protein | 134.816598 |
| ***Hapln3*** | hyaluronan and proteoglycan link protein 3 | 134.851846 |
| ***Mfge8*** | Lactadherin | 134.87003 |
| ***Abhd2*** | abhydrolase domain-containing protein 2 | 135.025144 |
| ***Rlbp1*** | retinaldehyde-binding protein 1 | 135.122063 |
| ***Polg*** | DNA polymerase subunit gamma-1 | 135.197016 |
| ***rno-mir-9-3*** | rno-mir-9-3 | 135.254133 |
| ***Rhcg*** | Ammonium transporter Rh type C | 135.36142 |
| ***Kif7*** | Uncharacterized protein | 135.473063 |
| ***Plin*** | Perilipin-1 | 135.497431 |
| ***Pex11a*** | Peroxisomal membrane protein 11A | 135.513735 |
| ***Wdr93*** | WD repeat-containing protein 93 | 135.527818 |
| ***Mesp1*** | mesoderm posterior protein 1 | 135.571777 |
| ***Mesp2*** | mesoderm posterior protein 2 | 135.59002 |
| ***Anpep*** | Aminopeptidase N | 135.600751 |
| ***LOC683402*** | similar to AP-3 complex subunit sigma-2 (Adapter-related p | 135.653108 |
| ***RGD1311021*** | RCG24599Uncharacterized protein | 135.69698 |
| ***Znf710*** | zinc finger protein 710 | 135.861678 |
| ***Idh2*** | Isocitrate dehydrogenase | 135.876058 |
| ***Sema4b*** | semaphorin 4B | 136.001235 |
| ***Cib1*** | Calcium and integrin-binding protein 1 | 136.031865 |
| ***NGRN_RAT*** | Neugrin | 136.07546 |
| ***Vps33b*** | Vacuolar protein sorting-associated protein 33B | 136.085931 |
| ***Prc1*** | protein regulator of cytokinesis 1 | 136.112674 |
| ***Rccd1*** | Uncharacterized protein | 136.134226 |
| ***Unc45a*** | Protein unc-45 homolog A | 136.143886 |
| ***Hddc3*** | HD domain-containing protein 3 | 136.161425 |
| ***Fes*** | tyrosine-protein kinase Fes/Fps | 136.199523 |

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|---|---|---:|
| ***Furin*** | Furin | 136.209969 |
| ***Iqgap1*** | ras GTPase-activating-like protein IQGAP1 | 136.552363 |
| ***Crtc3*** | Uncharacterized protein | 136.763502 |
| ***Wdr73*** | WD repeat-containing protein 73 | 137.088348 |
| ***Nmb*** | neuromedin-B | 137.097463 |
| ***Sec11a*** | Signal peptidase complex catalytic subunit SEC11A | 137.109468 |
| ***Znf592*** | zinc finger protein 592 | 137.188336 |
| ***Alpk3*** | alpha-protein kinase 3 | 137.256805 |
| ***Slc28a1*** | Sodium/nucleoside cotransporter 1 | 137.323995 |
| ***Pde8a*** | high affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic | 137.415852 |
| ***SNORA44*** | Small nucleolar RNA SNORA44 | 137.444624 |
| ***LOC100365810*** | 40S ribosomal protein S17 | 137.552232 |
| ***Cpeb1*** | Cytoplasmic polyadenylation element-binding protein 1 | 137.556774 |
| ***SCARNA15*** | Small Cajal body specific RNA 15 | 137.743986 |
| ***Fsd2*** | fibronectin type III and SPRY domain-containing protein 2 | 137.749268 |
| ***SNORA50*** | Small nucleolar RNA SNORA50 | 137.759109 |
| ***Whamm*** | WASP homolog-associated protein with actin, membranes a | 137.785814 |
| ***Homer2*** | Homer protein homolog 2 | 137.827128 |
| ***Fam103a1*** | family with sequence similarity 103, member A1 (Fam103a1 | 137.980239 |
| ***RGD1305713*** | UPF0235 protein C15orf40 homolog | 137.998479 |
| ***Btbd1*** | BTB/POZ domain-containing protein 1 | 138.006567 |
| ***Tm6sf1*** | transmembrane 6 superfamily member 1 | 138.058059 |
| ***Hdgfrp3*** | Hepatoma-derived growth factor-related protein 3 | 138.098819 |
| ***Sh3gl3*** | Endophilin-A3 | 138.398334 |
| ***Fam154b*** | family with sequence similarity 154, member B (Fam154b), | 138.905988 |
| ***Eftud1*** | elongation factor Tu GTP binding domain containing 1 | 138.92062 |
| ***SNORA15*** | Small nucleolar RNA SNORA15 | 138.942384 |
| ***Tmc3*** | Uncharacterized protein | 139.842574 |
| ***Stard5*** | stAR-related lipid transfer protein 5 | 139.896272 |
| ***Il16*** | pro-interleukin-16 | 139.908061 |
| ***RGD1310371*** | similar to RIKEN cDNA 1700026D08 (RGD1310371), mRN | 140.036328 |
| ***Mesdc1*** | mesoderm development candidate 1 | 140.157974 |
| ***Mesdc2*** | LDLR chaperone MESD | 140.167851 |
| ***RGD1305254*** | Uncharacterized protein | 140.20304 |
| ***Fam108c1*** | abhydrolase domain-containing protein FAM108C1 | 140.382431 |
| ***Arnt2*** | Aryl hydrocarbon receptor nuclear translocator 2 | 140.535823 |
| ***Zfand6*** | AN1-type zinc finger protein 6 | 140.885729 |
| ***Vom2r40*** | vomeronasal 2 receptor, 40 | 141.602289 |
| ***Vom2r41*** | vomeronasal 2 receptor 41 | 141.861806 |
| ***Vom2r42*** | vomeronasal 2 receptor 42 | 142.010227 |
| ***Vom2r43*** | vomeronasal 2 receptor 43 | 142.267794 |
| ***Folh1*** | Glutamate carboxypeptidase 2 | 142.936379 |
| ***Nox4*** | NADPH oxidase 4 | 143.415816 |
| ***Tyr*** | tyrosinase | 143.641257 |
| ***U7*** | U7 small nuclear RNA | 143.647155 |
| ***Grm5*** | Metabotropic glutamate receptor 5 | 143.863506 |

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|---|---|---|
| ***Ctsc*** | Dipeptidyl peptidase 1Dipeptidyl peptidase 1 exclusion dom | 144.629802 |
| ***Rab38*** | ras-related protein Rab-38 | 144.783909 |
| ***Tmem135*** | Transmembrane protein 135 | 145.664797 |
| ***Fzd4*** | Frizzled-4 | 145.953746 |
| ***Prss23*** | Serine protease 23 | 146.081557 |
| ***Eed*** | polycomb protein EED | 146.563964 |
| ***Picalm*** | Phosphatidylinositol-binding clathrin assembly protein | 146.754045 |
| ***Ccdc89*** | Coiled-coil domain-containing protein 89 | 147.091688 |
| ***Crebzf*** | CREB/ATF bZIP transcription factor | 147.124224 |
| ***Tmem126a*** | Transmembrane protein 126A | 147.129335 |
| ***Tmem126b*** | transmembrane protein 126B | 147.146187 |
| ***Dlg2*** | Disks large homolog 2 | 148.051658 |
| ***Ccdc90b*** | Coiled-coil domain-containing protein 90B, mitochondrial | 149.410497 |
| ***Ankrd42*** | ankyrin repeat domain 42 | 149.423846 |
| ***Pcf11*** | Uncharacterized protein | 149.475611 |
| ***SNORA73*** | Small nucleolar RNA SNORA73 family | 149.551354 |
| ***Rab30*** | ras-related protein Rab-30 | 149.656373 |
| ***RGD1559690*** | nitric oxide-inducible gene protein | 149.685958 |
| ***SNORA70*** | Small nucleolar RNA SNORA70 | 149.697952 |
| ***Prcp*** | lysosomal Pro-X carboxypeptidase | 149.711289 |
| ***Fam181b*** | family with sequence similarity 181, member B (Fam181b), | 149.955641 |
| ***U6*** | U6 spliceosomal RNA | 152.647115 |
| ***rno-mir-708*** | rno-mir-708 | 153.476669 |
| ***Odz4*** | teneurin-4 | 153.808625 |
| ***Nars2*** | probable asparaginyl-tRNA synthetase, mitochondrial | 154.216134 |
| ***Gab2*** | GRB2-associated-binding protein 2 | 154.348781 |
| ***Kctd21*** | BTB/POZ domain-containing protein KCTD21 | 154.587686 |
| ***Alg8*** | probable dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha- | 154.607442 |
| ***Ndufc2*** | NADH dehydrogenase | 154.635889 |
| ***Thrsp*** | Thyroid hormone-inducible hepatic protein | 154.647341 |
| ***Kctd14*** | Uncharacterized protein | 154.684785 |
| ***RGD1561459*** | similar to RIKEN cDNA 1810020D17 (RGD1561459), mRN | 154.786525 |
| ***Clns1a*** | Methylosome subunit pICln | 154.946673 |
| ***Aqp11*** | Aquaporin-11 | 154.973798 |
| ***Pak1*** | Serine/threonine-protein kinase PAK 1 | 155.057622 |
| ***Capn5*** | Calpain-5 | 155.366703 |
| ***B3gnt6*** | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransfe | 155.435459 |
| ***Acer3*** | Uncharacterized protein | 155.455466 |
| ***Tsku*** | Tsukushin | 155.61107 |
| ***Lrrc32*** | leucine rich repeat containing 32 | 155.761334 |
| ***Prkrir*** | 52 kDa repressor of the inhibitor of the protein kinase | 155.982782 |
| ***Wnt11*** | wingless-type MMTV integration site family, member 11 | 156.126223 |
| ***RGD1561870*** | similar to ribosomal protein L27 (RGD1561870), mRNA | 156.142284 |
| ***Dgat2*** | Diacylglycerol O-acyltransferase 2 | 156.447588 |
| ***Mogat2*** | 2-acylglycerol O-acyltransferase 2 | 156.516533 |
| ***Map6*** | Microtubule-associated protein 6 | 156.592504 |

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|---|---|---|
| ***Serpinh1*** | Serpin H1 | 156.667042 |
| ***B5DF39_RAT*** | Gdpd5 protein | 156.703241 |
| ***Klhl35*** | Uncharacterized protein | 156.801077 |
| ***Rps3*** | 40S ribosomal protein S3 | 156.811473 |
| ***SNORD15*** | Small nucleolar RNA SNORD15 | 156.812188 |
| ***Arrb1*** | Beta-arrestin-1 | 156.871562 |
| ***rno-mir-326*** | rno-mir-326 | 156.887513 |
| ***Slco2b1*** | Solute carrier organic anion transporter family member 2B1 | 156.992493 |
| ***Q5RJS1_RAT*** | Olr35 protein | 157.074498 |
| ***Neu3*** | Sialidase-3 | 157.172548 |
| ***Spcs2*** | signal peptidase complex subunit 2 homolog | 157.199447 |
| ***SNORA20*** | Small nucleolar RNA SNORA20 | 157.319772 |
| ***LOC100360934*** | chordin-like protein 2 | 157.391482 |
| ***Pold3*** | DNA polymerase delta subunit 3 | 157.453059 |
| ***Lipt2*** | lipoyl(octanoyl) transferase 2 (putative) | 157.538704 |
| ***Kcne3*** | Potassium voltage-gated channel subfamily E member 3 | 157.558044 |
| ***Pgm2l1*** | glucose 1,6-bisphosphate synthase | 157.605906 |
| ***P4ha3*** | Prolyl 4-hydroxylase subunit alpha-3 | 157.663338 |
| ***Ppme1*** | protein phosphatase methylesterase 1 | 157.725633 |
| ***Ucp3*** | Mitochondrial uncoupling protein 3 | 157.896001 |
| ***Ucp2*** | Mitochondrial uncoupling protein 2 | 157.922179 |
| ***Dnajb13*** | dnaJ homolog subfamily B member 13 | 157.931501 |
| ***Chchd8*** | coiled-coil-helix-coiled-coil-helix domain-containing protein | 157.965119 |
| ***Mrpl48*** | 39S ribosomal protein L48, mitochondrial | 157.979818 |
| ***Rab6a*** | Ras-related protein Rab-6A | 158.041088 |
| ***SNORA4*** | Small nucleolar RNA SNORA4 | 158.048843 |
| ***Plekhb1*** | Pleckstrin homology domain-containing family B member 1 | 158.08193 |
| ***Fam168a*** | family with sequence similarity 168, member A (Fam168a), | 158.140473 |
| ***Relt*** | tumor necrosis factor receptor superfamily member 19L | 158.293361 |
| ***P2ry6*** | P2Y purinoceptor 6 | 158.381128 |
| ***P2ry2*** | P2Y purinoceptor 2 | 158.440062 |
| ***Fchsd2*** | FCH and double SH3 domains protein 2 | 158.54883 |
| ***Q6QI52_RAT*** | LRRGT00156 | 158.590389 |
| ***LOC100364491*** | ribosomal protein L7a (Rpl7a), mRNA | 158.694172 |
| ***Atg16l2*** | ATG16 autophagy related 16-like 2 | 158.787779 |
| ***Stard10*** | PCTP-like protein | 158.81997 |
| ***Pde2a*** | cGMP-dependent 3',5'-cyclic phosphodiesterase | 158.921607 |
| ***rno-mir-139*** | rno-mir-139 | 158.976576 |
| ***Art2*** | T-cell ecto-ADP-ribosyltransferase 1 | 159.055461 |
| ***Clpb*** | Caseinolytic peptidase B protein homolog | 159.126512 |
| ***5S_rRNA*** | 5S ribosomal RNA | 159.2668 |
| ***Phox2a*** | Paired mesoderm homeobox protein 2A | 159.273524 |
| ***Inppl1*** | Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2 | 159.27813 |
| ***Folr2*** | folate receptor beta | 159.295773 |
| ***Folr1*** | folate receptor alpha | 159.315192 |
| ***RGD1311634*** | similar to RIKEN cDNA 3200002M19 (RGD1311634), mRN | 159.35911 |

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|---|---|---|
| ***Lrtomt*** | Transmembrane O-methyltransferase | 159.36201 |
| ***MGC72560*** | Ragulator complex protein LAMTOR1 | 159.367471 |
| ***Lrrc51*** | Leucine-rich repeat-containing protein 51 | 159.373973 |
| ***Il18bp*** | interleukin-18-binding protein | 159.471809 |
| ***Rnf121*** | RING finger protein 121 | 159.475046 |
| ***TRPC2_RAT*** | Short transient receptor potential channel 2 | 159.54282 |
| ***Art5*** | Ecto-ADP-ribosyltransferase 5 | 159.576991 |
| ***Art1*** | GPI-linked NAD(P)(+)--arginine ADP-ribosyltransferase 1 | 159.586246 |
| ***Chrna10*** | Neuronal acetylcholine receptor subunit alpha-10 | 159.590904 |
| ***Nup98*** | Nuclear pore complex protein Nup98-Nup96Nuclear pore c | 159.598048 |
| ***Pgap2*** | Post-GPI attachment to proteins factor 2 | 159.69692 |
| ***Rhog*** | rho-related GTP-binding protein RhoG | 159.724016 |
| ***Stim1*** | Stromal interaction molecule 1 | 159.761567 |
| ***Trim21*** | 52 kDa Ro protein | 160.175882 |
| ***LOC293190*** | bcl-2-like protein 1 isoform 3 | 160.254067 |
| ***SNORA2*** | Small nucleolar RNA SNORA2/SNORA34 family | 161.283594 |
| ***LOC689064*** | Hemoglobin subunit beta-2 | 161.578128 |
| ***Hbb*** | Hemoglobin subunit beta-1 | 161.584858 |
| ***Hbb-b1*** | hemoglobin, beta adult major chain | 161.590671 |
| ***Hbg1*** | hemoglobin, gamma A | 161.64024 |
| ***Hbe2*** | hemoglobin, epsilon 2 | 161.647651 |
| ***Hbe1*** | hemoglobin, epsilon 1 | 161.651306 |
| ***LOC499219*** | LRRG00121 | 161.788384 |
| ***RGD1562433*** | similar to ubiquilin 1 isoform 2 (RGD1562433), mRNA | 161.962308 |
| ***Ubqln3*** | ubiquilin-3 | 161.974585 |
| ***Ubqlnl*** | Ubiquilin-like protein | 161.985144 |
| ***RGD1310717*** | similar to RIKEN cDNA E030002O03 (RGD1310717), mRN | 161.990223 |
| ***Trim6*** | tripartite motif-containing 6 | 162.066157 |
| ***Trim5*** | tripartite motif-containing protein 5 | 162.096454 |
| ***Trim30*** | Uncharacterized protein | 162.173307 |
| ***U4*** | U4 spliceosomal RNA | 162.457008 |
| ***Fam160a2*** | FTS and Hook-interacting protein | 163.110928 |
| ***Cnga4*** | Cyclic nucleotide-gated cation channel alpha-4 | 163.137544 |
| ***Cckbr*** | Gastrin/cholecystokinin type B receptor | 163.156914 |
| ***Prkcdbp*** | Protein kinase C delta-binding protein | 163.212922 |
| ***Smpd1*** | sphingomyelin phosphodiesterase | 163.27897 |
| ***Apbb1*** | Amyloid beta A4 precursor protein-binding family B membe | 163.282918 |
| ***Hpx*** | Hemopexin | 163.319509 |
| ***Trim3*** | Tripartite motif-containing protein 3 | 163.331603 |
| ***Arfip2*** | Arfaptin-2 | 163.364861 |
| ***TIM9B_RAT*** | Mitochondrial import inner membrane translocase subunit T | 163.369752 |
| ***Dnhd1*** | Uncharacterized protein | 163.462348 |
| ***Rrp8*** | Ribosomal RNA-processing protein 8 | 163.47703 |
| ***Ilk*** | Integrin-linked protein kinase | 163.481299 |
| ***Taf10*** | TAF10 RNA polymerase II, TATA box binding protein (TBP)- | 163.487518 |
| ***Tpp1*** | Tripeptidyl-peptidase 1 | 163.490393 |

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|---|---|---|
| ***Dchs1*** | dachsous 1 | 163.49734 |
| ***RM17_RAT*** | 39S ribosomal protein L17, mitochondrial | 163.554719 |
| ***Syt9*** | Synaptotagmin-9 | 164.722168 |
| ***Olfml1*** | Olfactomedin-like protein 1 | 164.953064 |
| ***Ppfibp2*** | protein tyrosine phosphatase, receptor-type, F interacting pr | 164.979709 |
| ***NB5R2_RAT*** | NADH-cytochrome b5 reductase 2 | 165.131108 |
| ***LOC499235*** | LRRGT00141 | 165.181656 |
| ***Nlrp10*** | NACHT, LRR and PYD domains-containing protein 10 | 166.411647 |
| ***Ric3*** | resistance to inhibitors of cholinesterase 3 homolog | 166.494113 |
| ***Lmo1*** | LIM domain only protein 3 | 166.706026 |
| ***snoU13*** | Small nucleolar RNA U13 | 167.002996 |
| ***Trim66*** | tripartite motif-containing protein 66 | 167.04954 |
| ***Rpl27a*** | 60S ribosomal protein L27a | 167.115389 |
| ***SNORA3*** | Small nucleolar RNA SNORA3/SNORA45 family | 167.117372 |
| ***St5*** | suppression of tumorigenicity 5 protein | 167.119711 |
| ***RGD1306959*** | similar to C11orf17 protein (RGD1306959), mRNA | 167.324919 |
| ***LOC499240*** | similar to predicted gene ICRFP703B1614Q5.5 (LOC49924 | 167.333129 |
| ***Tmem9b*** | transmembrane protein 9B | 167.355899 |
| ***Nrip3*** | nuclear receptor-interacting protein 3 | 167.380328 |
| ***Dennd5a*** | DENN/MADD domain containing 5A | 167.519649 |
| ***Tmem41b*** | Transmembrane protein 41B | 167.608205 |
| ***Ipo7*** | importin-7 | 167.658312 |
| ***SNORA23*** | Small nucleolar RNA SNORA23 | 167.68657 |
| ***Zfp143*** | Zinc finger protein 143 | 167.704313 |
| ***Wee1*** | Wee1-like protein kinase | 167.769797 |
| ***Swap70*** | switch-associated protein 70 | 167.888783 |
| ***RGD1559442*** | SET binding factor 2 | 167.974268 |
| ***Adm*** | ADMAdrenomedullinProadrenomedullin N-20 terminal pept | 168.380255 |
| ***Ampd3*** | AMP deaminase 3 | 168.533491 |
| ***rnf141*** | RING finger protein 141 | 168.572375 |
| ***Lyve1*** | lymphatic vessel endothelial hyaluronic acid receptor 1 | 168.60146 |
| ***Mrvi1*** | protein MRVI1 isoform b | 168.627363 |
| ***Ctr9*** | Ctr9, Paf1/RNA polymerase II complex component, homolog | 168.784377 |
| ***snoU97*** | Small nucleolar RNA U97 | 168.834306 |
| ***E9PSI9_RAT*** | putative polypeptide N-acetylgalactosaminyltransferase-like | 169.251525 |
| ***Usp47*** | ubiquitin specific peptidase 47 | 169.836253 |
| ***Dkk3*** | dickkopf-related protein 3 | 169.924618 |
| ***Mical2*** | protein MICAL-2 | 170.076006 |
| ***Micalcl*** | MICAL C-terminal-like protein | 170.178141 |
| ***Parva*** | Alpha-parvin | 170.232441 |
| ***Tead1*** | transcriptional enhancer factor TEF-1 | 170.557393 |
| ***LOC687311*** | NADH dehydrogenase | 170.580048 |
| ***Arntl*** | Aryl hydrocarbon receptor nuclear translocator-like protein | 171.062181 |
| ***Btbd10*** | BTB/POZ domain-containing protein 10 | 171.163522 |
| ***Pth*** | Parathyroid hormone | 171.240596 |
| ***Far1*** | Fatty acyl-CoA reductase 1 | 171.392301 |

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|---|---|---|
| ***Spon1*** | Spondin-1 | 171.70072 |
| ***Rras2*** | ras-related protein R-Ras2 | 172.026263 |
| ***Copb1*** | Coatomer subunit beta | 172.199677 |
| ***Psma1*** | Proteasome subunit alpha type-1 | 172.237763 |
| ***Pde3b*** | cGMP-inhibited 3',5'-cyclic phosphodiesterase B | 172.409282 |
| ***B5DFA4_RAT*** | vitamin D 25-hydroxylase | 172.593057 |
| ***Calca*** | Calcitonin | 172.68617 |
| ***Calcb*** | Calcitonin gene-related peptide 2 | 172.777347 |
| ***Insc*** | inscuteable homolog (Drosophila) (Insc), mRNA | 172.804412 |
| ***7SK*** | 7SK RNA | 173.002191 |
| ***Sox6*** | transcription factor SOX-6 | 173.556967 |
| ***RGD1311703*** | small acidic protein | 174.173969 |
| ***Plekha7*** | pleckstrin homology domain containing, family A member 7 | 174.204979 |
| ***Rps13*** | 40S ribosomal protein S13 | 174.425816 |
| ***SNORD14*** | Small nucleolar RNA SNORD14 | 174.427277 |
| ***Pik3c2a*** | phosphatidylinositol-4-phosphate 3-kinase C2 domain-cont | 174.430831 |
| ***Nucb2*** | Nucleobindin-2 | 174.605677 |
| ***SNORA17*** | Small nucleolar RNA SNORA17 | 175.033994 |
| ***YBOX1_RAT*** | Nuclease-sensitive element-binding protein 1 | 175.17944 |
| ***Xylt1*** | Xylosyltransferase 1 | 175.68736 |
| ***Rps15a*** | 40S ribosomal protein S15a | 176.321901 |
| ***Arl6ip1*** | ADP-ribosylation factor-like protein 6-interacting protein 1 | 176.332758 |
| ***SYT17_RAT*** | Synaptotagmin-17 | 176.599608 |
| ***Itpripl2*** | inositol 1,4,5-triphosphate receptor-interacting protein-like 2 | 176.70669 |
| ***Coq7*** | Ubiquinone biosynthesis protein COQ7 homolog | 176.741638 |
| ***Tmc7*** | transmembrane channel-like protein 7 | 176.761053 |
| ***Tmc5*** | Transmembrane channel-like protein 5 | 176.84398 |
| ***Cp110*** | centrosomal protein of 110 kDa | 176.937287 |
| ***LOC361635*** | UPF0505 protein C16orf62 homolog | 176.965214 |
| ***SNORA24*** | Small nucleolar RNA SNORA24 | 177.060142 |
| ***RGD1565096*** | similar to TSG118.1 (RGD1565096), mRNA | 177.084712 |
| ***Gprc5b*** | G-protein coupled receptor family C group 5 member B | 177.205905 |

**Supplementary table 1.** List of genes within the QTL region on chromosome 1

**Supplementary Table 2: Candidate genes in the QTL region previously reported to be associated with psychiatric and behavioral disorders.**

| Gene symbol | Gene description | Gene location (Mbp) | Associated disorder |
|---|---|---|---|
| *Rgma* | Repulsive guidance molecule A | 128.547399 | Depression[1] |
| *Chd2* | Chromodomain-helicase-DNA-binding protein 2 | 128.609727 | Autism[2] |
| *St8sia2* | Alpha-2,8-sialyltransferease 8B | 129.158714 | Schizophrenia[3]; Bipolar[3]; Autism[4] |
| *Sv2b* | Synaptic vesicle glycoprotein 2B | 130.683153 | Depression[1] |
| *Homer2* | Homer protein homolog 2 | 137.827128 | Schizophrenia[5] |
| *Folh1* | Glutamate carboxypeptidase 2 | 142.936379 | Depression[6]; Schizophrenia[7] |
| *Tyr* | Tyrosinase | 143.641257 | Bipolar[8] |
| *Grm5* | Metabotropic glutamate receptor 5 | 143.863506 | Schizophrenia[9]; ADHD[10]; Addiction[11]; Autism[12] |
| *Dlg2* | Disks large homolog 2 | 148.051658 | Schizophrenia[13]; Autism[14] |
| *Odz4* | Teneurin-4 | 153.808625 | Bipolar[15]; Schizophrenia[16] |
| *Arrb1* | Beta-arrestin-1 | 156.871562 | Depression[17]; Addiction[18] |
| *Plekhb1* | Pleckstrin homology domain-containing family B membrane 1 | 158.08193 | ADHD[19] |
| *Folr2* | Folate receptor beta | 159.295773 | Autism[20] |
| *Chrna10* | Neuronal acetylcholine receptor subunit alpha-10 | 159.590904 | Addiction[21] |
| *Hbb* | Hemoglobin subunit beta-1 | 161.584858 | Depression[22] |
| *Cckbr* | Gastrin/cholecystokinin type B receptor | 163.156914 | Anxiety[23]; Suicide[24] |

| | | | |
|---|---|---|---|
| *Ilk* | Integrin-linked protein kinase | 163.481299 | Addiction [25] |
| *Ric3* | Resistance to inhibitors of cholinesterase 3 homolog | 166.494113 | Bipolar[26]; Schizophrenia[26] |
| *Lmo1* | LIM domain only protein 3 | 166.706026 | Addiction[27] |
| *Rps15a* | 40S ribosomal protein S15a | 176.321901 | Anxeity[28] |

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| **Gene Name** | **SNP ID** | **Chromosome** | **Position(Mbp)** | **Reference Allele** | **Alternative Allele** | **Location** |
|---|---|---|---|---|---|---|
| ***Chd2*** | 1_128649115_G/C | 1 | 128.649115 | G | C | INTRONIC |
| ***Sv2b*** | 1_130835497_C/A | 1 | 130.835497 | C | A | INTRONIC |
| ***Sv2b*** | 1_130837654_G/A | 1 | 130.837654 | G | A | INTRONIC |
| ***Akap13*** | 1_131315604_G/A | 1 | 131.315604 | G | A | INTRONIC |
| ***Ntrk3*** | 1_134268648_G/T | 1 | 134.268648 | G | T | INTRONIC |
| ***Acan*** | 1_134840489_T/C | 1 | 134.840489 | T | C | INTRONIC |
| ***Abhd2*** | 1_135088391_G/C | 1 | 135.088391 | G | C | INTRONIC |
| ***Iqgap1*** | 1_136631739_C/T | 1 | 136.631739 | C | T | INTRONIC |
| ***Pde8a*** | 1_137547830_C/T | 1 | 137.54783 | C | T | DOWNSTREAM |
| ***Cpeb1*** | 1_137582309_A/G | 1 | 137.582309 | A | G | INTRONIC |
| ***Cpeb1*** | 1_137609354_C/G | 1 | 137.609354 | C | G | INTRONIC |
| ***Homer2*** | 1_137882265_A/G | 1 | 137.882265 | A | G | INTRONIC |
| ***Homer2*** | 1_137882278_A/G | 1 | 137.882278 | A | G | INTRONIC |
| ***Homer2*** | 1_137882369_A/G | 1 | 137.882369 | A | G | INTRONIC |
| ***Homer2*** | 1_137882379_A/G | 1 | 137.882379 | A | G | INTRONIC |
| ***Tm6sf1*** | 1_138079519_A/G | 1 | 138.079519 | A | G | INTRONIC |
| ***Sh3gl3*** | 1_138430747_A/G | 1 | 138.430747 | A | G | INTRONIC |
| ***Sh3gl3*** | 1_138451888_C/G | 1 | 138.451888 | C | G | INTRONIC |
| ***Sh3gl3*** | 1_138512033_C/T | 1 | 138.512033 | C | T | INTRONIC |
| ***Arnt2*** | 1_140531141_C/A | 1 | 140.531141 | C | A | DOWNSTREAM |
| ***Arnt2*** | 1_140531145_C/A | 1 | 140.531145 | C | A | DOWNSTREAM |
| ***Arnt2*** | 1_140651827_A/G | 1 | 140.651827 | A | G | INTRONIC |
| ***Olr11*** | 1_141494096_C/A | 1 | 141.494096 | C | A | UPSTREAM |
| ***Vom2r40*** | 1_141659141_T/A | 1 | 141.659141 | T | A | INTRONIC |
| ***Vom2r40*** | 1_141659143_T/G | 1 | 141.659143 | T | G | INTRONIC |
| ***Folh1*** | 1_142966763_G/T | 1 | 142.966763 | G | T | INTRONIC |
| ***Folh1*** | 1_142966968_G/A | 1 | 142.966968 | G | A | INTRONIC |
| ***Grm5*** | 1_143859713_A/T | 1 | 143.859713 | A | T | UPSTREAM |
| ***Grm5*** | 1_144005117_T/C | 1 | 144.005117 | T | C | INTRONIC |
| ***Grm5*** | 1_144032182_A/T | 1 | 144.032182 | A | T | INTRONIC |
| ***Dlg2*** | 1_148421815_C/A | 1 | 148.421815 | C | A | INTRONIC |
| ***Dlg2*** | 1_148443210_A/T | 1 | 148.44321 | A | T | INTRONIC |
| ***Dlg2*** | 1_148476775_A/G | 1 | 148.476775 | A | G | INTRONIC |
| ***Dlg2*** | 1_148502976_G/A | 1 | 148.502976 | G | A | INTRONIC |
| ***Dlg2*** | 1_148562440_A/G | 1 | 148.56244 | A | G | INTRONIC |
| ***Dlg2*** | 1_149203589_A/G | 1 | 149.203589 | A | G | INTRONIC |
| ***Dlg2*** | 1_149203594_A/G | 1 | 149.203594 | A | G | INTRONIC |
| ***Odz4*** | 1_153937181_G/A | 1 | 153.937181 | G | A | INTRONIC |
| ***Nars2*** | 1_154235371_C/G | 1 | 154.235371 | C | G | INTRONIC |
| ***Aqp11*** | 1_154978188_G/A | 1 | 154.978188 | G | A | INTRONIC |
| ***Fchsd2*** | 1_158557777_G/A | 1 | 158.557777 | G | A | INTRONIC |
| ***Pde2a*** | 1_158930569_A/G | 1 | 158.930569 | A | G | INTRONIC |
| ***Pde2a*** | 1_158930585_T/C | 1 | 158.930585 | T | C | INTRONIC |
| ***Olr119*** | 1_161435537_T/C | 1 | 161.435537 | T | C | UPSTREAM |
| ***Hbb*** | 1_161590423_T/A | 1 | 161.590423 | T | A | UPSTREAM |
| ***Ppfibp2*** | 1_165008099_C/G | 1 | 165.008099 | C | G | INTRONIC |
| ***Olr237*** | 1_165247608_T/C | 1 | 165.247608 | T | C | SYNONYMOUS_CODING |
| ***LOC690767*** | 1_166068612_C/T | 1 | 166.068612 | C | T | NON_SYNONYMOUS_CODING |
| ***Ric3*** | 1_166523757_T/C | 1 | 166.523757 | T | C | INTRONIC |
| ***St5*** | 1_167138083_A/G | 1 | 167.138083 | A | G | INTRONIC |
| ***Mrvi1*** | 1_168714374_A/G | 1 | 168.714374 | A | G | INTRONIC |
| ***Spon1*** | 1_171742726_T/C | 1 | 171.742726 | T | C | INTRONIC |
| ***Spon1*** | 1_171777726_C/G | 1 | 171.777726 | C | G | INTRONIC |
| ***Spon1*** | 1_171904938_G/T | 1 | 171.904938 | G | T | INTRONIC |
| ***Spon1*** | 1_171904941_G/A | 1 | 171.904941 | G | A | INTRONIC |
| ***Spon1*** | 1_171998337_T/C | 1 | 171.998337 | T | C | INTRONIC |
| ***Pde3b*** | 1_172463519_T/C | 1 | 172.463519 | T | C | INTRONIC |

**Supplementary table 3.** List of genes in the QTL region that present SNPs

| **Gene Name** | **INDEL ID** | **Chromosome** | **Start(Mbp)** | **End(Mbp)** | **Reference Allele** | **Alternative Allele** | **Location** |
|---|---|---|---|---|---|---|---|
| ***F1M810_RAT*** | 1_129608899_TG/- | 1 | 129.6089 | 129.6089 | TG | - | INTRONIC |
| ***Sv2b*** | 1_130739698_-/CA | 1 | 130.7397 | 130.7397 | - | CA | INTRONIC |
| ***Sv2b*** | 1_130742599_-/AC | 1 | 130.7426 | 130.7426 | - | AC | INTRONIC |
| ***Sv2b*** | 1_130826672_-/GT | 1 | 130.82667 | 130.82667 | - | GT | INTRONIC |
| ***F1M811_RAT*** | 1_131129015_-/T | 1 | 131129015 | 131129016 | - | T | INTRONIC |
| ***F1M811_RAT*** | 1_131134284_T/- | 1 | 131134284 | 131134284 | T | - | INTRONIC |
| ***Klhl25*** | 1_131540432_TG/- | 1 | 131540432 | 131540433 | TG | - | UPSTREAM |
| ***F1M814_RAT*** | 1_132456191_-/CA | 1 | 132.45619 | 132.45619 | - | CA | INTRONIC |
| ***F1M814_RAT*** | 1_132675878_-/TG | 1 | 132.67588 | 132.67588 | - | TG | INTRONIC |
| ***Ntrk3*** | 1_134035794_-/AC | 1 | 134.03579 | 134.0358 | - | AC | INTRONIC |
| ***Mrps11*** | 1_134518244_-/CCACACA | 1 | 134518244 | 134518245 | - | CCACACA | DOWNSTREAM |
| ***Isg20*** | 1_134634753_G/- | 1 | 134634753 | 134634753 | G | - | INTRONIC |
| ***Mfge8*** | 1_134871094_-/C | 1 | 134.87109 | 134.8711 | - | C | INTRONIC |
| ***Abhd2*** | 1_135021727_-/G | 1 | 135021727 | 135021728 | - | G | UPSTREAM |
| ***Abhd2*** | 1_135029169_-/A | 1 | 135029169 | 135029170 | - | A | INTRONIC |
| ***Rlbp1*** | 1_135138240_-/TC | 1 | 135.13824 | 135.13824 | - | TC | UPSTREAM |
| ***Rhcg*** | 1_135362995_GAGAGAGAGA/- | 1 | 135362995 | 135363004 | GAGAGAGAGA | - | SPLICE_SITE,INTRONIC |
| ***Wdr93*** | 1_135549549_-/T | 1 | 135549549 | 135549550 | - | T | INTRONIC |
| ***Wdr93*** | 1_135549838_-/CA | 1 | 135549838 | 135549839 | - | CA | INTRONIC |
| ***Anpep*** | 1_135598576_-/A | 1 | 135598576 | 135598577 | - | A | DOWNSTREAM |
| ***Idh2*** | 1_135899068_-/A | 1 | 135899068 | 135899069 | - | A | UPSTREAM |
| ***D4A0Q8_RAT*** | 1_136069127_-/A | 1 | 136069127 | 136069128 | - | A | INTRONIC |
| ***Prc1*** | 1_136135140_T/- | 1 | 136135140 | 136135140 | T | - | DOWNSTREAM |
| ***D4A4J3_RAT*** | 1_136167005_A/- | 1 | 136167005 | 136167005 | A | - | DOWNSTREAM |
| ***Iqgap1*** | 1_136558664_-/CC | 1 | 136.55866 | 136.55867 | - | CC | INTRONIC |
| ***Iqgap1*** | 1_136641407_-/A | 1 | 136641407 | 136641408 | - | A | INTRONIC |
| ***Alpk3*** | 1_137269970_GTGTGTGTGTGTGT/- | 1 | 137.26997 | 137.26998 | GTGTGTGTGTGTGT | - | INTRONIC |
| ***Slc28a1*** | 1_137334547_-/TG | 1 | 137.33455 | 137.33455 | - | TG | INTRONIC |
| ***Homer2*** | 1_137882093_-/C | 1 | 137.88209 | 137.88209 | - | C | INTRONIC |
| ***RGD1305713*** | 1_138003252_-/GT | 1 | 138.00325 | 138.00325 | - | GT | INTRONIC |
| ***Sh3gl3*** | 1_138533714_AGAGAG/- | 1 | 138.53371 | 138.53372 | AGAGAG | - | DOWNSTREAM |
| ***F1M767_RAT*** | 1_138654884_TCTCTCTCTC/- | 1 | 138.65488 | 138.65489 | TCTCTCTCTC | - | INTRONIC |
| ***F1M767_RAT*** | 1_138713216_-/AC | 1 | 138.71322 | 138.71322 | - | AC | INTRONIC |
| ***D3ZFL6_RAT*** | 1_139143140_-/GT | 1 | 139.14314 | 139.14314 | - | GT | DOWNSTREAM |
| ***Tmc3*** | 1_139861479_-/TC | 1 | 139.86148 | 139.86148 | - | TC | INTRONIC |
| ***Arnt2*** | 1_140671403_AC/- | 1 | 140.6714 | 140.6714 | AC | - | INTRONIC |
| ***FAAA_RAT*** | 1_140858554_TC/- | 1 | 140.85855 | 140.85856 | TC | - | INTRONIC |
| ***Nox4*** | 1_143476690_T/- | 1 | 143476690 | 143476690 | T | - | INTRONIC |
| ***Nox4*** | 1_143480318_-/TCTA | 1 | 143.48032 | 143.48032 | - | TCTA | INTRONIC |
| ***Nox4*** | 1_143599429_-/AT | 1 | 143.59943 | 143.59943 | - | AT | INTRONIC |
| ***Grm5*** | 1_143897429_-/A | 1 | 143897429 | 143897430 | - | A | INTRONIC |
| ***Grm5*** | 1_144083448_-/TA | 1 | 144.08345 | 144.08345 | - | TA | INTRONIC |
| ***F1LUQ4_RAT*** | 1_146362231_AC/- | 1 | 146.36223 | 146.36223 | AC | - | INTRONIC |
| ***LOC680270*** | 1_146899406_-/CAATCA | 1 | 146.89941 | 146.89941 | - | CAATCA | INTRONIC |
| ***Dlg2*** | 1_148190578_-/CA | 1 | 148190578 | 148190579 | - | CA | INTRONIC |
| ***Dlg2*** | 1_148347335_-/A | 1 | 148.34734 | 148.34734 | - | A | INTRONIC |
| ***Dlg2*** | 1_148476682_-/TA | 1 | 148.47668 | 148.47668 | - | TA | INTRONIC |
| ***Dlg2*** | 1_148487662_AG/- | 1 | 148.48766 | 148.48766 | AG | - | INTRONIC |
| ***Dlg2*** | 1_148487707_GT/- | 1 | 148.48771 | 148.48771 | GT | - | INTRONIC |
| ***Dlg2*** | 1_148539160_-/T | 1 | 148539160 | 148539161 | - | T | INTRONIC |
| ***Dlg2*** | 1_148883316_CT/- | 1 | 148.88332 | 148.88332 | CT | - | INTRONIC |
| ***Dlg2*** | 1_148988102_ATATATATATATATAT/- | 1 | 148.9881 | 148.98812 | ATATATATATATATAT | - | INTRONIC |
| ***Rab30*** | 1_149659105_-/TG | 1 | 149.65911 | 149.65911 | - | TG | INTRONIC |
| ***RGD1559690*** | 1_149703024_A/- | 1 | 149703024 | 149703024 | A | - | INTRONIC |
| ***Odz4*** | 1_153843731_GT/- | 1 | 153.84373 | 153.84373 | GT | - | INTRONIC |
| ***Nars2*** | 1_154271062_-/ACAGAC | 1 | 154.27106 | 154.27106 | - | ACAGAC | INTRONIC |
| ***Nars2*** | 1_154284900_T/- | 1 | 154284900 | 154284900 | T | - | INTRONIC |
| ***Gab2*** | 1_154478186_-/CACACACAC | 1 | 154478186 | 154478187 | - | CACACACAC | INTRONIC |
| ***D3ZZQ6_RAT*** | 1_154718553_-/G | 1 | 154.71855 | 154.71855 | - | G | INTRONIC |
| ***D3ZGQ8_RAT*** | 1_154823313_-/A | 1 | 154823313 | 154823314 | - | A | INTRONIC |
| ***D3ZKE1_RAT*** | 1_156295478_-/GT | 1 | 156.29548 | 156.29548 | - | GT | INTRONIC |
| ***D3ZKE1_RAT*** | 1_156328047_-/TCTCTCTCTC | 1 | 156.32805 | 156.32805 | - | TCTCTCTCTC | INTRONIC |
| ***Map6*** | 1_156638174_-/A | 1 | 156638174 | 156638175 | - | A | INTRONIC |
| ***B5DF39_RAT*** | 1_156738188_-/GT | 1 | 156.73819 | 156.73819 | - | GT | INTRONIC |
| ***Lipt2*** | 1_157537693_T/- | 1 | 157537693 | 157537693 | T | - | UPSTREAM |
| ***Fam168a*** | 1_158235825_-/CT | 1 | 158.23583 | 158.23583 | - | CT | INTRONIC |
| ***D4ADZ1_RAT*** | 1_158314584_A/- | 1 | 158314584 | 158314584 | A | - | DOWNSTREAM |
| ***Fchsd2*** | 1_158582535_C/- | 1 | 158582535 | 158582535 | C | - | INTRONIC |
| ***Fchsd2*** | 1_158755377_-/A | 1 | 158755377 | 158755378 | - | A | INTRONIC |
| ***F1LM60_RAT*** | 1_158878464_TT/- | 1 | 158878464 | 158878465 | TT | - | INTRONIC |
| ***Il18bp*** | 1_159477723_-/C | 1 | 159477723 | 159477724 | - | C | UPSTREAM |
| ***Rnf121*** | 1_159492697_-/AC | 1 | 159.4927 | 159.4927 | - | AC | INTRONIC |
| ***Nup98*** | 1_159629524_A/- | 1 | 159629524 | 159629524 | A | - | INTRONIC |
| ***Nup98*** | 1_159631695_-/T | 1 | 159631695 | 159631696 | - | T | INTRONIC |
| ***Stim1*** | 1_159764629_-/AGAGAGAGAG | 1 | 159.76463 | 159.76463 | - | AGAGAGAGAG | INTRONIC |
| ***Stim1*** | 1_159884343_AC/- | 1 | 159.88434 | 159.88434 | AC | - | INTRONIC |
| ***Olr111*** | 1_161323284_-/CG | 1 | 161323284 | 161323285 | - | CG | DOWNSTREAM |
| ***Olr135*** | 1_161762982_T/- | 1 | 161762982 | 161762982 | T | - | DOWNSTREAM |
| ***Trim6*** | 1_162061328_-/A | 1 | 162061328 | 162061329 | - | A | UPSTREAM |
| ***Olr154*** | 1_162220333_-/GA | 1 | 162220333 | 162220334 | - | GA | UPSTREAM |
| ***Olr154*** | 1_162223980_TG/- | 1 | 162.22398 | 162.22398 | TG | - | UPSTREAM |
| ***Olr168*** | 1_162489797_-/G | 1 | 162.4898 | 162.4898 | - | G | DOWNSTREAM |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***Olr180*** | 1_162735896_A/- | 1 | 162735896 | 162735896 | A | - | DOWNSTREAM |
| ***Olr180*** | 1_162735898_A/- | 1 | 162735898 | 162735898 | A | - | DOWNSTREAM |
| ***LOC100362148*** | 1_162868053_-/T | 1 | 162868053 | 162868054 | - | T | UPSTREAM |
| ***Olr193*** | 1_162893376_-/A | 1 | 162893376 | 162893377 | - | A | DOWNSTREAM |
| ***Olr193*** | 1_162901538_GT/- | 1 | 162.90154 | 162.90154 | GT | - | UPSTREAM |
| ***Olr194*** | 1_162932668_C/- | 1 | 162.93267 | 162.93267 | C | - | UPSTREAM |
| ***Olr201*** | 1_163075087_-/AC | 1 | 163.07509 | 163.07509 | - | AC | UPSTREAM |
| ***Cckbr*** | 1_163157222_C/- | 1 | 163157222 | 163157222 | C | - | INTRONIC |
| ***Apbb1*** | 1_163297794_TT/- | 1 | 163297794 | 163297795 | TT | - | INTRONIC |
| ***F1LZ18_RAT*** | 1_163701435_TT/- | 1 | 163.70144 | 163.70144 | TT | - | UPSTREAM |
| ***Olr229*** | 1_164358981_C/- | 1 | 164358981 | 164358981 | C | - | DOWNSTREAM |
| ***Syt9*** | 1_164770760_T/- | 1 | 164770760 | 164770760 | T | - | INTRONIC |
| ***Ppfibp2*** | 1_165047610_-/GTGT | 1 | 165.04761 | 165.04761 | - | GTGT | INTRONIC |
| ***Ppfibp2*** | 1_165076240_TACACACACACA/- | 1 | 165.07624 | 165.07625 | TACACACACACA | - | INTRONIC |
| ***D4A7R5_RAT*** | 1_165190282_-/AGGAAGGAAGGAAGG | 1 | 165.19028 | 165.19028 | - | AGGAAGGAAGGAAGG | DOWNSTREAM |
| ***Olr239*** | 1_165268528_T/- | 1 | 165268528 | 165268528 | T | - | UPSTREAM |
| ***Olr245*** | 1_165438665_-/GTGTGT | 1 | 165438665 | 165438666 | - | GTGTGT | DOWNSTREAM |
| ***Olr260*** | 1_165809567_AAAGA/- | 1 | 165.80957 | 165.80957 | AAAGA | - | DOWNSTREAM |
| ***Olr262*** | 1_165823727_ACATGC/- | 1 | 165823727 | 165823732 | ACATGC | - | UPSTREAM |
| ***Olr281*** | 1_166472403_G/- | 1 | 166472403 | 166472403 | G | - | FRAMESHIFT_CODING |
| ***Olr282*** | 1_166487497_GTGTGTGTGTGTGTGTGT/- | 1 | 166487497 | 166487514 | GTGTGTGTGTGTGTGTGT | - | DOWNSTREAM |
| ***Ric3*** | 1_166648228_TCTCTCTCTC/- | 1 | 166.64823 | 166.64824 | TCTCTCTCTC | - | INTRONIC |
| ***Lmo1*** | 1_166702862_T/- | 1 | 166702862 | 166702862 | T | - | DOWNSTREAM |
| ***Lmo1*** | 1_166729026_-/CA | 1 | 166.72903 | 166.72903 | - | CA | INTRONIC |
| ***Tmem9b*** | 1_167367043_-/TC | 1 | 167367043 | 167367044 | - | TC | INTRONIC |
| ***Swap70*** | 1_167911659_-/G | 1 | 167911659 | 167911660 | - | G | INTRONIC |
| ***Swap70*** | 1_167927999_C/- | 1 | 167927999 | 167927999 | C | - | INTRONIC |
| ***F1M683_RAT*** | 1_168065753_T/- | 1 | 168065753 | 168065753 | T | - | INTRONIC |
| ***F1M683_RAT*** | 1_168115964_T/- | 1 | 168115964 | 168115964 | T | - | INTRONIC |
| ***F1M683_RAT*** | 1_168147706_-/A | 1 | 168147706 | 168147707 | - | A | INTRONIC |
| ***E9PSI9_RAT*** | 1_169263659_A/- | 1 | 169263659 | 169263659 | A | - | INTRONIC |
| ***E9PSI9_RAT*** | 1_169346363_-/AC | 1 | 169.34636 | 169.34636 | - | AC | INTRONIC |
| ***E9PSI9_RAT*** | 1_169368882_-/C | 1 | 169.36888 | 169.36888 | - | C | INTRONIC |
| ***Usp47*** | 1_169891406_-/A | 1 | 169891406 | 169891407 | - | A | INTRONIC |
| ***Mical2*** | 1_170117853_-/CA | 1 | 170.11785 | 170.11785 | - | CA | INTRONIC |
| ***Parva*** | 1_170305167_-/AC | 1 | 170.30517 | 170.30517 | - | AC | INTRONIC |
| ***Parva*** | 1_170357189_-/TG | 1 | 170.35719 | 170.35719 | - | TG | INTRONIC |
| ***Far1*** | 1_171389151_-/T | 1 | 171389151 | 171389152 | - | T | UPSTREAM |
| ***Spon1*** | 1_171777715_-/ACAGACAGACAGAC | 1 | 171.77772 | 171.77772 | - | ACAGACAGACAGAC | INTRONIC |
| ***Spon1*** | 1_171818052_GT/- | 1 | 171.81805 | 171.81805 | GT | - | INTRONIC |
| ***Spon1*** | 1_171857492_-/A | 1 | 171857492 | 171857493 | - | A | INTRONIC |
| ***Spon1*** | 1_171934624_-/CA | 1 | 171.93462 | 171.93463 | - | CA | INTRONIC |
| ***Spon1*** | 1_171992012_A/- | 1 | 171992012 | 171992012 | A | - | INTRONIC |
| ***Spon1*** | 1_172005216_CA/- | 1 | 172005216 | 172005217 | CA | - | INTRONIC |
| ***Rras2*** | 1_172061298_AC/- | 1 | 172.0613 | 172.0613 | AC | - | INTRONIC |
| ***Rras2*** | 1_172087391_-/CACA | 1 | 172.08739 | 172.08739 | - | CACA | INTRONIC |
| ***Pde3b*** | 1_172488706_-/CT | 1 | 172.48871 | 172.48871 | - | CT | INTRONIC |
| ***Calcb*** | 1_172783191_-/T | 1 | 172783191 | 172783192 | - | T | DOWNSTREAM |
| ***Insc*** | 1_172823765_TATA/- | 1 | 172.82377 | 172.82377 | TATA | - | INTRONIC |
| ***Insc*** | 1_172830913_-/TG | 1 | 172.83091 | 172.83091 | - | TG | INTRONIC |

**Supplementary table 4.** List of genes in the QTL region that present INDEL

| GeneSymbol | Description | GeneID | Chrom | Location (Mbp) |
|---|---|---|---|---|
| Akap13 | A kinase (PRKA) anchor protein 13 | 293024 | 1 | 131.224569 |
| Alg8 | probable dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase | 293129 | 1 | 154.607442 |
| Ampd3 | AMP deaminase 3 | 25095 | 1 | 168.533491 |
| Ankrd42 | ankyrin repeat domain 42 | 293117 | 1 | 149.423846 |
| Apbb1 | Amyloid beta A4 precursor protein-binding family B member 1 | 29722 | 1 | 163.282918 |
| Aqp11 | Aquaporin-11 | 286758 | 1 | 154.973798 |
| Arfip2 | Arfaptin-2 | 293344 | 1 | 163.364861 |
| Arl6ip1 | ADP-ribosylation factor-like protein 6-interacting protein 1 | 293551 | 1 | 176.332758 |
| Arnt2 | Aryl hydrocarbon receptor nuclear translocator 2 | 25243 | 1 | 140.535823 |
| Arntl | Aryl hydrocarbon receptor nuclear translocator-like protein 1 | 29657 | 1 | 171.062181 |
| Atg16l2 | ATG16 autophagy related 16-like 2 | 308865 | 1 | 158.787779 |
| Btbd1 | BTB/POZ domain-containing protein 1 | 293060 | 1 | 138.006567 |
| Btbd10 | BTB/POZ domain-containing protein 10 | 308890 | 1 | 171.163522 |
| Ccdc90b | Coiled-coil domain-containing protein 90B, mitochondrial | 308820 | 1 | 149.410497 |
| Cckbr | Gastrin/cholecystokinin type B receptor | 25706 | 1 | 163.156914 |
| Chchd8 | coiled-coil-helix-coiled-coil-helix domain-containing protein 8 | 499214 | 1 | 157.965119 |
| Chd2 | chromodomain-helicase-DNA-binding protein 2 | 308738 | 1 | 128.609727 |
| Cib1 | Calcium and integrin-binding protein 1 | 81823 | 1 | 136.031865 |
| Clns1a | Methylosome subunit pICln | 65160 | 1 | 154.946673 |
| Clpb | Caseinolytic peptidase B protein homolog | 65041 | 1 | 159.126512 |
| Copb1 | Coatomer subunit beta | 114023 | 1 | 172.199677 |
| Coq7 | Ubiquinone biosynthesis protein COQ7 homolog | 25249 | 1 | 176.741638 |
| Cp110 | centrosomal protein of 110 kDa | 361634 | 1 | 176.937287 |
| Cpeb1 | Cytoplasmic polyadenylation element-binding protein 1 | 293056 | 1 | 137.556774 |
| Crebzf | CREB/ATF bZIP transcription factor | 293112 | 1 | 147.124224 |
| Ctr9 | Ctr9, Paf1/RNA polymerase II complex component, homolog | 293184 | 1 | 168.784377 |
| Dchs1 | dachsous 1 | 308912 | 1 | 163.49734 |
| Dennd5a | DENN/MADD domain containing 5A | 308942 | 1 | 167.519649 |
| Dgat2 | Diacylglycerol O-acyltransferase 2 | 252900 | 1 | 156.447588 |
| Dkk3 | dickkopf-related protein 3 | 171548 | 1 | 169.924618 |
| Dlg2 | Disks large homolog 2 | 64053 | 1 | 148.051658 |
| Eed | polycomb protein EED | 293104 | 1 | 146.563964 |
| Eftud1 | elongation factor Tu GTP binding domain containing 1 | 308789 | 1 | 138.92062 |
| Fam103a1 | family with sequence similarity 103, member A1 (Fam103a1), mRNA | 293058 | 1 | 137.980239 |
| Fam108c1 | abhydrolase domain-containing protein FAM108C1 | 361601 | 1 | 140.382431 |
| Fam160a2 | FTS and Hook-interacting protein | 293343 | 1 | 163.110928 |
| Fam168a | family with sequence similarity 168, member A (Fam168a), mRNA | 361614 | 1 | 158.140473 |
| Far1 | Fatty acyl-CoA reductase 1 | 293173 | 1 | 171.392301 |
| Fchsd2 | FCH and double SH3 domains protein 2 | 308864 | 1 | 158.54883 |
| Folh1 | Glutamate carboxypeptidase 2 | 85309 | 1 | 142.936379 |
| Fsd2 | fibronectin type III and SPRY domain-containing protein 2 | 308779 | 1 | 137.749268 |
| Furin | Furin | 54281 | 1 | 136.209969 |
| Gprc5b | G-protein coupled receptor family C group 5 member B | 293546 | 1 | 177.205905 |
| Grm5 | Metabotropic glutamate receptor 5 | 24418 | 1 | 143.863506 |
| Hbb | Hemoglobin subunit beta-1 | 24440 | 1 | 161.584858 |
| Hddc3 | HD domain-containing protein 3 | 308758 | 1 | 136.161425 |
| Hdgfrp3 | Hepatoma-derived growth factor-related protein 3 | 252941 | 1 | 138.098819 |
| Homer2 | Homer protein homolog 2 | 29547 | 1 | 137.827128 |
| Idh2 | Isocitrate dehydrogenase | 361596 | 1 | 135.876058 |
| Il16 | pro-interleukin-16 | 116996 | 1 | 139.908061 |
| Il18bp | interleukin-18-binding protein | 84388 | 1 | 159.471809 |
| Ilk | Integrin-linked protein kinase | 170922 | 1 | 163.481299 |
| Inppl1 | Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2 | 65038 | 1 | 159.27813 |

| | | | | |
|---|---|---|---|---|
| Ipo7 | importin-7 | 308939 | 1 | 167.658312 |
| Kif7 | Uncharacterized protein | 293047 | 1 | 135.473063 |
| Klhl35 | Uncharacterized protein | 308850 | 1 | 156.801077 |
| Lipt2 | lipoyl(octanoyl) transferase 2 (putative) | 365314 | 1 | 157.538704 |
| Lmo1 | LIM domain only protein 3 | 245979 | 1 | 166.706026 |
| LOC361635 | UPF0505 protein C16orf62 homolog | 361635 | 1 | 176.965214 |
| LOC683402 | similar to AP-3 complex subunit sigma-2 (Adapter-related protein complex 3 sigma-2 subunit) (Sigma-adaptin 3b) (AP-3 complex sigma-3B subunit) (Sigma-3B-adaptin) (LOC683 | 683402 | 1 | 135.653108 |
| LOC689064 | Hemoglobin subunit beta-2 | 689064 | 1 | 161.578128 |
| Map6 | Microtubule-associated protein 6 | 29457 | 1 | 156.592504 |
| Mesdc1 | mesoderm development candidate 1 | 308795 | 1 | 140.157974 |
| Mesdc2 | LDLR chaperone MESD | 308796 | 1 | 140.167851 |
| Mesp1 | mesoderm posterior protein 1 | 308766 | 1 | 135.571777 |
| Mfge8 | Lactadherin | 25277 | 1 | 134.87003 |
| Mogat2 | 2-acylglycerol O-acyltransferase 2 | 681211 | 1 | 156.516533 |
| Mrpl46 | 39S ribosomal protein L46, mitochondrial | 293054 | 1 | 134.498792 |
| Mrpl48 | 39S ribosomal protein L48, mitochondrial | 293149 | 1 | 157.979818 |
| Mrps11 | 28S ribosomal protein S11, mitochondrial | 499185 | 1 | 134.507836 |
| Mrvi1 | protein MRVI1 isoform b | 308899 | 1 | 168.627363 |
| Ndufc2 | NADH dehydrogenase | 293130 | 1 | 154.635889 |
| Nmb | neuromedin-B | 499194 | 1 | 137.097463 |
| Nrip3 | nuclear receptor-interacting protein 3 | 361625 | 1 | 167.380328 |
| Ntrk3 | NT-3 growth factor receptor | 29613 | 1 | 133.92553 |
| Nucb2 | Nucleobindin-2 | 59295 | 1 | 174.605677 |
| Nup98 | Nuclear pore complex protein Nup98-Nup96Nuclear pore complex protein Nup98Nuclear pore complex protein Nup96 | 81738 | 1 | 159.598048 |
| Olfml1 | Olfactomedin-like protein 1 | 361621 | 1 | 164.953064 |
| P2ry6 | P2Y purinoceptor 6 | 117264 | 1 | 158.381128 |
| Pak1 | Serine/threonine-protein kinase PAK 1 | 29431 | 1 | 155.057622 |
| Pcf11 | Uncharacterized protein | 361605 | 1 | 149.475611 |
| Pde2a | cGMP-dependent 3',5'-cyclic phosphodiesterase | 81743 | 1 | 158.921607 |
| Pde3b | cGMP-inhibited 3',5'-cyclic phosphodiesterase B | 29516 | 1 | 172.409282 |
| Pex11a | Peroxisomal membrane protein 11A | 85249 | 1 | 135.513735 |
| Pgap2 | Post-GPI attachment to proteins factor 2 | 116675 | 1 | 159.69692 |
| Pgm2l1 | glucose 1,6-bisphosphate synthase | 685076 | 1 | 157.605906 |
| Picalm | Phosphatidylinositol-binding clathrin assembly protein | 89816 | 1 | 146.754045 |
| Pik3c2a | phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing subunit alpha | 361632 | 1 | 174.430831 |
| Plekhb1 | Pleckstrin homology domain-containing family B member 1 | 64471 | 1 | 158.08193 |
| Pold3 | DNA polymerase delta subunit 3 | 293144 | 1 | 157.453059 |
| Polg | DNA polymerase subunit gamma-1 | 85472 | 1 | 135.197016 |
| Ppfibp2 | protein tyrosine phosphatase, receptor-type, F interacting protein, binding protein 2 | 308918 | 1 | 164.979709 |
| Ppme1 | protein phosphatase methylesterase 1 | 361613 | 1 | 157.725633 |
| Prc1 | protein regulator of cytokinesis 1 | 308761 | 1 | 136.112674 |
| Prkcdbp | Protein kinase C delta-binding protein | 85332 | 1 | 163.212922 |
| Prkrir | 52 kDa repressor of the inhibitor of the protein kinase | 308845 | 1 | 155.982782 |
| Prss23 | Serine protease 23 | 308807 | 1 | 146.081557 |
| Psma1 | Proteasome subunit alpha type-1 | 29668 | 1 | 172.237763 |
| Rab30 | ras-related protein Rab-30 | 308821 | 1 | 149.656373 |
| Rab38 | ras-related protein Rab-38 | 252916 | 1 | 144.783909 |
| Rab6a | Ras-related protein Rab-6A | 84379 | 1 | 158.041088 |
| Relt | tumor necrosis factor receptor superfamily member 19L | 361615 | 1 | 158.293361 |
| RGD1306959 | similar to C11orf17 protein (RGD1306959), mRNA | 361624 | 1 | 167.324919 |
| RGD1311021 | RCG24599Uncharacterized protein | 308765 | 1 | 135.69698 |
| RGD1311634 | similar to RIKEN cDNA 3200002M19 (RGD1311634), mRNA | 293155 | 1 | 159.35911 |
| RGD1311703 | small acidic protein | 293160 | 1 | 174.173969 |
| RGD1561459 | similar to RIKEN cDNA 1810020D17 (RGD1561459), mRNA | 361606 | 1 | 154.786525 |

| | | | | |
|---|---|---|---|---|
| Rgma | repulsive guidance molecule A | 308739 | 1 | 128.547399 |
| Rlbp1 | retinaldehyde-binding protein 1 | 293049 | 1 | 135.122063 |
| Rnf121 | RING finger protein 121 | 308871 | 1 | 159.475046 |
| rnf141 | RING finger protein 141 | 308900 | 1 | 168.572375 |
| Rras2 | ras-related protein R-Ras2 | 365355 | 1 | 172.026263 |
| Rrp8 | Ribosomal RNA-processing protein 8 | 308911 | 1 | 163.47703 |
| Sec11a | Signal peptidase complex catalytic subunit SEC11A | 65166 | 1 | 137.109468 |
| Sema4b | semaphorin 4B | 293042 | 1 | 136.001235 |
| Serpinh1 | Serpin H1 | 29345 | 1 | 156.667042 |
| Sh3gl3 | Endophilin-A3 | 81921 | 1 | 138.398334 |
| Slco2b1 | Solute carrier organic anion transporter family member 2B1 | 140860 | 1 | 156.992493 |
| Smpd1 | sphingomyelin phosphodiesterase | 308909 | 1 | 163.27897 |
| Spcs2 | signal peptidase complex subunit 2 homolog | 293142 | 1 | 157.199447 |
| Spon1 | Spondin-1 | 64456 | 1 | 171.70072 |
| St5 | suppression of tumorigenicity 5 protein | 308944 | 1 | 167.119711 |
| Stard10 | PCTP-like protein | 293150 | 1 | 158.81997 |
| Stard5 | stAR-related lipid transfer protein 5 | 502348 | 1 | 139.896272 |
| Stim1 | Stromal interaction molecule 1 | 361618 | 1 | 159.761567 |
| Sv2b | Synaptic vesicle glycoprotein 2B | 117556 | 1 | 130.683153 |
| Swap70 | switch-associated protein 70 | 293410 | 1 | 167.888783 |
| Taf10 | TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor | 293345 | 1 | 163.487518 |
| Thrsp | Thyroid hormone-inducible hepatic protein | 25357 | 1 | 154.647341 |
| Tm6sf1 | transmembrane 6 superfamily member 1 | 361600 | 1 | 138.058059 |
| Tmem126a | Transmembrane protein 126A | 293113 | 1 | 147.129335 |
| Tmem126b | transmembrane protein 126B | 293114 | 1 | 147.146187 |
| Tmem41b | Transmembrane protein 41B | 361626 | 1 | 167.608205 |
| Tmem9b | transmembrane protein 9B | 293415 | 1 | 167.355899 |
| Tpp1 | Tripeptidyl-peptidase 1 | 83534 | 1 | 163.490393 |
| Trim3 | Tripartite motif-containing protein 3 | 83616 | 1 | 163.331603 |
| Trim5 | tripartite motif-containing protein 5 | 308906 | 1 | 162.096454 |
| Trim6 | tripartite motif-containing 6 | 293294 | 1 | 162.066157 |
| Ucp2 | Mitochondrial uncoupling protein 2 | 54315 | 1 | 157.922179 |
| Ucp3 | Mitochondrial uncoupling protein 3 | 25708 | 1 | 157.896001 |
| Unc45a | Protein unc-45 homolog A | 308759 | 1 | 136.143886 |
| Usp47 | ubiquitin specific peptidase 47 | 308896 | 1 | 169.836253 |
| Vps33b | Vacuolar protein sorting-associated protein 33B | 64060 | 1 | 136.085931 |
| Wdr73 | WD repeat-containing protein 73 | 308751 | 1 | 137.088348 |
| Wee1 | Wee1-like protein kinase | 308937 | 1 | 167.769797 |
| Zfand6 | AN1-type zinc finger protein 6 | 293067 | 1 | 140.885729 |
| Zfp143 | Zinc finger protein 143 | 361627 | 1 | 167.704313 |
| Znf592 | zinc finger protein 592 | 293038 | 1 | 137.188336 |

**Supplementary Table 5:** Genes within the linkage region represented on the array

| Locus_Name | Sequence | Var | Chr | Coord | Final Score |
|---|---|---|---|---|---|
| 1000316809 | ATAATTTTTATTTTTATAGATGTCTAAATTTTAAAATAGGATACACTCAAGCAATATACA[T/G]GTGGTTAAGACAAATTAATACTTTTATAAATGACCATTCTCAGTTACAAGCACCAAAAT | T/G | 1 | 316809 | 0.493 |
| 1002439384 | TGGCGAGTCTGGGGATGATAGACAGTAGAGTCCATGATTGGAGATGGGGTTTTAAATATC[T/C]GTTTTATCTGTAAGTTTTTCTGCTGTTTTCTCAGAGCCGTCTGGGTATAAGATGATAGG | T/C | 1 | 2439384 | 0.903 |
| 1006529087 | GGCAAAAGGCTAAGCTCCATCTTTGTGCATCAGAGACAGACAGGTACCTTCTGTCAGTCA[A/G]AAGCCAGCTTTGGATGTCAAGAATGTGGCTGGGTTGCTTTTAGGAGTTTTCATCTCACA | A/G | 1 | 6529087 | 0.981 |
| 1010631560 | ACTAGGCGACATAGTCTCACAGAAAACTTCCTGATCCTCTGTCTCTTATAATCATTGTGCA[A/G]TTCCATTTTAACATAGTGTGCCTTCAATCATAATTCTGCTAAGAATTTTAGTATTGGGAAC | A/G | 1 | 10631560 | 0.771 |
| 1015047131 | TTCTTTAATGGTCTAATGCGGGGTTCCCAACCTGTGGGTCTCGAACCCTTTGGAGGTCAAA[T/C]GATACTTTCAGAAGGGTTGCATAGCAGACATCCTGCACATCAGATGTTTACATTACAATCC | T/C | 1 | 15047131 | 0.625 |
| 1017126515 | GAACTTGCAAACTTAATAGTTAGCCCAGGCTAACATCAACCTCAAAATTCTCCTGCGTCA[A/G]ATTGGTAAGTTCTAGGGCTACAGGGAAGCAATCCCATACTGGCCTAGGTTTGAATTTCA | A/G | 1 | 17126515 | 0.984 |
| 1019324003 | CAGTCAATACTCTTAACCCCCCCCGCCCCCGAGCCATCTGTACAGCACCACTAATTGAGG[A/G]TTTTAACTTTTAAAAAATCTAATGGTTGTGGAGGAAAAGTTCTTTGACTAAGACTACTTCA | A/G | 1 | 19324003 | 0.835 |
| 1023571501 | ATTAGGGCTGAAGATATAACTCAGGCTAAAGAAGAACTAGCTTTAGCCACAGCAACTCACA[A/G]AATAGGTGTGCCTGTCCTTGCTAGCAATCCCAGCATGTGGAAGTAGAGCCACTGGTTCCTC | A/G | 1 | 23571501 | 0.881 |
| 1028061199 | AAGGCACATCCAAAGCCTGAAAAGGCAAGCTGGTAAAGGAATGGACTTTTGGTGGGTCAGA[T/C]AGACTTTGGTGCATATCTCTCATTTACTGGTTAGTTAAGAGCAGGCTCAGTGCTCTCCTTG | T/C | 1 | 28061199 | 0.984 |
| 1043141868 | ACAGAGAGAGACAGATACAGAGACCGAGACCACAAACATAGGCAAAGAGATGCCCCCAGGG[A/T]TCTGTTCCTCTCACCTGAACCTTGTCAACTAAAGGTTCCATTATTCCCAAAACAGTGCTGC | A/T | 1 | 43141868 | 0.865 |
| 1045244987 | CAGCATTTTGACTTTGCATGATGTACAAAGCAGGCAGGAAATATCAGTTTCCGTAGATGTG[A/T]ATAGCCCTACTTCTGTGTAAAAGAGGCATCACGCATTGAAAGAATTTGTGTCTTTGTTTCT | A/T | 1 | 45244987 | 0.898 |
| 1047282515 | TTCTGCTGCTGGTCCTATCTTCCTGGTTAGAGCAGGAAAAGTGAGGTCAAAGATTGGATCC[T/C]GAGGTACCATCCCACCAGGTCCCTTCAGCCTTTGTGGGCACTTCTTTCTCCTGGCTGTCAC | T/C | 1 | 47282515 | 0.959 |
| 1049404004 | TCTAGACTAGCCTTTCACTCAGCAAAGATAGATTACTGAGTGTTGAGAGGTGAGGGGTTTT[A/C]AAAGATATCTTGTTGTTGAGGTTGTGACATTAAAAGCTTAGTTCTATGCTGGAAATAGACT | A/C | 1 | 49404004 | 0.982 |
| 1053099529 | GCTCAGCCTGCTTTCTTATACAACCCAAGGATATCTGTGGAGAGTAGTACCACACACAGT[A/G]AACTGGACCCTCCCTAAAAATCATGAATCAAGGACATGCCCTACAGATGGCCTACAAGG | A/G | 1 | 53099529 | 0.965 |
| 1055185526 | GATTTATTCCTAAGTACCCAGATATATTTATTGTTTTGACATGAGAAATCTAAGTATGTT[A/G]TATAATGACTTGTTACTATGGAGGGTTATGTTTGTTATTTTGATATGGAATGTCCAACC | A/G | 1 | 55185526 | 0.711 |
| 1065906423 | CAATCGTGATGAGTTTATAAACCCTACTGTGCCTGGACCTCCACACAGCTGCCCTTGGTAT[T/C]GCTGCTTTCTGTAGAACGAGCAAAGATGGAGGTTCTCTTCCTACAAGCTTTTAACAATTAT | T/C | 1 | 65906423 | 0.727 |
| 1069420737 | GGTTGCTGTATGTGTAAGGCTTGTTTGCATAATAATGTACATATTTTACTTTGTATTCCTC[T/C]TTCAGAGAAAGTTCTCCCTGCCAAGGTTATTGGGGAATGTTCTCCTTGCTGAAGTTAATGA | T/C | 1 | 69420737 | 0.579 |
| 1071824081 | TAGGTCTTCCTTTGCAAAGAAGTTAACATGATACATTCTGATTTTCATAGCTTCTCTCTAG[A/G]GCCTTCTCCTTCCATTCTTTAATTTCCTCTTTATTTGTTAGAATTTGTTACTGTTTTCTCA | A/G | 1 | 71824081 | 0.814 |
| 1081561140 | AAGTCTTAGTAATGTTTCTTTTACAAATGTGTGTGCCAATTTGGAGCATAGTTGTTCAGAA[T/C]TGAGATCTCTTTTTTTCCTTTGATGTGTATGAAGTATCCTTCCTCATGTCTTTTGGTTACT | T/C | 1 | 81561140 | 0.943 |
| 1085654787 | GAGGTTGATGGTGTCCAAGGGCCGCAGAGAAGCAGGAGCTTTGGGCAGAGCTGCGTGCATC[A/T]GTGGTCCCCCTTCCTCCTCAGAGAATGGTGTAGAAATACATGGCTATCATCATCACAGGGA | A/T | 1 | 85654787 | 0.637 |
| 1091980360 | TAGAACCTGTACCCTGAAATTGCATCCCCCAACAGCCAGGTCCATGTAAGGCAGAAAGGC[A/G]TTTCTTGTGTAAACCTTTTATGCAGGAAGTTGGGATGCCAGGCAAAGGTGTAGCTTCTG | A/G | 1 | 91980360 | 0.99 |
| 1096098605 | TTCTAAACTGACAACTCCAAGTTGGAGTCGGGCAAAACAATGTCCAGAGTTAAGAGCCTTT[A/T]TTTCTCCACAGGCACAAACGCCCCATCTTGGCGGACCCAGAAGAATAGGTCTCGGGCAGCA | A/T | 1 | 96098605 | 0.976 |
| 1098244859 | CTAATTTCTTTCTCAGCCTGTTAATCATTTGTATAAAGGAAGGCTACTGATTTAGAGTTA[A/C]ATTTATATATGGCTGCTTTGCTGAAGTTGTTTATCAGCTGCAGAAATCCTCTGGTAAAA | A/C | 1 | 98244859 | 0.49 |
| 1100506123 | ATATCAGGCTTGACATGACTTATCTGTCCCCTAATTTTATATGAAGCTCTCCTACAATTTA[A/G]GAGGAAAATCAGGCAATGCCCTAGAATCTAGTCAAGGTCAGGAAAGCAATTTATATCCGTG | A/G | 1 | 100506123 | 0.964 |
| 1102564198 | CCACTGGCAGTTTATTACATTTACCTTCCCATATTACTGTCATCATTTTGCTTTGGTTTA[A/C]TTTTGCCACAGAATTGTATATATGTTAATGAGATTCTCTATCTGCTTAATTACAACTTT | A/C | 1 | 102564198 | 0.8 |
| 1104596221 | TGAGTGACTCTTTATGGAAAATGACAATGTATTAGTTTTCTTTTCAGTAGTTAAAACTAAC[A/G]CAGCAGATTTGTGCAATTTATCCTAAATTGCACCCTGAGAATCAGGTGTTCATAGCCGCTG | A/G | 1 | 104596221 | 0.772 |
| 1106667964 | TTCTGGGGAATCAGAAATACTGAGACTAAAACAACAGCATCACATCTCTTTATTTCTTTAA[T/C]TGTTACTTACATAGAAACGCATATAATGGAATAATCGGGCCTAATTTTAATCAAGGAATTT | T/C | 1 | 106667964 | 0.71 |
| 1110776278 | TATTTTTATCTTTTTTTTATCTGATAGCTATGACTGGATTTGTGCTTTACTATTTAGAGGT[A/G]GTGAGAGTAGATATTTCTCCTTCTCTTCCCCTTCCTCTTTTTAAAATTTATCTTATGTGTA | A/G | 1 | 110776278 | 0.75 |
| 1112858894 | ACTAATGACACAAGGCAGGCAGATGTGAGCTTTAAGCTGCCCTATTGCTAGTATGAAAGCA[C/G]GGAGTCTTCATAAACCCCTGTATAAATTGATCAGGGATAAGTTCAAGGTGCTTTCTGGGCA | C/G | 1 | 112858894 | 0.505 |
| 1114894731 | CTGCTTAGAGTTACAAAATATTTTAAGGGAGTGCAATATACTACTAGCAATTAGTCAAGAT[A/T]GGTTTATTTATGTATACCCTTGATCTGATCTCATGGAATACAGTGTAAGGCTAATTTCTGT | A/T | 1 | 114894731 | 0.585 |
| 1119329729 | CTACTCTGCAGAACAGACTTTACCAGCACATTCTCCCATCTACAGAAAGGGTCTTTCCCCA[T/C]GAGAAAAGAGCTAAGAAGCATTTGTGATGACCATAGCCAGGTACATGACCTGCAAAAGTCT | T/C | 1 | 119329729 | 0.98 |
| 1124142467 | CAGTGGTTAAAAGCACTGGATACTCTTGAAGAAGAGACAGGCTTGGTTCCCATTACCCACA[T/C]GATTGTATAAACCATCTTTAACTCCAGTTTTCTACATTTACCAAGCACCAACACGATACAC | T/C | 1 | 124142467 | 0.867 |
| 1126194113 | TCACCGAACTCTACATGAATGACATGAGGAAAAGTTGCATGGGCCCCAACACATAGGAGG[A/G]AGCAAGAGAGGTCCCACATGCCCAGCTATGATTCCTGAAGTAGGAATGAAATGCACTAA | A/G | 1 | 126194113 | 0.75 |
| 1128220967 | AGCCTGGAATTACGAGCCAACTTAACCCCTATTCTTCTAAGTTGATTTTGGTTAGGGTATT[A/T]AAGCATAGCAATAGAAATGAAACTTGTAAATGTCCACTAAGGCCTGGTCTTAGGAGACTCT | A/T | 1 | 128220967 | 0.604 |
| 1132288249 | GTGTGATGGTTTCAGCATTGTGTTCCCCTCCCCTGCATTTCAGAATTTCTTGGTTGCTTTG[C/G]GTCCCTTTGTGTGCACTTCCACATTGCTTTTCCTCTTTGATAGTATTTTTCAGAATCGCTT | C/G | 1 | 132288249 | 0.948 |
| 1134312415 | AGAAAGCAAACCAGTACCAGGAGCAAAAGAAGCAGTGAGGAAAGGCCATTAGGGTTGGGAA[A/G]CTTCATTTCCCTGTGCCAGGCTGAATTAGAAGCCGTGATTTTAATCCATTAACCAATACAA | A/G | 1 | 134312415 | 0.725 |
| 1136332511 | CTAGAAGGACAAGGTAGGAAGACTGCAAGCTTAAAGCGTATGTGGACAATTTGGTAAAAT[C/G]CTGTCACAAAGTAAACAGTAAATAAAAACCTGAAACTATAATTCAATGATAGTGTTTGT | C/G | 1 | 136332511 | 0.856 |
| 1138338108 | TGCGCATACTACTGCTATAGTTTGAATGTAGAAGGGTCTCTGCTGGCTCATGTGACTGAGC[A/G]CTTGGTCCTTAGCTGGTGGCCCTTCTTTGGCAGGAGGTGGAACATTGAAAAGCAGGAGTCA | A/G | 1 | 138338108 | 0.719 |
| 1146593376 | CTATGCAGTAAGAAAAAAAGAAAGAAGAAAATCCTATTTTTGTCGAAGGGGACTTTGAGAT[A/G]GAAGGTGTTCTTTTCAACTGTATCAAAGCCAGCACAATGTTTTAAGATGCTAAGACAAAAA | A/G | 1 | 146593376 | 0.97 |
| 1148739042 | CTGAGACCCAAGAAGCTAGTTGAGTTGAAAATTCTCCATTGCCTTGAAGAACAGTACTAAA[A/G]TATCTTCAGCTTTTCTAATGCTTTAGCCTGTGTTTTACTATATCTGCTTCTGAAAAACTGT | A/G | 1 | 148739042 | 0.903 |
| 1150822909 | TAATGGAGAATCTATTCCTGACATTTTTCTTAACCAATATAATTTACAACTGTACAGGTC[A/G]ACCCTCATCATAAAAACTTCTTTCAACCCTGAAGATTGTCACAGATATTGTAATCTAAT | A/G | 1 | 150822909 | 0.809 |
| 1152856366 | TTTTTATGGACTGGATTGGGCAGATGGCTGTTGACATTTAATGACTTTTAATGAAGCCTCC[A/G]AAGATGCAACCCCTCGATCCTCCAGAAAGTGAAATAAGTCGTTACCAATAAATAAAAATAT | A/G | 1 | 152856366 | 0.989 |
| 1154943209 | TGCCAAGCCATCTTTTTAAACCACAGCCCTAACAATTTAAGAGTCTTAGTTGAGCATGGG[A/G]CTAGAACATAGCTGTTAACTTTTGTCTTAGATTAAGAGACCTGAGGATTTGATGCACTA | A/G | 1 | 154943209 | 0.825 |
| 1156997876 | CTGCTTCTTTACTTGCAGGGGTAGCTGGGGTGGATGGACACCAAGGCTGGACACTGCTTT[T/C]TAGATTCCTCCTCAAGCTTCCCTCATAGGCATCAATGTCCATGGTGAGAAGTGCTCACA | T/C | 1 | 156997876 | 0.881 |
| 1161067665 | ACTCAAGTGAATAAAATACATTCTTTTTTGGTCATTATGAACAATCTGGTCTTTATTATCT[T/C]TCTGGACAGTGAAAGTTCCCTTATGACATCTACTTCATTCATTTCTTCTATTTTTATCTCA | T/C | 1 | 161067665 | 0.809 |
| 1163084697 | TTAATGGGGCAAAACTCGCAATTTGGAAACTGTTTACCTCTTAACGTACTGATGCAAATTC[A/G]GATTTAGTCCTCACTCCTGCCCACAGGCACTTAGACAGTGTGCCCTCCATCTTCACAATCT | A/G | 1 | 163084697 | 0.991 |
| 1167133721 | TTGCTCTTTGGGGAGAAAAAAAGTTTCTATTTTCAAAATTCTATCTTTCCACTAAGTTCAA[A/C]ATATTTCTCCAAGAACCCCAGAGGAGGTGTGCATCTCAGTCCCTGCTCGAATGGCAGCTCT | A/C | 1 | 167133721 | 0.935 |

| | | | | | |
|---|---|---|---|---|---|
| 1169175540 | TCATATTCTCTTATAGCCTGGTTATCTTGTTTGGTTATTGCAAGGATACTTTACTGTCAGG[C/G]TATAATAATTACCATTAGGATATGTCCCAGTTTTGATCATTTGGGGGTCAGTTTTCCCTAC | C/G | 1 | 169175540 | 0.751 |
| 1171186665 | ATTGTTTGGATATTATGTTACCAAGGACTAAACTCAGAGCCAGCCCCACATATACGTGAA[T/C]ATTTCACCTCTGAGCTATATGCTCAGCCCTACTGCAATATTTAGCAGAGGAAGCAGACA | T/C | 1 | 171186665 | 0.824 |
| 1173205180 | CCCATTGCTCATTAGAGGACATATTTGTATTAGATGAGGCTGGGTGGGGGCCTTGCTTGT[A/C]CTCCCACTACCTAAACCAGTAAGGAAGCTCAGGAGTCAAAGGAAGTAGCTGAGGCTGCC | A/C | 1 | 173205180 | 0.919 |
| 1175234094 | AGGTTTATGTTAAGCAAGTTACAGTCCATTCTAGAAATCAAGGCAGCAGGAACTTAAAGT[T/C]GCTAGTCACATTGCAACCATAGTCAGAAGTAAAGAGGGATAAACACATTCATGCTTTGA | T/C | 1 | 175234094 | 0.791 |
| 1177281844 | GCATATGCAAACCATCACAGCCCCTAAGAGTAGACTTAATGCCTTTATAGGAGGAGGCTTA[T/G]AACTTTCTCTGCTTCCCTGCTATGGAAGGATTCAGTAGGATGGTAGACATCTGTAAACAAG | T/G | 1 | 177281844 | 0.88 |
| 1179326548 | CCCCAGAGAACATGTGGGACCGTGACCTCTAGATGAGTGTTTTCTTCCTTGCCTGAAAGTT[T/C]CAGGTACAGTCTCCCTTGTCTTTGTCCTCATCCTCCTTGCAGTCACTGCCAGTCTTGAGAA | T/C | 1 | 179326548 | 0.85 |
| 1181376481 | CCCCTTCGCCAACACCTTCTCAGTGCCTTTCAGGGTCGGTGATAGACCTCCATGCATATGA[A/G]TCTAGACTCATGAAGCCCACTGAACCAGGACACCATCCTCGGAGGTCAAATTTACATTCAA | A/G | 1 | 181376481 | 0.93 |
| 1183474096 | GCAGGTCAGAGGGAGGTCAACTTATCCTGAGGCAGTGGCTAAACATTTGAAAGTACATTG[A/T]GTTCTGAACTAATTGCAAACCTATTGCCTCCCTTCCGTGGCTGCAGCAACATCCTTGTT | A/T | 1 | 183474096 | 0.872 |
| 1185536653 | AGGGGGAGGCCGCGCGCTGCAGGACTAAGGCCAGGCGTTCCAGGAGGTGGCCTCGAGTGG[A/G]GCCTGAGAAGACTCTTGAGGCACCAGAAGAAGACTACGGAAGACCGGGAGCGCTCCGAG | A/G | 1 | 185536653 | 0.869 |
| 1187786202 | ATCACCTGCCATTGTGCCTCTTAGCAGACTCAGGGGCTGAGTGGCTCCTTCCCCTCCTTT[T/G]CAGCAAGCTGCAGTCAGGGCTGGGAAGTGGTTTGGTGGGAGAGGATCAGGAGCACAGCC | T/G | 1 | 187786202 | 0.668 |
| 1193936251 | ACCGGGAAGTTTTATGAAGGGAACACAACTGGGGAGTCACTACGCTGATGAATAAAAGGG[A/G]GGTGAGACCTTCATGCCTGTCTGCTTTAGGCTCACTGCCCAGCTAAGCAATCCCACTTT | A/G | 1 | 193936251 | 0.976 |
| 1196046075 | CACCAGCTAGCAAATGAGGAAAAATTACTGTGCGGCACCTTCTGAAGAGTCTCATCATATA[C/G]TTTTGAATTCTGAACTCTGCACACTTTTTACATATTTAGACATAAAATGATCATAATTGAA | C/G | 1 | 196046075 | 0.914 |
| 1198066256 | AAAACTGTTTCTAGAATTTTCTTCCACGTAACAAATAGAGAAAGATTCTCTGTGCTTCTAA[A/C]CTGGGAAGGATAGATAAATTTTGAGTTGTAGTTTCCATTTTTAAAGGATTTAAAGAATGCT | A/C | 1 | 198066256 | 0.841 |
| 1202376557 | GGCAGGGAGGAAGGTAAGGAGTGAGGAAGGCAGGGAGGAAGTTAGGGAGGAAGTTAGAGAG[A/G]AAGGTAAGGAATGAGAAAGGCAGGAAGGAAGGTAAGGAATGAGGAAGTTAGAGAGGAAGGT | A/G | 1 | 202376557 | 0.832 |
| 1204394931 | TTCCAACTTTATTTTTATGAGAGTCTTTGCCACAGATAGATGCTAAATTTTGTTTAAAAAA[A/T]TTTTTCAGGATAACACCTTTTAAAAATGAACTTTTAATAACAAAATATTGAACCAGCCTTG | A/T | 1 | 204394931 | 0.741 |
| 1206440830 | AGCCTGAGGCTACCCAGAGCAACAGTCATACCAGAGGGTGAGCAGGTTGGAAGACTGTCTG[T/C]TCTCAGGCCAGTGCCAGCTGGGTTCAGAAGACTCTGAGGGAGGTTGGCCCTCTCTGCTGAA | T/C | 1 | 206440830 | 0.872 |
| 1208614539 | ACTGAAGAGTCCTCAAAGACACACTTGGTATTGAATTGCATCTAGTTCTTACCCTAGCTGC[A/G]TGGCCTTGAAAAATCATGGCCCCTCTCTGGGCTGTACTTCAGTTCCCCCTTTACAAAATGC | A/G | 1 | 208614539 | 0.979 |
| 1211246657 | TGAAAGGATTTACAAGCAAGAGGCTGGTGAGACTCTGCAATACCAGGCGTCTACCGTAAGA[A/G]GGAGCTGCGGGAGGCTTTTCGATTCAACAGGGACAATTAAACTTTGTTGGTTTGGAACTGC | A/G | 1 | 211246657 | 0.863 |
| 1213607625 | GGATAAGGGTAAGGGATTAATGTCAACTCTAGATAGAGAGAAGTGTGACATTTTTATGTA[A/C]CACCTCTGCCTCTTAACTGCTGAGCCACCCCTCTGTCTTTTGCTTTGGTAGATATTTTT | A/C | 1 | 213607625 | 0.865 |
| 1217741264 | TTGACACTTTTACTACATCTTTTCTAGTCATAAAGATAGACATTTAAGAAAAGTAGTTTAT[A/T]GGACCGAGGCAATGGTTCAGCCCTTAGGCCTGCTTGCTGCTCTTACAGGGAACCAGAGTTT | A/T | 1 | 217741264 | 0.703 |
| 1219832931 | TTTCAAACTGGCCTTGAACTCTGTGGTTTATATAATTGTCCACCTGCTTCAGTGTCCCTAG[T/C]AACTAGGATCACAGGTCTGGACCACCAACTCTTGCTGATACTGTTTAAATTGTGCTTGCAT | T/C | 1 | 219832931 | 0.861 |
| 1234713288 | TCTTTAGCCTGTGGCAAAGTAGCCCATGGTAGTTGGTGCTTGTAATTAGGCAGAACCTCAT[T/C]TTCTCAGCCAGGAAGCAAAGGGGAATGAAGAAAGGACTCCTTCAAGACCCTATTCCCAATA | T/C | 1 | 234713288 | 0.976 |
| 1236768740 | GGAATTTGGAAAGTTCCCCAACTAGGACCACACGTGACCTCCTCCTGAAAGTAGTTCCGAC[T/C]GCGGCTCATGTATCCTTCCACCTAGCCTTTGAGCCCTCCCAGGCCTGCTCGCCCCGCCCAC | T/C | 1 | 236768740 | 0.891 |
| 1238809544 | TTTTCTTGTTTGCTCCTTAAATACTTTTTAAAAAAAGTCTTTGTTTGAATTTTCAGCTTCA[A/G]TACTTTTTGTCCCTGACGATCTTTGGACCAAGGCATTCAACCACCAACTCCAAATGTAGGC | A/G | 1 | 238809544 | 0.937 |
| 1241096569 | ACAGACTCAGAAAAAGCATCCCATTTTCTGTCATATATGGGACCTAAGTTTATGCTTGCAC[A/G]TCACAAAACTAGAAAGCGGATGAGAAGAGGGGAAGAAGAGATCTTAAGAAAGATGATGGCA | A/G | 1 | 241096569 | 0.909 |
| 1245376209 | ACGTATTTACAAATCAAGCATCCTTTTTCAGTATTGCAAAAGACTTCCCTCCTGCCAATCA[T/C]ACAGCAATGGTCTTAGTCCAGTTTCAGATTTTATTAGCATGGGTTTTTTTTTCTCTTCAAG | T/C | 1 | 245376209 | 0.704 |
| 1247601695 | ATTTGCAAGCAAAGAAGTGTGGATAAATGGGTATACTGTGGTGCACAGTGTGACACATTAC[A/G]GGACGAGATGTTCATTTCTCTGTTGGGGTTGAGGCTGCAATGGTGAAAGTGGGTAGGAGGG | A/G | 1 | 247601695 | 0.862 |
| 1249679196 | GTCCTCTCTTGTCTTCTTACTGTCCTGAGCCTACTGAGGATTTCTGCTGACCTTTCAAGGC[T/C]CTGACTGGTTTTTCTTCCTCCAGAAAGCCTTCCCTAACTCCCTAAACCCACAGCGTATGAG | T/C | 1 | 249679196 | 0.891 |
| 1254170679 | TTATTAGCTTAGCAGTTCTTAACAGCATCCCATGCAGACATAAGTAATCAAATGGGCTGGG[T/C]TCACTAAGTCAGCTTATCAGTCCATCAGACTAAACTCCAAACACTAGGAACATAGATCATC | T/C | 1 | 254170679 | 0.96 |
| 1256243539 | CGTTATTCTTGCTGAGCACGGCATCTTCATGAAGAGAAGAGATGTGTGCTTCTGGCCTCT[A/G]AATGCTTGGTATGTGCCAAATCTACGCTGGGTGTAGTACCTGCAGCATCCTCAACCCTT | A/G | 1 | 256243539 | 0.865 |
| 2000011883 | AACAAAAGGGTTCAGACTGTTTCTGAGCTCCTCTTCCAAGAGATCATCCCCAATTTTCAT[A/C]CCGTCAGTGAGACAATGGTCCCGAATTTACTTCCCAAATTTCTGAAATTCTGTCTAAGG | A/C | 2 | 11883 | 0.55 |
| 2002466457 | TAGGAAGAGGGTCTAATGGACCACACCCATAGTGACACAACTAAACCAACAACGCCACACC[A/T]GTTTCAACACGACCACACTTTCTAATAGTGCCACTTCCTTAGCCAAGCATATTCAAACCAT | A/T | 2 | 2466457 | 0.525 |
| 2005314110 | GGTTTAAACTGGTGTTAAACTCCTCCTGTTGAGGTGTCAATGTTAGCTCAGGCAGAAAAT[A/G]TTATCAAAGTTCTGAACTCCATTCTTCCCTCTAGGTAGCCCCACAGTGTGTTCTTATGT | A/G | 2 | 5314110 | 0.944 |
| 2007385642 | GTTGCTTCTAAGGCTGCTGTGGAGTCAGTACAGTAAGGCAGGATGCTACTCAAACCCAGA[A/G]GCTAGGAGCCAAGGTTCAGGACACAGAGAAGTGCCCAGAGTAGGTTGGCGCTAGGAGCA | A/G | 2 | 7385642 | 0.894 |
| 2009622034 | CAGCTGAGGATGATGGTAAACTCCTACTCCTGTGGCTCTATCACCTGAGTGCTAGGATCA[A/G]ATGCAAATATTACCACCTCGGTTTACATGGTGCTAGGGTTTGTATCCAGGGCTTTGTGA | A/G | 2 | 9622034 | 0.927 |
| 2011645767 | TTCCCTAAAGCTTGAGACATAGCTTCCTGAGGTTGGTGCTAGGAACCAAATTTCATCACTG[A/C]TCTTAACTATGGAACCATTTCTCTAGCCCCAAATTTCTTTTATGTCCACCACATTATTTTA | A/C | 2 | 11645767 | 0.596 |
| 2016098166 | TGATTTGAGCATGCATTCACCACTCTGTGTTCTTCAATATCCAACTACAGAGTCTCAGTT[T/C]TACTGGGAGGTTAGTCCTGCTGACCATCTTTCTCTGTCCTTCAAGTCTGAAACTAGCAG | T/C | 2 | 16098166 | 0.944 |
| 2018274737 | GCATATACCCACATCAAACACACAAGTGATTAATTGAAAAATAAAAATGAATGTCAAAAGC[A/C]ATAAAGTATTGTTGTTTATTCACCTTGAGACATGAAGCTTTGGCCTTTTGATGATTTGTTT | A/C | 2 | 18274737 | 0.698 |
| 2020856498 | ACTCTTGCCCACCTAGAAATGAACAGCTCTGAGACTTGTCTAAATGCTTTAAATTTGATTC[T/C]ATAATTTTGTGTCTAGACAGACGTCAGGAAAGTTCTAGAAGATGGTAGCCAACTTCCCTGG | T/C | 2 | 20856498 | 0.821 |
| 2022884169 | CTTTGGGGCCCCGCTCTCTGGGGAAGAAGAGGAGGGGGGTGTAGGGTGTCGGAGTAGGGG[A/C]TCTACTGATAGGAACATGAAGAGTAAATTGGTCTACGTGAGTGGGCAGGAGGGACTCCA | A/C | 2 | 22884169 | 0.94 |
| 2027169154 | AACAACTGTTGGGAATCTGTTCTCTCCTTCTATCATGAGTACTCTGAGGATCAGACTCTGA[T/C]CATGAGGATTCATGGCCAGCATCTTGACTGGCTGAGCTATATCTTGCTGGACCATAAGCAT | T/C | 2 | 27169154 | 0.977 |
| 2031259633 | ACCTGTCATCTGAGTCTGAGGATCCTCCTAACCTTGCCTTGATCGTTTGGCAAAGCATTC[C/G]TGTGGTCTTAACTCTGCTGTTTACTCTGGCCACTGGTTCCACATCCCAAGACATCCCTG | C/G | 2 | 31259633 | 0.894 |
| 2033357629 | GGTCTGGGCGCCACTTACTGTCCTATCATTCTTAATAACAGCCGTGCTTTCGAATGGGAC[A/C]ATGTTTCTCCTGCCACAGATCAAAAGGACTGTGTCCCATCATCCTATCTGAGAAGCCAA | A/C | 2 | 33357629 | 0.806 |
| 2035402978 | CATACATTCCAAAGGCTTGGCTTACTGTGACCAACACATGACAACTGATGCTTGCCCAAGA[T/G]GGAGGCAGCCTCTGGAGAAGTATCTGGTGCCTAATTCTTCAGGGAAAAGTTTCCTTTGTCA | T/G | 2 | 35402978 | 0.766 |
| 2037535509 | GGCTAAGGTATGTGTTGGGATCCCATCCAACTATGCTCAGGTACTTTGCTGGCCTGGTAGT[T/C]TGTGGGCTCAGATATAAATACACAAAGTCTAGGTCGCATTATATTATATCAGTTGACCTTC | T/C | 2 | 37535509 | 0.989 |
| 2039576817 | GCATCAGTTTTTGAGTTGGCTGTTCTACTCCTTAGTTTGCTTCTCTCATTTGAGACATTGG[T/C]GCCTGTTGGCGTTTTTGAGTAAGGCCCACTTGAAGACAGCTTTACAAACGAAAGTCCTCAA | T/C | 2 | 39576817 | 0.973 |
| 2041585226 | AGCTAGCCAAGGAAGGCCCTATTACTCTGTAGTTTGCACAGTTATCCCATAGGCAGGCTT[C/G]TTTCTCTTTAAATACCAACATGTGCTTTTATAAAGAAATTGATTTCAAGATGTATCTAC | C/G | 2 | 41585226 | 0.958 |
| 2043600678 | GAGTCCTTCTCTGCCTTAATTTCTTGAAACTGCTGTAAGATTATCGCAAGCTTGGTGGCT[T/C]CCATAACCAACCAAAACTTACAGTCTAGGAACGAGAAAAATCAAGGTGTTGAGAAAGCC | T/C | 2 | 43600678 | 0.997 |

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|---|---|---|---|---|---|
| 2047930597 | AGGAAAGAAGGGAGGGTGGGAAGAAACCAGGAAACCTTTCATTCACTCCAAGACAACAACC[A/G]GAAAACCAGCATAGTTCATTATTCTTGAGGGTAGAATTGTGCACAACATTGTACAATGGAG | A/G | 2 | 47930597 | 0.956 |
| 2050000379 | GTGCATTTGATTTCTAACAGATTTTAATACTCTTGACTTTCTATTTTAAGTGCAGAACTC[A/C]AACAGAACCCTAGTGTCCAAAAGATTCACAAACCTTTCTTGTCATATGATACATTCCCC | A/C | 2 | 50000379 | 0.867 |
| 2052066591 | CAAAGATATTGGCTTCACCCAGGATCGCAGGTTTCTAGGATTCAAGGGAAGGCCAGGAAGA[T/C]GGCAACCCTGATACAACCTGCAGTGGGAAGGCAGCTCTGGCTTCATGTTTCTAGCAGTTCA | T/C | 2 | 52066591 | 0.674 |
| 2054131845 | CCCCATCACCTGCAGCAGGCAAGAGACCTGGTCCTGGGGTTATGAGAACAGGAGGACTAGT[T/C]CTGCCCCTCAGCAGCACTCAAGAGAGCAGGCACCTCACCTAGGCAGCACGGTAGAGCTGAC | T/C | 2 | 54131845 | 0.961 |
| 2056283433 | ATATGGCCTTTTGTTAAGTGGTACCCAATCCCCTTTGAAACAAGATACTCTATCAGTACA[A/G]TGTGCATTCCCAGTCAGAGCAAAGGTAGGCCACACACAAGAAGTATGTTTTGAAATGCT | A/G | 2 | 56283433 | 0.874 |
| 2060415706 | CCATATCAGTACCTGTGTTTCCATTTCAGGGCTCATTTCTCTTTTCCCTCTGCTCATATT[A/C]TACTTCTTTTCACTGTCCAGGAGAAAGTTGGTTCCTGCCATTCCTATTATATATCCTTA | A/C | 2 | 60415706 | 0.868 |
| 2066704298 | AAGCATTAGTAAATTTCTTTTCCAAATGGGGTTGATATCTTACATGTAGTTACTAGCACCA[A/G]AGTGATTTCCTGTAGAACAGGTTCTTCTGCTGGAGTTTTGGGGCTTTTGTGTATATCTATC | A/G | 2 | 66704298 | 0.72 |
| 2070774696 | ATGTATTTGAAGAAATAAAAAATGCTTGTAGTAGAATGAAACTGCATCTTTCACATCTTG[T/G]ATTTTAATGGTATTGTTTTGCCTCTCCATTCATAAGAAAATTACCATCTTTAAATTATG | T/G | 2 | 70774696 | 0.919 |
| 2074816527 | AATGATAGTGGAGAGAATAAGTGAATGGCTGACCAAAGACTGCCCCAAACTGAGAGCCAT[T/C]CCACAAGAAAAATCAATCTATGACACTATTATGATACTTTGTTATGTTTGGAGGCAGGA | T/C | 2 | 74816527 | 0.701 |
| 2076840315 | CTCAAGGGACAAGTGGTTGCCATAACTGAGAAGACTAACAGAGGGATTTTAGTCCTCTAT[A/G]AGCAAGTATTTTAGATCAGTCTGGGGAATAAAATAAGAAATAAAAGCAACAATTCTGGT | A/G | 2 | 76840315 | 0.906 |
| 2078881254 | TAAAGTAACTAAGTTAATATGTAAGCACTCTACCAACTGAACTATGTTGCCAGGCCCGGTC[A/T]TCTGGTTTTCATGCTAATGGTCTCATCTGTGAAGTGCTCTACAAACACTCCATAATGCTCA | A/T | 2 | 78881254 | 0.901 |
| 2081114629 | AGGACATTCAGCAGAATCAACCAACCTCAAACCTTGGGGCTTTCAGAGTCCAAACCACCAC[T/C]CAAAGATCATACACAAGCTGAACCTAGGCCTTCCTGAACATATATAGCAGATGTGCAACTT | T/C | 2 | 81114629 | 0.566 |
| 2087350375 | AGCTAATATGAAAGAGCTGAAAGTGATCCAGCCTGACAAATCAGTTTCTGTTGATGCTGGA[A/G]GATCAGTCACTCTGAATTGCACGGTGACATCTCTCATCCCTGTGGGGCCCATTAGGTGGTT | A/G | 2 | 87350375 | 0.744 |
| 2089384684 | CTATGTTCTTCACACATATATAACATGTAGGCAAATGTTTGCTTGCAAACACATGTGCATA[C/G]CACTCCACACATAGACACAGATAGACAATATACATAATCCACATATATTTAAAAATATAAA | C/G | 2 | 89384684 | 0.993 |
| 2091485272 | CCCATTCAACAATTCCGTCTACGAGCATCCAAGTGAGTATGGCCTGCCTTGCTGATGGAA[A/G]CACAGTGAGCAGTGAGTCCGCATGGCAATGAGATGGAAGAGGTAAAGAGAAGGCAACTC | A/G | 2 | 91485272 | 0.585 |
| 2095616472 | AACAATGGGTTTCAATATGACATTTTCATATACATACATGTTCTACTTTGATCATCCATG[A/T]TCAGCCTCCATTACTCTTTCTCAAGGCTTTAAGTATTGAGTGTCACAATGTGAAGCATA | A/T | 2 | 95616472 | 0.949 |
| 2097793508 | GTGTTGACTATCACTTACATTATTATTTGATTCCATAAAAATTCCCGTTTGAAGTCTGGCT[T/G]GAAGATGAATCCATTTTAAGATACGAAAAATATGCTGTCTCTCCGGAAGCATCTACTTCTT | T/G | 2 | 97793508 | 0.614 |
| 2102112098 | TAAGTTCTTCATCTTCACTTAAGACAAGACTGCCATCGAGAAATTGAAACATCCATCAAA[T/C]TATTCAACAATTCAGATTGAAAAGGGCCTTTAAAAATTATTCTAAGCTGCACATCCTAA | T/C | 2 | 102112098 | 0.963 |
| 2104290705 | AAAAGAAAAAAGAATGAAAGAAGGAAGTAATTCAACCTGGTTTTCTTCTAGCTGTGTCTC[T/C]TTTTTAACAATTTAGGTTTTAAAAAAAAGGAATAACTGAATAACACTATTTGGGACCTT | T/C | 2 | 104290705 | 0.849 |
| 2106347084 | TATATGTATATATTATAGAAAGCTACTACTGTATTAGGTTTGCTTTTGATCCCCCAAGTG[A/G]CACTTAGTTTTAGTTGTCCCTCCTAGTATTCCCTCCATGTCCCTTCCTCTCTCCCTGCA | A/G | 2 | 106347084 | 0.733 |
| 2108423278 | CCACTTTGGCTAATTTACAAAGTTTTAAGAGGTTGATTTTGACTATATTTTTCTTTTGTT[T/C]GTTATGTGTAACTGCCTTTCTGAAAAGACTTATTTGGGGGGATTCTTATTCCATCATTC | T/C | 2 | 108423278 | 0.779 |
| 2110513518 | AAAGAGACCAGAAATTGATGGGTGGTGGGAAATTTAAGAATCAGAATCGTTCTGGAAAAC[A/T]CCTCAGGATTCTTTCTACCTAAGGAGTAGGTAGGAGACCCACCACTGTTTTTGGCCTGA | A/T | 2 | 110513518 | 0.876 |
| 2112598040 | GCCAGCTGGTGTTCATGGGCCATTCTGCCACCAGGGAAAATATTTAAATGAGTGGCTTCTG[T/C]TGCCACCTGAGGTCCAGGCTGCCCCTGAGAGCATTGTCTGGGTCCATGGTCTTACAGTAGC | T/C | 2 | 112598040 | 0.926 |
| 2114705253 | GCCACGGAGGCATGTGTGCCACTACTGCACCTGAGGAGTTACTGCCTCATCCTCACTGCC[A/G]TGACTCACAGCTGTCTTAGTTGGGTTGATTGTTGCTTGCTTCTCTTAGAAGCTTACATG | A/G | 2 | 114705253 | 0.799 |
| 2116734555 | AAAGGACACCGCTTTAATGTCCTGTAACATTTGATACAGAAATAACTAAATTCCTGTGCA[T/C]ATTAATAACCATGTCAGCTTTAATTTTACTTGTATTTATTTCTATTTATTTGAGACAGG | T/C | 2 | 116734555 | 0.779 |
| 2120976129 | GAGGGACCATTCGTTTTATGACCCCATCTGCTTGTCTATAGCGAGTCAAGTGGACACGGA[T/C]GTATAAAGATTTCGGCGCTTTGAACCACTTTTGCTTCTCTAGGCCCAGGTTCGGCAGGG | T/C | 2 | 120976129 | 0.903 |
| 2123134658 | GATTCCCCAGCGCATACAGACGGCTAAGCATGGATTGCTGGAAAGTCTTGATCCACACATG[T/C]CCTGCACTGGATGCACCCTGGCTGCTAGCCAAACACACGGCAAGCAGGGTGGACTCTGAGG | T/C | 2 | 123134658 | 0.917 |
| 2125287256 | AAAAAAAAAAAAAAAAAAAAAAAAAAAAACCAGAGAGCCTGAGATCGTTTCACATTTGAACT[A/G]GAGACACAACTAACCTGACCAGCTTGCATCTGGCCACCATAACACAGTGTGGGAAGCATCT | A/G | 2 | 125287256 | 0.902 |
| 2128187827 | ATGGGAGGTGCTTTCTTCTCCCCAGCTACTTGTCTTGAGAGTCTCAACTTCCCCCTCCATT[A/T]CTTCATTCAGAGTCAGTGTCAGCCATAGGTGCCAACAAGAACATATGGTCTGTGACATGAG | A/T | 2 | 128187827 | 0.93 |
| 2131121098 | TAAGGCAAACTTGTTTGTCTTTGATAAGAAGTCTGGCCACCTTAACTAGTTAACAAATTGA[C/G]CAATGAACTGATACTGCGGTAGATTACATTGCAGTAAGGACCTAGAGGTCTGTTTTTGAGC | C/G | 2 | 131121098 | 0.861 |
| 2133968266 | CATCCAGAAGGCTAAATGTCCTCAAAGGAACACAAGCAAAAACTGCCAGGGCTATGTGACA[A/C]CTTCAGAACACAGCCACCCTCCTGTAGCAAGCACACCTAACAGTGTCAAAGCACAAGAAAA | A/C | 2 | 133968266 | 0.778 |
| 2144715765 | CCGAGTCATCTCCCCAGCCCCGACATTGCCATTTTTGTGAGCATCTACATCCTATTGTAT[A/G]AACACCCTCATTGTTTGATCAGCACATTTCCACTTGCCATTCCTTCATTGCTTCTAATG | A/G | 2 | 144715765 | 0.978 |
| 2146756377 | GATGTCCCTCTTTTTAATACATGATTTAAAAAAAAAAAAACCATAAGCCACAACTTACAC[T/C]GTGGCTGTCAATCTGCTGCCCTCTAGAGCTCACTGGACATTCCCGGGTACATTCTCACC | T/C | 2 | 146756377 | 0.964 |
| 2157090038 | CATTGTTTATGTCCTCCTAATAGAAATCCTATTTTATAAATGCATTGGCTCATTTTTTAA[T/C]GTTTCTTGACTGCCATTTGCAAGTATCTATTATATATTGGGAGATTTTCAGGGTGCCTA | T/C | 2 | 157090038 | 0.828 |
| 2159122474 | GTGTTAGAAGTTCATAAATGATACAAAATTCCAAGAATCTCTGTGCAGAAAGGAATAGTAA[T/G]ACCTCACCTATAGACTATGCTAGAAGTACATTAGGTTGAGAAAAATTAAAGATAGTAGGAT | T/G | 2 | 159122474 | 0.793 |
| 2161342675 | CCTTGTAAAGAATGAGAGGATTGAATGGTAGGCCAGTTTTTTGACCACCAATGGGAGAAGA[T/C]AATACTTTTATCTGCTCCTGTATCTAGAATGCCTGTGAATTGCTTTCCATCAATTAGCAAC | T/C | 2 | 161342675 | 0.765 |
| 2163515761 | AATGAGACATGGGTTTAGACAGGTTGGATAGAGACATTAATTTCCACAGGCTGTTTGGAAA[A/T]GACAATACAGAAATCCCGTTTTCAACTATAACTCAAGTACTCCTTGTCTATCTTCATATCT | A/T | 2 | 163515761 | 0.944 |
| 2169717338 | AGGGCAAAGAATACACAAGCTCATACAGTGCTCCTATTTAGTTTTTCACACCAAGCCCTG[A/C]AAGTCCTTTGTCAAGATCATGTAGAAAAGAAGACCTTTAAAAAATGAGAGGAGAGATAA | A/C | 2 | 169717338 | 0.976 |
| 2171951621 | TCCCTGTCTCTTAAGGAACACATTTTACAAAGTCTTGACACCAGCTTTGAAAGCATCTTC[A/G]CCTGGGCCTGAGCCCTGGGAATTCTCACCTGACAGAATTTCCTTACCTCTAATTTGTGA | A/G | 2 | 171951621 | 0.813 |
| 2173966193 | TGTGTTGTCTGTAGACAAGTTCTAAAAGAATATGACCTTTAGTTGCCAGCGAAAGCAACGA[A/G]AAAGGAAAAAAGCTACAGCTGTGGTAAACGTTACTCAGGGCCAAGCTTCTGATCTTCAGGG | A/G | 2 | 173966193 | 0.932 |
| 2180060571 | GTAGATGGGGATTCCTGGTCCTCAGGGGAAGACTAGAAACTGCCCCTCTGGCTCTGAGGA[T/C]GTACTGGTGGGGATGTCCCTCCCTGCTCTGGGTGACCACTCTTAGCTTTGATAACTTGA | T/C | 2 | 180060571 | 0.682 |
| 2182080587 | GACAATGGACACCCATCCTCTCTCTACTTCTGCTCTGCTTCTCTCCTGAAGTCCTGAGAT[T/C]GAAGAAAATAAAACCTCAAGTCAGCAGTGCCTAGGATTACTATTCACATTTAAAAACTG | T/C | 2 | 182080587 | 0.944 |
| 2184309455 | CCTTGTTTGGTGATCATCAGAGAAGGAATACAAGAAAGAAGAAACAGGTCAAAGAGGAAGA[A/G]AAGCCATTATGGGATAGATAAGACATTACAATATTGTTATGAGGCCGAGACCAATTAGAAT | A/G | 2 | 184309455 | 0.652 |
| 2186441049 | CTTACAGACTGCTTCCTACACAGGATAGAGGTAGTCAAGATGTATTAACCTGAGAGGATC[A/G]GTTAGCAAATGGTAGCAGAAGGAACTTGGGGGGAAATTCAGAAACCAAGAATGGGAGTC | A/G | 2 | 186441049 | 0.908 |
| 2192611280 | AGTTCTTACTGGTATACAAATTTTACATGTAGCGTATGTATGCCTCAAAAATCCCACTTC[A/G]TTGCAATCTCAACTTCATTCATTACCAGACTGTAATTCTGGACCCCTGTTGACTGAGGA | A/G | 2 | 192611280 | 0.95 |
| 2196682421 | ACAGGTGGTTAGGAGCCTGGGAAGCAAGCGGACTGCTGGGCCGGAAGTGGGCAAAGGTGCT[T/G]ACTGGCTTCAGAAGCGCAGCTTGGTGCCATGGAAGCACGACAGGGAGCATGCAAACAGAGG | T/G | 2 | 196682421 | 0.638 |
| 2198706857 | AAAGAACAGTAGCAAGTAAAGTTAAGAAGGTTGGAAAGGATTTCTTAGGAAAACTGATAA[T/C]TGATAACTTCAGCCCACAGGAGGGGATGCTCTGTGAGTCTGATGGTGGCTTTGGTCTTG | T/C | 2 | 198706857 | 0.984 |
| 2205116571 | GTCAAATCATGATAACAGGTTAAGAAGCTGGCTGATCACATTTTTATCTAGACACAGGAA[T/G]CAAAGATTGAGAACAGGAAGTAAGGTGAGGGTGAGTAACATTAAAGACTGTCCCCAGTG | T/G | 2 | 205116571 | 0.709 |

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|---|---|---|---|---|---|
| 2209434768 | CCATGACTCCAGTAGAATCGCCCTGCTCTACCAGTGGACATGCTGGTATCGAGAGCCACC[A/G]GGCAGGTCCTAGGGCAGACCACAAATTTCCTCAGAGTCCCTTCAACCTGCCCCAACAGT | A/G | 2 | 209434768 | 0.641 |
| 2211589987 | GATAACTGTCCCAGGTACTCTCAGAGGCATGTCTCTTAGTTGATCCTGGATCTAATCAAGA[T/C]GACAACCATGATTAACCATCACATTGTGTATGACAGGGAATTTGAAGAAAAAATCTTCTAA | T/C | 2 | 211589987 | 0.84 |
| 2220105538 | AAAAGCACATAAATCCTGTAGTCTCTAAAATATTTTATGTTCTTTTCCTAATTAACTTAA[A/G]AATCCACCTGAGAAAGAATTCAGAACGAAACATAAACACCAACTTACTACTCTCCCAAG | A/G | 2 | 220105538 | 0.774 |
| 2222168234 | GATTTTAAACATTTTATAGACTTAAAAATAATGTATTCAGTCTACACAACCTGTGTGAGTC[A/G]GATGTTAAATACTTGGTCTACCCAACACAGGATTATCCCCCAGAATTGGGAAGATTTAGTA | A/G | 2 | 222168234 | 0.898 |
| 2226297591 | GAAGAAGGAAGAGGGAGGAAAGAATGGGGGATAGAAAGGGAGAGACAGGAGAAGATGGAGG[T/C]GGGAATGGAAATACAAAAGCTAAGGGAAGTGACTGTGTCTGTTTAAAACCATGCAAGTATG | T/C | 2 | 226297591 | 0.981 |
| 2228473263 | TAAATGGGATGTCTCTTTTAAGCCCCTCCCCCAGAGCTCAAGTGACATGTGGAAGAAGAG[A/G]CGAAAGAGGTAAGAGCGGAGGTCATGGAGACTCTGAAGAAACAGTATCGTCCAGACGTG | A/G | 2 | 228473263 | 0.952 |
| 2230682421 | TCGGTCTTGCCCCGACACTGTGCTCAGGACGGATGTACTCAGGCCATGCTCAGATGCTGA[T/C]GGTGCCGAGATTGAGGGCAAAGTTCCTGTGTGTGCAGGGCATAGCGTCTGACTTCACCC | T/C | 2 | 230682421 | 0.644 |
| 2234764832 | GGAAAGTGGGGGAAGGAATAAAAAAGAAAAAGTAGGGATATAGGAATAATAGAGAAAAAA[A/G]GTAAATTATTGAATCTACATTTAGGCCAAAAAGTACTAGCCAGGAAAAATATTATATTG | A/G | 2 | 234764832 | 0.573 |
| 2240905173 | GAAGACCCGACAGAACATCCTCCGTGGGGCCTGGACTTGGGGAGTGCACACAGTCAGCAC[A/G]GTACCTTGGTCCCGGCTGCCCAGAGCCTGGCTGAGACTGTGAGTGGGCGCTGGCGCTCC | A/G | 2 | 240905173 | 0.739 |
| 2245080775 | GGATCCACTTCCGTCCTTCTTTCTTGGGTTATGACACTGGGGCTCCACTGAGGCAGTTGG[T/C]TCTAAAGGGTCTCTGGTAGGGGAAGGGAGACAAGGGGTATGACTACTATGGAGGACACA | T/C | 2 | 245080775 | 0.894 |
| 2249118552 | TGTAATACTGGAACTCTTAATGGAAACTTAATGGAAACAAAATAAAATCTAAAAACATTTG[A/G]CACATAGTTAAATATTCCAGAAAGAGACATTCATATGTAGTAAATGAATAAATTTAAGGAA | A/G | 2 | 249118552 | 0.65 |
| 2251155448 | GAATTCTCAGAGTAATCAAATTGTTTTCCAGGAAAACATCAGAAGCAGCAAAATATAAAAA[T/C]ACCGAGAGCAAGAATATTTTAAATGCCCCCAAGGAAGCAGCTAGAAAACCCGATGTGTGGT | T/C | 2 | 251155448 | 0.913 |
| 2255556330 | GAAGGAAGCCAGGTCAGTAGTCAACAGGGAAGCCTCACCTAGGCTTGCTGCAGTTAAATG[A/G]ACCATCTCTCTCAGTTTAGCAAAGCTCATTGTACTTGTCCTTGCAGAATCTCATGCTCC | A/G | 2 | 255556330 | 0.955 |
| 2257673789 | CCCATAGGCTGCAGTTTCTGGTTTCAGAGGAACTCAAACAGGCAGGTCAACTACTGAAGC[A/T]AAGTAATTTAGACTTAAAACAGGTAAACTTTTATTATGAAACAACAACTCTAAATATAT | A/T | 2 | 257673789 | 0.623 |
| 3000090664 | CTATTAGTAATAATAAAAGATTCTTCTATGAATAATTTAGACAGTTACATGTTGTCTCTGC[T/G]CATAGCTCCACATGTACTGTGGGGTCAGACTTCGAGAGATTCATTATGTGGGAGTGACGTT | T/G | 3 | 90664 | 0.595 |
| 3004079793 | CCTGTGTCCACATCCCTGACAGTGATCCCCACAAGAGACCCCACAGCTATGACCGTGGGGC[A/C]CATCAGAGTTCATAGACCTCACCACAGGACCCACAAGGGGCTACATGTCGATGACTAAGGG | A/C | 3 | 4079793 | 0.82 |
| 3005824425 | GGCTAGAAAGAAAGTGCTGGGATGTCCGCACAGCCTGTATGACCTAAAGCCAGGTAAAGAC[A/G]CCAGCAATGACTGCAGTGAAACTCACGTGTCCCAATCACCATCAAAGGGCAGTTCTGAAAG | A/G | 3 | 5824425 | 0.975 |
| 3009068961 | TCCGAGCCTGGACACCGACTTGCCCTGTGCTAGAAACTCGTGTTTGAGGCGGAGTGGGGGG[T/G]AGTCGCTTTCCAGTTTCTCGCTCTGAGCCTAAGCGCTCCTTATCTGAAGCGCTGCTGGCCG | T/G | 3 | 9068961 | 0.674 |
| 3016151838 | ATCACTTACTCCAATTCTTTGTTTATGCTTGTCTGAATTCTCAAGGGATTTATTAATTTC[T/C]TCATTAAAAATTCCAATCATCTGCAAAAAGCTGGTTTTATGGTCTTTTTCTTGTGTTTC | T/C | 3 | 16151838 | 0.896 |
| 3017874135 | ATTATGTCAATAAAGATGGCAAAAGTCAATTGCTAGGCGAAGAAGGTACAGAGGTCCAGG[A/T]CCCAGGAGGAAGAGGTGGAAAAGATATAGAGAAAGGGCTTTTTGGCCAGGTTTTGGAGA | A/T | 3 | 17874135 | 0.804 |
| 3019581047 | TAATATAGTAGTGGATTACCTTAGGGTATGAGCTAGGTCTGCTTGCTAGCTGTCAAGCTAC[A/G]GTTACCTTAGCTGTTAATGTAGTTAGAAATCTGGGAAGATAAATTATAGTCTAGGACTCAT | A/G | 3 | 19581047 | 0.531 |
| 3021115954 | CATCATTGCATAGACAACTGCAGATAATGCCTTCTCTTCAGGAGATATCAGTAGTCAATA[A/G]TTTGTCAGAGAGTGGTGGTCTCTATTAGCCTCTTATAAGTCCATGACTGACTACTAAAA | A/G | 3 | 21115954 | 0.871 |
| 3022640856 | GGGTGGTAGAAGTAGGGAGTGTGAGTAGGGCTGCAGAGCTCAGGTCAATCAAAGTTTGTC[A/C]CAACTATGAAGAAGGTGATGATTTACTTAACAAAATAAAGAAAAGAGAAAAGTTCTCAG | A/C | 3 | 22640856 | 0.915 |
| 3032072437 | CATTTTCTCATTTTGCTATTTATAGAGTGAAAATTATTACTGTCCGTGTAACTTCAGCGCA[T/C]TCTGTGCCAGTGCCTGTACTGGGCTCTGCTGATTTATAGCAGTTGTTTCCAGAGGGAAACT | T/C | 3 | 32072437 | 0.821 |
| 3033793044 | CTGAAGGGTTATCAGAAGACCAAAAAAAACCAGATCTAAATGTAACACAGGGCTGGCTTCA[A/G]CCTCAGTGAATTTCCAAGGATGGTCTTGAACTCCTGATCCTCTCGTTGCTGCCTCCTGAAG | A/G | 3 | 33793044 | 0.935 |
| 3035446267 | TTCAAATACTCACAGGGATGGTACTGGACGGGGAACCTCACAGTAGTTAAGAACTAATACC[A/G]TTGTCTAGCTACGTTGTGACTGAAAACACAGAGAGTGGTAAAAAGGAGACTTATTTACACA | A/G | 3 | 35446267 | 0.731 |
| 3038942593 | GAGGATGAAAATCGGGGCACGGAAATGAAGAAGCCAGGTATAATTCTCACGTGCAGACAC[A/T]GAGGATGTGGAGATGGCTCCTGGAAGGCAGTCATCTGCTTGCATTTCCCACTTCTCGGG | A/T | 3 | 38942593 | 0.986 |
| 3040597508 | GAGCTCTTAGCCATTAGCTGACATGCCTGCTGCTTGCTGTCATTCTGTCCCACCACAAAG[A/G]ACTCTTAGTCTCTGGGACCAAAGGGCAAAATAAACTATTTCTTAAGTTGTGTTGGTCAT | A/G | 3 | 40597508 | 0.965 |
| 3045763581 | AAGAAATTTATTGAGAAATGGCAAATAAATAATTATTCAGAGACCAAATGGAAGGTAGTA[T/C]TGACAACCATTAAAGCCCACATCCAACACAGAAAAACTAAGAGACAGGAGTATTGGTGG | T/C | 3 | 45763581 | 0.948 |
| 3047346760 | ACAAATGTCACGTGCACACCCCTCACTTTTCATCAAATTTAACATGAAAACAGTTAAATC[A/G]AAAGCCAAGCGGGGAACACGTGGAGTTCCTCCCTTGTTTATTTACTGTTTTCAAGTTAT | A/G | 3 | 47346760 | 0.768 |
| 3048920359 | TGGTTACAGAAGATGTGCAGTTCAGGCTCCATATGATTCATTATTAGGAGTGCTTACCAAG[A/G]TCATCCTCATAGACACCACAAAGTTTCTACTAGACTAGGTTTCCACATTGTCTGTATATGT | A/G | 3 | 48920359 | 0.911 |
| 3050437769 | AAAAGAGAAATCAAAAGTTGCTCTTTCCTTATAAAATTACAGAGGCCAAGGTCAGTGTCC[T/C]GCTTGCCCTGCTGTCCACTCTCACCGGAGGGTCCACAGAGAGCACGAGGGGCAAACAGA | T/C | 3 | 50437769 | 0.799 |
| 3051998320 | CCCCTGCCCCCCTTTACACTTTTACACATCTGTGGCCAGTTTTATTAAGCTGTAGGTTGGC[T/C]TCAGTGGCTGAGCTCTTGCCCAGTGGGTAGCTCTCTGTACTGTTAGAGCAAGGAGATCTTA | T/C | 3 | 51998320 | 0.971 |
| 3053681912 | GAACAGCTGATGGGTAGGAAGAAAATCAATACACAGACAGGGGAAATGCAGCCTTCCTCA[A/G]CAACGTGATAATTCTTTCCCTGAGAGCCCTGTGACTGCACAGTAGTGTGGATTTATGAC | A/G | 3 | 53681912 | 0.942 |
| 3055246649 | GGAGGCATTTTCTCAGCTGAGGTTTCTTCTTCCCAGACCACTCTGCCTTGTGTCGAGTTGA[T/C]ATAAAACAATCAGCACAGTGAAGCTGAACATCTTTCGCTTATCTACTGGCTCTCTGAGTAT | T/C | 3 | 55246649 | 0.708 |
| 3056914987 | CCTGGCTGCTGTCCTGGAATATGTGACCACAACCCCCACAAGAAGGTCATGACCACTAGTC[A/G]TGTAGCACGGAGTTCTCCATACCAATGTGGTATCTATACGGGCCCAGAGGGTTTAGCCAAT | A/G | 3 | 56914987 | 0.822 |
| 3058625138 | ACCAGACACAGGCAAACTAAAAACTGGCATTTTGATTGATCACTTACTGGCTTCCTATGAT[T/C]GCTAATTCTAGTAGTTTCTCCACTGTTTTAGAGAGTGGGATGGATTCTTACGCCATGGCTC | T/C | 3 | 58625138 | 0.801 |
| 3060223303 | CTTTTGGAGAACGATCCAATGATGTCTCCTAAAATCAGACAGTAGGCTCCCCTTTTCTCTT[T/C]TAAGCTAACTGTAGTTCCAATTAGGGGGCGTAATGCGGAGTTGATCATTACCAGGTAGATA | T/C | 3 | 60223303 | 0.949 |
| 3061784861 | TTTGTGGTTCTAAGTGAATATTCTGTGTGGTGGGAGAATACTGATTTAAAATTACACTTC[T/C]GTTTTTAAGAGTTCACCCCAGGGGTTGATATTAACAAGTACAACATGTGGGGAATTGGT | T/C | 3 | 61784861 | 0.862 |
| 3063309021 | TCCGCCCGTGGAATGAAAATACTAACACCTCCTCCTGGGGCTAGCATTAGGACTCAATAGA[T/G]TCATACACACAAGAAGCTTAAAACAGGGCCCACCATACAGCAAGAAAATACATTTATGTGC | T/G | 3 | 63309021 | 0.943 |
| 3064922447 | CTGGGAATTAGAGCTCTATAACTCACTCTTACCCAGTATATACTTTATTGATATATTGAA[T/C]GTTTTACAGGCACGGTGACAATCCTTTATGAAAGTGATTTTGTATTAGAGCCAGAAATA | T/C | 3 | 64922447 | 0.666 |
| 3066438824 | TTCTTCTGGTTTTTCAAACAGCTGAAACTCTCTGGCCTGGGTGAAAACCTAAAATTCCAG[A/G]CTACCCAAAATTAATTCAACTGGCTCAACCCATTGCCTGGTCAAGAAACTGCATCTCAG | A/G | 3 | 66438824 | 0.96 |
| 3067974744 | TTTGATCAAAATAGATCAGAACCCTAGGCTTTGCTTATGCTTCAATGCAGAACCTCTAAC[C/G]TCTAACCTCTAGTCCTGCTGTTAACAGGTACATAGGACTTTCTTATTTTAACATCTTCT | C/G | 3 | 67974744 | 0.904 |
| 3069585117 | CTCTGTATTTGAGCAGACCAAAGATAACAAAGGAAGACTGTCACAGTAGAAATGACTGAT[A/G]ACATTGGAGCCACAGAAAGACAAAGTGAAAATCTTAGTTGTGATTAGAAGAGCAACAAG | A/G | 3 | 69585117 | 0.752 |
| 3071302240 | GGACATTGCGATTGTATAGAGCAAGGGATTGCAGATAGCAACATAGCGACCATAGGCCAT[T/C]ACAGCTAGCATGAGGCATTCAACATCTCCAAAGGCTGCAAAAAAATACATTTGAACAGC | T/C | 3 | 71302240 | 0.55 |
| 3073091270 | ATCATATTATTAATTGGATGTACCCAAATTATGCAAAGGTGCTTCACCAATGTTTCTAAG[A/T]CTTTATGTTTAATTTCATACATCTTCAAAAGCATCTTCATCATCTCTACCTCTTCAGAC | A/T | 3 | 73091270 | 0.847 |
| 3074637142 | AGTTCTATGGAAAATCATAATTTATTTCCTACATTATTTTCATCTTAAAAATAAAAATCAG[T/C]GCCCATTTAAAAAAAGAAAATTAATCGCACGTGAGTAAGGGAAGAAGAGACGACTGTTGGA | T/C | 3 | 74637142 | 0.666 |
| 3079526168 | GTTTGTTTTTGTAGGTACATAGCCTAAGCTATTTGACACTATTGGCACAGGTGCAAGAAGC[C/G]ACAGTAAAAATGGAGAAAAGTATGTTGACTTCTGAGTTTCTATAAAAAGAAAATGCTTCAA | C/G | 3 | 79526168 | 0.97 |

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|---|---|---|---|---|---|
| 3081263952 | GTTTTTGAATCACCTGAAATTAACAAAAAATTTCTCCTCTAGTATCTCATTAATTCAAGT[A/C]TTCTTATAAGATGTTGGGAAGAATGGGCATGATAACTTCAGTAAAAATCCAGCAAAGCC | A/C | 3 | 81263952 | 0.83 |
| 3082915876 | ATATGATGGTAGATAAAATATTCTGTAAATATGTATGCATATAATGGTTCTGGTAGAACTG[A/G]CGTGAGTCAGTTTGGAATTGAATCAGTTCATCCATCAGTTGGGAGTCAGTGAAATTAGCAC | A/G | 3 | 82915876 | 0.966 |
| 3084726779 | ATCATATTTGTTTTACTTACTAGTTTTGAAAGTTGAAAACTTGACATACAAGAATACGTG[A/G]AGATATGGAGACAGTTTGAAACTTGTTGAGATTTTAAATGATCCATTTGCACAAAATTG | A/G | 3 | 84726779 | 0.817 |
| 3086289128 | CATCCTTGCCAACATGTTCTGTCACTTGAGTTTTTGATCTTAGTCATTCAGTCATTCATTT[C/G]TATATGACTAAATGATCATGATCAACAAATTATATAGAAAAGTATGTCTGTGGTTTATGTA | C/G | 3 | 86289128 | 0.748 |
| 3087797914 | ACTCTTATTCTAAGAGCACAGTCTAGGTACAGGAGGTATTCCTGGCTTTTGGTTTGTCATT[A/G]TTAATTAGTGATTATTTAAAGTTATTTAACAGGGCCTGGGGATTTAGCTCAGTGGTAGAGC | A/G | 3 | 87797914 | 0.689 |
| 3089363019 | CGCTATAATGGACAAGGGGATGGTAGCGTGGAAGGGTGAGATAGGAAGTGTACCAGACCAC[A/G]TGAGACAGAAGCATTTCTGAATGAGAGTGTCCTGGCACCCGGTGAGTGTCTCTGCCTGGCA | A/G | 3 | 89363019 | 0.929 |
| 3090974446 | GCTAAGATATACTACCAATGAGTCATGGTTTTGTCCCATTTTTCAGTTTTTAAAGATTCTC[A/G]ACCAGCAAATGTCACATAATGGGGAGTTTCTGGGTTGATTTCCAATCTCTTTCTTGTTCTC | A/G | 3 | 90974446 | 0.953 |
| 3092549463 | ATCTGGGAAAATCTGAAACCTCCCTCTGGTCCTCAGCTTCTCTGCTGATTCTAAGGAAACA[C/G]TTCCCAGGATGATTTCCCCTCAGTGATGCTGGTCTCTTCTTAGCCACGGCTAATTTCTCAA | C/G | 3 | 92549463 | 0.786 |
| 3094071447 | GTTCACTTTGCCTCTTGTTTACTCTTTTGAAAATGGCAAATAAGAAAGCTCCATGTGGATT[T/C]TGGAGGCAGACAAACTTCTTCCAAGTGCAATCAAGAATCTCTATCCTCTCTTCAGTCAAAT | T/C | 3 | 94071447 | 0.689 |
| 3105451747 | ACTGTGTGTCGAAAACTTTACCCATTTTAGGATTAGGGTCAATGGTTTTCAGCTGGGGTCC[T/C]CTTAGGGGATTTGGAAATAATCAAAGGGGTAAATTTCAAAGAAAGCTACACAATTTTTATA | T/C | 3 | 105451747 | 0.955 |
| 3112264059 | TGATTCTGTTAGATATTTTGTCACAGCTATGCACTGAATAAATAATATAGTATATATCAG[T/C]GATGTTTTGATGTCCTAAAGCCCAATAACCCAGAATATGACTGTGGTTAGATTTGGCTA | T/C | 3 | 112264059 | 0.648 |
| 3115483838 | ACATGTACCACAGGGCTCATATCAGGGTCATGTAGCATCAGAGGACAGCTTGGAGCAGTC[A/G]ATTCTCTTCTTGCACTGTGTAGGCCCTGGGCACGGCGCTACAATGCTCACACTTGGTGC | A/G | 3 | 115483838 | 0.864 |
| 3117024540 | TGGGGATTGAACTGAGTCTTCTGTGTGCACGGTAAGTGCTAAGCTATGCCCTGATCCCCA[A/T]GGTCATAGGCTTTGTTTTTTACCACTGCTTAGATGAAGCCTGTCTTCATTTGGGGGTTC | A/T | 3 | 117024540 | 0.98 |
| 3118842691 | AGGGACTTCAAACTCTGGTATTGGTCTGCTCTTAGAAATAATCATGGGACAGGGTCTTAT[T/C]GGAGCCCTTGGCATCTCTAGGACTCCTCATTGGCCAAAAGACTAAAGAATGGACCTCGG | T/C | 3 | 118842691 | 0.956 |
| 3120434693 | CATTTCCTTGCATTTGCATCCACTAGTGACTGGTTCCTTAGTCACTTTGCTGCTTCCTTC[C/G]ATTCAAGATTCAAGAAATGCCTTCCATTTGCTCTTCGATGGATTTTCGATTTGGAGGCT | C/G | 3 | 120434693 | 0.918 |
| 3123525182 | GTATTTGATGCTCTCAAAATGTACATATTTGGGTTCTTCTATCTCAAATTATTTAAAATGC[A/G]TAATTCACATTTTTTTGTAATCATTCTATGCAATTTTGTGGCATGACGTTTCTTCCACTTG | A/G | 3 | 123525182 | 0.595 |
| 3126820406 | GAAATATTTAATCAACATCAGAGAATGGATCTCAGCAAAGAAGTCACCTGCCTGAGGACAC[A/T]TTTTCCAGCGCAGTTCTTCTGCTCCATATTCTGCTTTATGATAGCCTGGGAAGCACACAGC | A/T | 3 | 126820406 | 0.741 |
| 3128386941 | AATATTTAGTGGGAAGACATGAAAAACATTTCACCCTGGATAAGGCACCAACAACAGACCA[T/C]CCCAGTGTCCAGCTTGATGAGCCAATGAATTACTGGGCTTACTTAAAGGATAGTGGGTGAC | T/C | 3 | 128386941 | 0.86 |
| 3133286498 | CTGTAGAGATGTCTGTAGGACCAAACAGGGTCTGAATGACGTGGGGGCGTTCAGAGTTGG[A/C]CATACAAGAATATGTGCAAAGTGGATCACATACTTCTGAACAGCGTGTTGTTTTGTCTG | A/C | 3 | 133286498 | 0.952 |
| 3136767098 | CCTCCTTGGAGCTGGTCAGCGGTGTTTAGTTCTTTGGTGGCTTCCTCTCTCTCACTGGCG[A/T]GAGTGGATATCTTACGTTAAATTTTAAGTTCTTCTTAAGAGTTACATTTCCCCCCATTG | A/T | 3 | 136767098 | 0.905 |
| 3142347974 | AGGGGCCACCTCCTACCCCTCAGACCTCAGAGGAAGGACTCCTTCCTGATGGCATCCTTCG[A/C]ACACTGCTTAAGGTTACCCTGCTGACCTCATCTCCCTGCAAGAGTCGGAGCAGGATCCATC | A/C | 3 | 142347974 | 0.897 |
| 3143920365 | CGTGGCAGTAGCCTGCTCTGTGAACTAATCTGACCACCCCTGACAAACAGATGTAGGAGAC[T/C]GGAGGGCACTCGCCCTTGCTGCTTGGCTGTGTGACCCTAGGCAGAAGAATTGACATCTCTG | T/C | 3 | 143920365 | 0.896 |
| 3147613796 | GGGTTCAATGCAGTCTTTTCTCCATTCTGAATTCAACGAGCCTCTATTCACCCATGGAAAC[A/G]CACAACACGGGACCCCCTTCTCTAACGCTGCTTCCTATACAACAAACACATTAACTGCTCC | A/G | 3 | 147613796 | 0.852 |
| 3149186732 | AGTTAATCAGCAGAACTTACCATTTTCTTTGTTGTGTTTTGCTTTATTTTTGTTTTAAAAT[T/G]GAAAGAAACTTCATTTTGGGGAAATGCTTTAAAAGTACCTGTCTTATTTCAGTTAGAAGAG | T/G | 3 | 149186732 | 0.689 |
| 3156964356 | CATCCCCACCAGCTCTGTTCCGGCCCCGGTGCCCACCCTCAGCTCCTTCGGTGCCTCACTC[A/G]GCTCTGCACACCCATCTGTCCGGTCCACCTGCTAGCACATCCGGCCCCTCCTCTGGCCCTT | A/G | 3 | 156964356 | 0.809 |
| 3161912878 | TGCACCGGGCTTTTACATTTTTTTCTAGTTCGTATGTAGAAGTGTTTGCCTGCATGAATGT[A/T]TGTGCACTTGTGTGTGTCATGTCCACAAAGGTCAGAAGAGGGCACTACATCCTTGGAACCA | A/T | 3 | 161912878 | 0.715 |
| 3163501339 | AAGCTGCCTTCGAACGTGAAGCCCTCCTGTCTCCGATATGGGGTTACAGATATGAACTACC[A/G]GAGCAAGTACCTATACTCCCTGGGCCATCTGAGCTGCCCAGGTCTTTTAAAAAAAATTTCA | A/G | 3 | 163501339 | 0.85 |
| 3165014088 | CCTCTGACCACCTCCCAATGCCTGTTACTCCCTGTAGCTGGCTGATGACCGCATGGCGCT[C/G]GTGTCAGGCATCAGCCTAGATCCAGAAGCAGCAATTGGCGTGACAAAGCGGTCCCCTCC | C/G | 3 | 165014088 | 0.776 |
| 3168152874 | TCTGTTAAGATGCCGTTCTCTAATATTGATTCTCTGTGCACAGAGGTCACAGGTGACAACA[A/G]CTGTATTGTGAGGCTTTTTAAAAAAGATTGTGATTATATTTTATTTATAACTGTGTTGGGA | A/G | 3 | 168152874 | 0.891 |
| 4001510132 | TGGCATATCTTCTGAGGTCTTCCTCAAATGTCATTCTCAAGGGCATACCTTTGCCTGGTTT[A/G]AAGTTGGTACTTCCTCAAGGCTTTGGCTATCACTGTTTCAAGACTAATGAGTCAAGGCAAC | A/G | 4 | 1510132 | 0.849 |
| 4003183259 | CGTGAACGGCTTCCGGGGTCTGCCTCCTCTTCACAGGCTGCCATCTGCACTACTTCTGAG[T/C]GTTGGTGGTTCTGGAGAGCCGATGTAGACTCACTTCCGTCCTAGAACTCTGAGCTGACC | T/C | 4 | 3183259 | 0.889 |
| 4004770797 | ATCCCACGGGTGGCAGGAGAAAGGTGCCATTCAGGGCACCTCAACCACCAACAAAAGCCCT[A/G]GAAACCAAGGGCTTAATGAATCCAACCAACCAAGGAGGGCAGTGGTGGCTGTTCTGTGAAG | A/G | 4 | 4770797 | 0.94 |
| 4007954708 | TCTGTCCTAAAGGTTGTAAGTAAGCCTTATTGCCTAGTCACTATTAATGGTGTGTGCAGC[A/G]TGATCTTGGGTATGTAAGGTCATATTGCCTATTACCTTTTCCTCGGTATTCTCAGGCTC | A/G | 4 | 7954708 | 0.911 |
| 4011087981 | AGGCAGGGTGGTACTTGTAAAGTAGAGACATGTGATTTGTAATTAGGGCATTTGGGTACA[T/G]TGTGCTCAGGGCAGCTCAACGGAACACGTGTTCCACTCATGCAGGGCCCTGTTGCATGA | T/G | 4 | 11087981 | 0.558 |
| 4014153602 | ATATTTATAAATATTTTATATGAATACTAATAGCTGTTATGAGTATTCTACCCTCATGGCC[A/C]AAACTTACCCTAATGATTGTCAACTAGTGCTACCATCATCTTATGCATCATACATTTTTAA | A/C | 4 | 14153602 | 0.91 |
| 4015706671 | TCACGCACTCCGCGCACAGCATGCTGGAGACTTGAGTGTAGATTATCTAAAATCTCAGGC[T/C]GGTCCCTGTTGGGAAGAAAGGCAGCAGAGGGCAGAGAGCTCCATGCTCTGCTGCCTCCT | T/C | 4 | 15706671 | 0.904 |
| 4017323924 | ACCTAGCTGTATACTAAGAGCATATCTAAAGTCAACGCAGAGGGTTTAGAGAGTGTGCTAC[A/G]ATGGATAAACACCTCAACAACAAACAGTCTTTTTGGTAAACACACCATTTTGGGGGTTCAC | A/G | 4 | 17323924 | 0.908 |
| 4018914851 | CAAATAAATTATTAGTATAAAGGCCTCCATAAGGCTCTGTACTTCCCAGAGAAGGGGTCTG[T/C]TCACCATGTTGGATTCAGAAGGATGCTTACACAGAAAACAAAAGCACCTAATACCCCCTTG | T/C | 4 | 18914851 | 0.896 |
| 4021988111 | CTATACAAACAACTAGTTCAGCTGTAGCGTTTTGCGGTTGGCGGTCTTGTAGGAAGTGAAT[A/C]CTTGGTAACACGGTTTCAAAGAGAGTGTAAATTTCTGCCTGAACAATCGAACCAATAATTT | A/C | 4 | 21988111 | 0.905 |
| 4023502835 | CTTATTACATTAGGTTTTTCTCACCAATATTTATCAAAGTGATGCCTTTCTCCAACTTGT[A/T]TTTTTTTAGTAATTTTGTCAAAGATCGCTAGCAATTTATTTAACAACTTTATATTTTAT | A/T | 4 | 23502835 | 0.882 |
| 4027941759 | GGGATTAATTCCTCAACCAGACAGGATGACTTAAGTTATGGACTCTGAACACTGTTGAAA[T/C]TACCTAAGAGGAAGAATATTGGTCCAAAAAAATGCTGTGGCTGTTGGTCAGTGGGGCAC | T/C | 4 | 27941759 | 0.686 |
| 4031072166 | AGATAGAGCCCTTGAAGCTGCCTCGTGACTCTGAGGCGTTGGATCGTTGTGTCCTGGTCAC[C/G]TGTTCAGTAAAAAGCTGGAGAGCCCATGGCTCGTGGGAGACAACCTGTCAGTGCAATGTTC | C/G | 4 | 31072166 | 0.959 |
| 4035890150 | CTGTAATTGTGTTCATACCATGCATGTCCCATTTCGTCCGGGTTACCTCACTTGGGAAAAT[A/G]TTTTCCTGTTCCATTCCTTTGCCTGAAAGATTCATGATGTAAGAATTGTTTTAGCTATCAG | A/G | 4 | 35890150 | 0.759 |
| 4037413372 | CAGAGGTGTTCATATTATATTGTATTATTATAATGGTGTGACAACTATTCAAAAGCAAGG[A/G]GATGGGATGATTCTAGATCTTCACCAACTGATTATTAGATAAGAAAATATGATACATAC | A/G | 4 | 37413372 | 0.942 |
| 4039060333 | TATACTCCACTGACTGCTTACTGCTGCACTCATCTCAGACCAGTGCAGGAAGTAGAGAAG[T/C]GCTCCAGTGCATTCTTAGTCCTCTTAGAATCAGAGAATCTGTTTAGTCTGTGCTTTTCT | T/C | 4 | 39060333 | 0.911 |
| 4040902321 | TGTGGTACTGGAGAGTTCTACATCTAGATCTGAAGAGAGCAGGAAGAGAGAGCCACTGGGA[T/C]TAGTTTGTGTTTCCGAAAGCCCAAGGGCCACAGCAACACAGGTCCACCTACAAGGACATAC | T/C | 4 | 40902321 | 0.502 |
| 4045685149 | TTATCCCCCTTCCAATTTCCCCTCTGGAAACCCTCCATGTCATTCCATAGTTCCCTGCTCC[A/T]ATGAGGGTGCTTCCCCACCCACCGCTGATTCCATCCTGCCTCCTTGCCCTGGAATTCACCT | A/T | 4 | 45685149 | 0.602 |
| 4047510440 | CCTCCAGGTGCAACTGTGCAATATGGGTACGCCTGGCAGATGTTCACCTGGCTATGGACC[A/C]GGGGGCAATGAAGGGGGCCAGAAGAAGACCAGGGCCAAGAGGTATAATGTGCATATTGTT | A/C | 4 | 47510440 | 0.609 |

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|---|---|---|---|---|---|
| 4049098430 | CCACCTAGTGTTTGAAAAGCCATCAAATGCTCTATCTTTGTAGAATTCCTGAGCCAATTTA[T/C]GTCCAATCAGAGTGTTAGCAACAGTTGTAAATGTTCTGCCAAATAGATCTCTAATCTTGTC | T/C | 4 | 49098430 | 0.876 |
| 4050715446 | TGGAAACTTTTAAGAAGTGGATCCTAACGAGAAGTGCTCGAAAAGGGCAGAGTGGGATCA[A/C]CGGCTTCTATCTTGCTCCGTGACTCATAAGAGGTAAGGGTTTTTGCTTTTCCACATTCT | A/C | 4 | 50715446 | 0.824 |
| 4052313040 | GGGTTTTCCCACGGTGTCAAGTACCTTGACTGGTCTTTTACTGTGAGTCATCATTCTGTCA[A/C]TGTGAGAAATAGCCAAGACAATTGACTTATACCAAAACAAGGGGTTACATTGGTTTATGGT | A/C | 4 | 52313040 | 0.838 |
| 4055570079 | TCAGGAGGAAGTGACAGCAGTGATACAGATTGGTTCTAGTCAGGCATATGGATCCTGCGG[A/G]GAAGCACACTAAGGATAAACCTCTTACTTGGATGAGGAGAGTTAAAGGTATGGAAAGGA | A/G | 4 | 55570079 | 0.976 |
| 4057174499 | GGAGTTGGTTCTGAGTGGCTGTATTGGTGCTGGGATCTAACCCTGTCCTCTCCGGAAGAGC[A/C]GACAGTTCTTTTTGAATTGCTGAATCGTCTTTCTAGACCCCTTTATTTTCTTACCTTAATT | A/C | 4 | 57174499 | 0.956 |
| 4059071691 | ACATAGGCAGGCTAGAATGATTCAGCCTGGAGCAACAGACTCATACCAATATAAAGCTAA[T/C]GTTGGCTTGTTAAGAACAGATTCAATAGAACTTCCTTCAGTCGGTAAAGCCAGCTTCCC | T/C | 4 | 59071691 | 0.823 |
| 4060670736 | TAGTTACATGTATGCTACAGTATACCTATGGAGTTCTGATGTCAATTGAAGGAGTTAGTT[T/C]TCTCTTCCTACCATGTGGTGTCCCTTACTGAGACATCTTGCTTGCTTTAACGTTTGTTT | T/C | 4 | 60670736 | 0.986 |
| 4062198189 | AAAGATTAGTAAAGCACACCTCTGGGTATAACTGATAGGACATTTGAAGAGGATTAGATC[A/G]TGAGGGCTGTAACAGTTCATTCTATTGACAGATTCAAAACTTGGGGCTACTGGGAGATG | A/G | 4 | 62198189 | 0.908 |
| 4066812933 | CTAGGGTTGTAGGCATGCACTATCCACACTCACCCTGATGTAAGTTTGGCTAGAATAGACA[A/G]AAGAGCTCACAGCCAAGTGAAAGAATGGAGTCCTACCTTGCTGAGGGCAGGAACGCAGGGC | A/G | 4 | 66812933 | 0.955 |
| 4068343084 | TGCATTCCAGCACCATTACATTTACAGCTTCTCTAATTGTTAGAGCATTGCAGGCAGACTG[A/C]TGGTATTAGCCGTGGTAGTGAGGCATGGTAGTGGGGGGGAGCATGATGGTTGTGATAGGAA | A/C | 4 | 68343084 | 0.943 |
| 4069863554 | CACATCCAACATAGCTGATGCCAGTCTCTTCTGGAGTAGTGTTCTCAGAATCAGTCTGCC[T/G]GTCTACCCAGCTGGCCACTCAGTTTTACTGATTCAGAGCAACCCTGGCTTAAAAAGAAC | T/G | 4 | 69863554 | 0.982 |
| 4073009704 | CAAAATGGCTGAGTTTATATATGGAGGAGAAACTTGGAGAAGGGAAGTGAAGCTTCTGAA[T/C]TGGAGAGGTTGAGAGTAGCAGACAAGGCATGCTAGCTAGGTTGGCTCACTGTCGGTAGA | T/C | 4 | 73009704 | 0.937 |
| 4077641301 | TCTCTCAGCAAGCAAATATCAGTGAAAATGAGAGACCCACAAGCTTTACATAACTAGCTCT[A/T]TAAGCAAGCCAAACTCTGACACCATCACTGTCCCTTGAGTCCTTTTATACCTTCCAAACAT | A/T | 4 | 77641301 | 0.879 |
| 4079183914 | AATTTGAGATCTGGACAAAATTGGAGAACATATACTTTTTTTTGGATGAGGTCTTGAGATG[A/G]AAGTCCAAATTGTTTTAAAGGTACTGTTACCTGAGTCACCAGGCCCACCCACAGTCTCCTG | A/G | 4 | 79183914 | 0.93 |
| 4080742511 | TGTCCCATTTCACAGACAAGGAAAACTGAGGTTTTGCATGTTAAGTAACTAGCTCAAGAC[A/G]TGAAAACTGAGGTAGAGGGTATTAAACAATTACCCTGAGATAGAGTAGTCAATGAATAA | A/G | 4 | 80742511 | 0.816 |
| 4082266250 | TTTCCTCCCACATAAACATAGCAGAGAGAATGCCGGGACAGCTTGCTTTCTCCCACACAAC[A/T]CAAAATTGACATAGAAAGGATTTAGAAATATGGATACTTTCTGTTCCCAGTGACCCCATTT | A/T | 4 | 82266250 | 0.961 |
| 4088644702 | AAGATGCCAAAGTGAATTACTGAAATGGAGAGTTGAGAAAGTTACAGAATAAAAATAATGT[A/T]GATCATTAGAGAAACTACATTTCAGAGATTAATCTAGGAACCATGAACACTTTCAAAGTAG | A/T | 4 | 88644702 | 0.567 |
| 4090207324 | AACAATTAAAATGTACTGAAAATTTCTTAGTGATTTTGAATATTTGCAATAGAGCTAATC[A/G]TCTTTTCTATTTAATATGTTTCCAGGATCTGAAACATGAAACATGATCCATGAAAGAGA | A/G | 4 | 90207324 | 0.631 |
| 4091870538 | TGCTTGCTAGGCAAGTGCTCTACCACTGAGCTAAACTCCCAACCCCACTTCACTATCTTTT[A/G]GTCAGGAAATGAACTGATTTCAAATCAAATATCCTTGCACTTTCCCTTCCATTTCACAATT | A/G | 4 | 91870538 | 0.943 |
| 4093383134 | GATTATATATATCTAATATACTGAATCTACCTGAAATCTACACATTCTAACTTTAATTCC[T/C]CCATCTCTTCTCATGTACCAAACCCCTACTCTGGTTCAAATATATGTCCTCTTTTGTTT | T/C | 4 | 93383134 | 0.808 |
| 4094931788 | GGCATGTCTGACCAATTTTTTCTTTTCTTTTTCTTTTTTCATTTTTGGTTGTTTTATCTA[T/G]CTAGCTACAGAATCACTGTAAATTTTAAAATATCAGTTACTAGGACTACTCTAACACAT | T/G | 4 | 94931788 | 0.539 |
| 4096920596 | ATTGATAATACTATTATGTTGCAAAGTGAAAAGTATAAAATTAGTAAAGTGAGAACCCAC[A/G]TGTTCCATGAGAATTTACTTATATGAAATCATAAGTATGCTTGACGTGGTAGCACATAA | A/G | 4 | 96920596 | 0.676 |
| 4098619123 | TTCTGAAATGTTTTATATTGCTCATAGTATAAAAATAATAAGCTGACCTGAAGCCCCAAA[A/T]GTTTATAGTACATTGGACAATGAGGTCTCACTATATGATATTTTTTGTTACTGAGATAA | A/T | 4 | 98619123 | 0.835 |
| 4103249461 | TTTAAGTCTTACAAGGAAGAGGGATTTGTATTCTGGCCAACATGAATTCAGTTTGCTTTT[T/C]CCATAAGTGGAAAGTGAAGCTAAGGAACCATTTGATAATTGTTGATTGTTGAGTTGACC | T/C | 4 | 103249461 | 0.872 |
| 4104814037 | TATACATGTTAAGAATTAGTTCTGGGTAGAAATGAAAGAGATCACCACCACTCCTGAAGC[A/T]TGTCATGTCTGGGCAAGGCAAACTTCTATTATCAACCACGAAGGTATGCTCAGAAGAGT | A/T | 4 | 104814037 | 0.839 |
| 4109637514 | TAGGTGCTGTGTCTGATCTTTAATATTCTGGAAGGGCTCCACGTGCTTTTAACTGCTGAG[A/C]AATTTCTGTAAACCCCTTTTTCCTATAATCTATTAAGACAAATTAGAGTGTCTCTGTAT | A/C | 4 | 109637514 | 0.8 |
| 4114563241 | AAAAATAAGCAATAGAAAAATATTTGTATGAACAAATGTGAACAAAATGTGAAATGATTT[A/G]TTATTATGCAAGTTTGCATCCAGCCTCAATGCTATATTAATTCCAAGTAGTGAAAATGC | A/G | 4 | 114563241 | 0.955 |
| 4116166995 | GATGTACTCAAATACAGCTCTGTCGGGCTTGTAAACTGTTCATCTAATGTGTTGAAACAAC[A/G]GAAAGTCCATTTATCCTGTCCCCAGAACTCAGCTCTCAACTCTTCCCATTAGATTCTCTTT | A/G | 4 | 116166995 | 0.974 |
| 4119360890 | AGTCCCTCGGCCAAAACCTGCTGTTCTTCCAAAACCAAGCCCTACTGTAGGACCTGACGCA[C/G]CTTCCCAGGGTCCCACAGTCAAGTCTTGCACGATGTAAAAACGAAGGTCGTGAGGGGAGGG | C/G | 4 | 119360890 | 0.782 |
| 4124297354 | CTGGGACTGGACACTTCCAGTTTGTAGCTGGAGCCCCAACCTAGCTGATCCCAGCCCTCAG[T/C]TCACTACTCCCAAGTACCTTAGGAGAGAGAGTTCACCGCCCGGACAGGTGGGCACTCCTGA | T/C | 4 | 124297354 | 0.549 |
| 4127749824 | TTAAAAAAGCATACTTTTCGAGACTAGGAGACAAGTCTGCTAAATTGTCTTTTTGAAACCA[T/C]CCACGTGCATCCCATGCGACTTTTAAACACCTCTTCAAGTTTCAGTCCAGCCTGAAGACAG | T/C | 4 | 127749824 | 0.88 |
| 4129411553 | CACACACACACACACACACACACACACACACACACACTGTCCTTTGTTCTTTGGTTTAC[A/T]ACTTGGGCTGCTTAGGCCTTTGCTTTCACCCTTTGAGTTCAGAAACAGAGAGGACCCACAG | A/T | 4 | 129411553 | 0.982 |
| 4131221730 | TCAGAGTCATAGAGACAACCCTTCAGAGGGCGGGTAAACATAACTAATAAATCAAGCAGAC[T/C]GGGTTGGGAGTTTCGAGGGGCTATTGGGAGACAGTGGCAAACTGTTCAGATCATGCCTGTC | T/C | 4 | 131221730 | 0.898 |
| 4133375390 | TATTTTTCATAATTATAAGCCCTCCCTAACTCCCACTCTCTAGCTGGATGTGTAGACAAG[T/C]TGACTATCCTATAGCTTCATGAATCTTTTAGTTTTAAAAATGACAGAAGTTCATTTACT | T/C | 4 | 133375390 | 0.841 |
| 4134899865 | GGGGTCAAGACCAAGAGCTCACTGAAGAGCGGGTCTCAGAGGAGACTGGTTACAGCCTGGG[T/C]GAGGGAAGAATGTGTATCAGCCTCAGTCATGAGGGCTATTCAAGTCTGTCAACCGTGGACC | T/C | 4 | 134899865 | 0.905 |
| 4144487081 | TGCTGAAGACATTGCATGCTTAGGTTGCAGGACGTGGAAAAATTGAGCTGGAAGCTCTCC[A/C]TGGCTCTTGTGTTCTTTAAGCCTCCTCTTCCTCAGGGTTCCCTGAGCTCTCAGGGGAAG | A/C | 4 | 144487081 | 0.806 |
| 4146021397 | TTCTAGAGTAGAATTAATAAGCATTTAAATTATTATCATTTTAATGATTTTCTTTAAGTAC[A/G]CTCTCCACCTGTCAACTGAACCAGCCATGTAGTGATATTTCTCCAACTTCAGTCATAAGCT | A/G | 4 | 146021397 | 0.828 |
| 4147671667 | ACCAGTGTTGGGGTTCAGAAAGTGACATCCCCCATATTTGCTCTTTGATGAGCTGACAAA[T/G]TTGAGAGGTGGCCTCAGACCAAGATCCCCAGGGTCTTCTTTTTTCACTTCAAGACAGTG | T/G | 4 | 147671667 | 0.896 |
| 4152505867 | ATGTGTGGAGCAGGTATTGCTGCACTCATGGAGGATGGAGGATGGGATGTCAGGGGCCTG[A/T]CCAGCTGTTGGCATGCTCCTACCACATGTGCTCTCACGCACTGGCCGCTCTCTAGCCCC | A/T | 4 | 152505867 | 0.625 |
| 4154143910 | AATACAACTATTCACAGACACCCCCACTCCCAACTCCAGAGAAAGGAGGGAAGCAGGGGA[T/G]CCTGCGGCAACATTGGATCCAAGAGATCCCAGAAGCCCACAAACTTTATGTTTAACCTG | T/G | 4 | 154143910 | 0.7 |
| 4155805092 | TTCACCTCCCAGTATGACACAACCACTCCCTGTTTGGTTTGGTTTGGTCTTACCTTTGTT[T/C]GAGACATGGTGGAACACCAATGATCTACGATGCCATTTAGATTTTTAATGCTCTCTTTT | T/C | 4 | 155805092 | 0.762 |
| 4157312410 | CCGCCCCCACTGTCCAAGTGCTGGGGCTACAGATGCCAACCACTGCGCCTGGCTTTTGCC[A/G]TGCTGGGGACTGAAGTCCTCTGCCATTCTACTGGCCTTCTGCCCCTTACTTGTGCTTCT | A/G | 4 | 157312410 | 0.675 |
| 4160402821 | ACAGCTTGGATGTGGCTCTGCACTTCAAACACAGTCTAAGATCTACTCTAAAACCAAAAC[T/C]GAGGCAACAAATACGTGGCTCTTTCCTGGCTCTTGCAGTGGAAATGAAACTTCTCTTTG | T/C | 4 | 160402821 | 0.902 |
| 4162009988 | AAAATTAACATATGAGAAATATCCCAGGGGAGTCAGATAGTCTTTCATAGTGCTGAACTCA[A/G]GGGCATGAGCAAAGACTGCTGGAGGTGACCTGAACTCCTTCTTTCGAAGCACCAAAGACTC | A/G | 4 | 162009988 | 0.966 |
| 4163821233 | AGTAACTCACCTGCTTCTCGAATGGACCCACTTGAGGGTCCAGGGCCACTGAAGGGTCTTC[A/G]TACATAACTGAACACTGTCAAAGCTAGACTATTCATGTTTTAATATTCAAAGGCTTAGCAG | A/G | 4 | 163821233 | 0.991 |
| 4165454560 | TGATGACCTGGGGGGAAGGGAAGAAGGTGAGTACCTAGGGATGTGGGCAGAAGAGCCCCA[A/G]CTGTCCATAAGCCCCACCAAAGGCACAAACTGGATGGCCTCTGTTGTACCCACTGCCCC | A/G | 4 | 165454560 | 0.65 |
| 4168756464 | TTGGCACTCTTAGCAAATAAAAAACTGTCAGCCACAGGATGTACCATAACAAAGAGTTAAA[A/C]TTCATCAGCGAAAGATATGCTTTCTGAGATATTCTCTTGTAAACTTATGAGAAAGGGATAA | A/C | 4 | 168756464 | 0.742 |
| 4170447191 | ACCACATTAGGTGTTGCTCCAATATTTAAAGCACATTGAAAATCTCCCACACTCCAGCCT[T/G]CTGGGCTACAGTCCCAGTGAGAAATAATGAAGCAAGGTTGCCCAGTTGATGCTCAAAGA | T/G | 4 | 170447191 | 0.614 |

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|---|---|---|---|---|---|
| 4172050247 | TTGTTTAGCTGTAAAGGGCGCCAGCTGGTCATTGGCTCGCAGTCCTGTGTTCCCAGTTTC[T/C]GGCTTAGTCCTGTTATCGTGGACCCTGATTCAGCAGCAGAGGCATTCCCGGGTTGACTA | T/C | 4 | 172050247 | 0.935 |
| 4181963967 | GACTGCTATCTCTAATTAAATGTAGAATTAATTTTGGCAAACTAACCACAGATGCAGTTTA[T/C]GCTCAGTTTTATCAGACAGATTTATTTATAAGCTGTCAACTTCTTGAAAGACTTCATTTTG | T/C | 4 | 181963967 | 0.872 |
| 4183540141 | CTTCCTCTTGTCTACCTTATCTGTGGAGACCAACCTCCACAGTCTACCTGAGAAAAAAT[T/C]ATGAAATCCTTGATGGAAATCACAGGTTCAACTTCCTGGAACACCTCTCCATGCAAATG | T/C | 4 | 183540141 | 0.921 |
| 4185056116 | TTCTAAAATGATGTAGTGGCCGTTCCGGAATGGAGAGGCAGGGAGGGAGGGAAACAAAGC[A/G]GAAGTCTTTTAAAACTGTAGCTGGGGAAATCAGGCGTTCTCAGGTCAGTCTGCAGCCAC | A/G | 4 | 185056116 | 0.72 |
| 5005067054 | GATCCCTCCTGTACTTCTGAAAACATGGTTAGAGTGCAGGGAAGATCGGTGGCTGTCTAC[A/G]CAGGAGGTGGGTAGAAAGCTTCCAGTTTACCCCAATCTTTTAGGAACCAGGTAATTATT | A/G | 5 | 5067054 | 0.896 |
| 5006609907 | AAAATCAGGAAAGCTGCAGTGAGAAAGAAGTATTTTAGAAAAGTGACATTGATTTATTTC[A/G]TATTTTTTAGAATTAATTTTACTATGGCATCCAATAGGAAAGATGATCACCTTAAAGAA | A/G | 5 | 6609907 | 0.552 |
| 5009771971 | AACAGTTGTGAGTGTGTAGCTCTATTAAAAATGAGAAAAAGGAGAAGCCCACTCAATGGA[A/G]GGACCAGCAACCAGGTGCATCTACAACCCTGACGTACTTTCCAGGTTAAGTTTTATGAT | A/G | 5 | 9771971 | 0.745 |
| 5011423376 | CATTCTATCCCCAGAATATTGCTAGATAAAATTAGTTTAAAATATTAGCATTCCTGGGAG[A/T]GTCCCTTTATTATTCTCATTTGCCAGAATAAGATGAAATAGGAGGAAATTATATAACTT | A/T | 5 | 11423376 | 0.9 |
| 5014587097 | TTTAGTGACACCCAAAGTTTGTCCATGTTCTGAGTTGATATAAAGCCACTCTGTAGGGCCC[A/G]CTGCTTTGTTCATGTTCTTCTTGCACAAGTTAGGAAAAAGTAGCAACATTTCAGAATCACA | A/G | 5 | 14587097 | 0.934 |
| 5021092679 | GTGTGTGTGTGTGTGTGTGTATGAAAGTAATCTAACTGAAATCACCAAATATTGTTTGAGT[T/C]AGAGCCCTAACAGGCCATCTTTTGTCACCCAATGACATTTCAAGTCCAGAATTAGGTTATG | T/C | 5 | 21092679 | 0.987 |
| 5022847270 | TCCCAGACACACTGCCTGGGAACAACAACAGGACGTCTGAGATCAAGACTGGTTCGTTCTC[A/C]GCATTAAGTTTCCTCGGAAGACTTCCACGGTCGGCGCTGCTGCAGGAGGCCACGCAGATGC | A/C | 5 | 22847270 | 0.93 |
| 5024525099 | TTGAATGAAAATGAAAGCAAAACACAATACATCCATGGAACACAGCAAAGGGAGTCCGAA[A/G]AGAAGCGTTTCTATCTCTAAGTGCCTACATTGAAAAACCAGAAATGTCTCAATATAGAT | A/G | 5 | 24525099 | 0.991 |
| 5026080053 | AGGCTGAGTCAATGCCACCTACGTCTGTCTTATACTTCATGAATGGATGTCACCATTACAG[T/C]GTACTGATGAGAGAATGATACAAGAGAAGGCCCAGAGGTCTTGAGTCTTTGAGAACAATAC | T/C | 5 | 26080053 | 0.919 |
| 5027598108 | AGTCCTAATTGAACTTCATCTTTGCTGTGACTGAGACTCAGATAGAAACAAATGCAAAGT[T/C]TTATTTGCTTAATCTGTTTACCAGTAACTTTTCATTCTTGCAGCGTGTGCTTTTGTAGT | T/C | 5 | 27598108 | 0.807 |
| 5029291630 | TAAACTACTCTTAAGGGTAAGCTAGTGTTAGATGGCTAACAGAACATTGATTCAATGACGT[A/G]GTTGGAGGGTCCTTGTCTTATAACATCCTGTTTGGGATTTTTTTCTCTTCTAAATTTTATT | A/G | 5 | 29291630 | 0.877 |
| 5030844009 | GGATCCTTGTAGTTAGTCCTTGAGATGTAGATCATAGAGCTGCCAGGGTAAAGTGAAAGAG[A/G]TAGTGTAGAGCTGAGAAAGGTAAAAGTGGAACACCTGAAATTTGAAGGCCCCAGTAGCCAT | A/G | 5 | 30844009 | 0.837 |
| 5032389662 | ATAAGAATAGTGAATGATACTGAGAAACGAATAATAAAGGAGGGAAAATTTTGATAAGAC[A/G]TATTGACAAGAAGGTGAACATAAAATTTCATGTTCCTCAATTTCACATGTTAGAATATA | A/G | 5 | 32389662 | 0.81 |
| 5033983990 | TTTTTAAAATGTCAACAAATTTCAAGGTGATAAATCCAATTATGTCTTGTTCCATGTATG[T/C]TCTTACAAGTAGTCTTACCCACAGATTAACTTCTATCATCTCTTCTAGCCAGTGACTCC | T/C | 5 | 33983990 | 0.862 |
| 5039065030 | TAAAGCTATTTAGTTTCCCAGAATACAAAATTTTGTTTTGCTTTGTTATTATATTCCTGA[T/C]GGCAGGAATCATGCAAACAACAGGAAATAATGAATTTGACTCTGTATCTTATAAGGTTG | T/C | 5 | 39065030 | 0.64 |
| 5040663200 | AATAATCTGCATTTTACAGTGACACACCATCTACTAAAGTTTTCTAAACCTTCTCAAATC[A/G]TACCAAAATCTATGTTTCTATTAATGGTTCAAATGGATGAGTCAGATAGGACATTTCAC | A/G | 5 | 40663200 | 0.613 |
| 5046890247 | ACAGACTGATGAATCCCACCATTCCTGCAAGCAGAAAGACCGGAAGAAAGCTATAGGCAT[A/G]TTTTTTACAGCATCTTTCCTGCGTTTGCCAATGGTTGACCTATCATTAATGGTCTGATG | A/G | 5 | 46890247 | 0.904 |
| 5048449425 | AAGTACAGAAGTTTAGATCATCTGGGGTGAATGTCTGGGCTATTTCACCAGGCAAGCAACC[T/C]AGACCAGTAAAACTGCCTCCTGAGGAGATGGACAGCAATCAGGGACCTGGAGCAGCATTGA | T/C | 5 | 48449425 | 0.905 |
| 5050017626 | ATGCTGAACCCCAACTCTTTGCAAGAGAAACAGTTTTGCATAGGTAGAGAAACCCAGTGAT[T/C]ATCCTCCCTACCTCTTTGCGGTATTTATGTGATATACATCTGGGGTCAGAGATTAATGAGA | T/C | 5 | 50017626 | 0.986 |
| 5051833536 | TAGATGTAGTCATGTCTTAAGCGTTGTGCACATGGGCTTGAGTGAATTGTCACCAGGAAAC[A/T]TTTTAAAATATGACTAAAATACACTGCCTCTAGATGTCAGCCTCTAGAAAAGTGAAGCAAC | A/T | 5 | 51833536 | 0.765 |
| 5054983065 | AAGCAAAACTATTTGCAGATAGTTGGTATGTTCAAATCTTTCCAGGTCTCCTTTCCCACA[T/C]ATTTTTCTTCAGACACAGATATATTCTATTTTAATAAATATTTCAATAAAAACATTTCA | T/C | 5 | 54983065 | 0.846 |
| 5059722864 | GGACAACTTCCCACCCCCTTGCTGTGAGTCAGCAGACTCCACCACTAGTGGAGAGAGAGAT[A/G]GGGACCTGGCCCAACTTGGTAGCTTTGAGCAGCAAGCCAGTAGCCAACCTTCTCTGGCCTG | A/G | 5 | 59722864 | 0.915 |
| 5063069411 | TCAGAGAAGGGATTGAGAGGAATTGACCAATGCCCTGAAGAGCAGGCAAGGATGGCTGGG[T/C]TTAGAGTGCTGGGGGAGGGGAGTGTGGGAAGAACCCTACCAGGAAGCTGCCTGGGCTGT | T/C | 5 | 63069411 | 0.553 |
| 5066241199 | ACGCTAATTATGTTACCTAAAAACCTGTTTGCATTGTCCTGCATGTGTGACTAAAGGAAG[C/G]CTGTCCAGAGTTGGTTTTTGACTGGTCAGTAAAGTTACCAGCTGCTAATGGCTGGACAG | C/G | 5 | 66241199 | 0.648 |
| 5067878089 | GGTCCCACTTAGGCCAGGCTTTAGGTTGGGGGTATCTCACTTGTGAGCGTTGTTGTGAAG[T/G]AGCTCCCAGGAATTAAGCTCTCTCTATGTGTGAGAGGGGATCTGGAACACCAGCTCTGA | T/G | 5 | 67878089 | 0.873 |
| 5071110542 | GTGTGTGAGAGGTTCTTGTTGATCACTTCCGTTTCACTAATGGCTGGATGGTCTGAATTT[T/C]TCCATTTTTATTTATGGTAGAGCATTGTGTATAGGTCAGAGGACAGCTTGCAGGAATAG | T/C | 5 | 71110542 | 0.957 |
| 5072889821 | CAAAGTGAGAAGTTGATGATGTAGCTTTTAATGGCTAGTAGCTATGGGAAGGAGACAGGAT[T/C]GGCTCAGAGAACATGGGGGAAGAGAAAGAGCTTATGGTAGGACTGAACTGTAAGACCCGTC | T/C | 5 | 72889821 | 0.756 |
| 5074405238 | TCTAGCCAATTTATGTGGACTTTATCCCAGTAAGATAGACTTCATGCCTTCATATGTGTA[T/G]CAGCTAGAACAAAGATCTCGATACCGTTCCAATTAATATCCATCAGTAAAACAGCTGTG | T/G | 5 | 74405238 | 0.918 |
| 5076011393 | GTTCTAATTTACCTGCTTCTCTTGAGCAGGGAGAGGCTCTAACAAGCAGAAGGAGCGATG[A/G]ATCTGGAGGATGGAAGGACTGGGGACAGTGAGGTTTTTTCACTCTCTCACTGCTGATGA | A/G | 5 | 76011393 | 0.88 |
| 5077777345 | CCAAGAATGGATAAGCAAGCCAGTGGGACACCATGAACAACAACCCAGACATCTGTGATCC[T/C]GTCAATGGATTGTGCTGAGCAGTTAGACATGGAAAAAATGAACACTAAGCATGAGCACAGC | T/C | 5 | 77777345 | 0.923 |
| 5079291757 | CTCCTGGTTGGCAGTTTTGCACATTCATACAAGACAAAATCTCTAATGAATTTGCATTCA[A/G]GATGGATGCAGGGTCTGTTGAGACTTGTCTTCCCTTCTCCAGGGAGGACGGACGCTGAT | A/G | 5 | 79291757 | 0.993 |
| 5080882050 | GTATGAACCTCCTCTTTGAGGACAAGAATTGATTTGTAATGAAGTTTTCTTGAACATTATC[A/G]TTGGTCTTCCTTCTAAACATGTCTGTAGACTGCTTTACTGATAACATATTACATGAATATA | A/G | 5 | 80882050 | 0.829 |
| 5082405031 | ATATTTTTACCATTATGCAAACTGAATATTTTTTCACATCCATTTATACTTTTCTTTAGC[A/C]TCAGGGCAAGCGAACAATATGCTACTCTTGTTTCTGAGCTTGGGACACTACTGTAGCTT | A/C | 5 | 82405031 | 0.92 |
| 5084309584 | ATATCCTATTGATGGACGGGATGGTTTTGTACAGTTCACTCAGACAAGGAAAAAAATTAT[A/G]TTTCTGAAGTATATACAAGACCCGCTCTCATGACTTATTTATCCACTTCAGTCACAAAA | A/G | 5 | 84309584 | 0.875 |
| 5085968698 | TTAAAGGTGAAGACACCATTCCAGGATCACCTTACAGGTGAGATTAAGTTTCAGGATAGTG[A/G]AAGTAGAAATCATGTGACCCTTCCAAAGCCCTGTCTTAGTATTTATGCATTTCCTCAACCA | A/G | 5 | 85968698 | 0.923 |
| 5087557596 | TTTCTCATCTGGACAAAAAGGGACTTGCTTGGGTCACTAGTTTCAAAGCATATCTCTTGGA[T/C]CCCTAGTGTTTCTCAAGGGGTCTCAGGGCAGGAAAGGAAGCCTATTGGACTCTCAAGTCAT | T/C | 5 | 87557596 | 0.979 |
| 5089137795 | CCATTTTTTTCCTGCTGCAAAATCCCTGAAACTGGGTAACTTATAAATATAAGAAATTAA[A/G]TTTCATAGTTGTAAAGCTTAAGGGGCCCATATCTGGTAAAGGCTTTCTTGCACTTTTAT | A/G | 5 | 89137795 | 0.691 |
| 5090734317 | TGGTGCTATTGATTTTTCTGAATTATGCTTTGATATTAACATAACCATTCTACCTTTATTT[A/G]AATAATGCTCAAATGCTAAGATAGCTTATAAGTTGAAATTTTCCATCATGGAGAGATATTA | A/G | 5 | 90734317 | 0.652 |
| 5095772373 | GAAACTGTAAATAAAACACATGGCGTTGACCATCTTTTATTCATAATTTAAGATTATTTTA[A/G]TTTCTTGTGTGTTCTATATTTTCAAAGCATTGCTTTTGCATTGGTTCCTATTCTGTTTTCT | A/G | 5 | 95772373 | 0.562 |
| 5097348972 | GTGGGGGTAAAATCACCGAATAGGTAGAATTTTAATGATTAACACAAAGTGGTGCAGAGTG[A/G]CAGGGAGATTAAGGCTCATATTTGGGTGCATGAATGATTCAGAGTTATACATCACTTGGGC | A/G | 5 | 97348972 | 0.935 |
| 5099195367 | CAGGTCTCTGCGACTTTCTAGAGTTTCCCCCTGTCCCCTAACTCCCACTGCTACATATTTC[A/G]TTCATTCTTCTGGCCCTATTGGTGTCCCTCCAGTCTTTTCCCATACATAATCCTGCCCTTC | A/G | 5 | 99195367 | 0.651 |
| 5106168007 | TTTTAAAGGGGGCAAAAGAAGACGACTTTAGGCACCTACACAACTTCAACAATTCACGTGC[A/G]CAGAACGTTTTGAGCAGCTCCCACACACAGCAGAAAACCCACGACTCGGACTCGCAGGCCC | A/G | 5 | 106168007 | 0.954 |
| 5107857072 | GTGGCCTTGTAACCAGACAGCATGTAGTTGAGAGCAATGGTATTAGCTGTAACTCAGAAAT[T/C]TTGGCAAAAAGCTCAGTGTAGGCATCTGGCAAATGCCTCTCTCTTCTTCTTCTTTGTGAGA | T/C | 5 | 107857072 | 0.974 |
| 5109413667 | CCCTATATATCCTTACAAAGGAATAGGTCAGGTTGTGGTTTCTGGCTTCTTCAGTGGCTG[T/C]AACAGTTTTTGGAATCAGTGTTCTAACCTTTGGAATACCCCTCCTATGTGGATTTCCAC | T/C | 5 | 109413667 | 0.986 |

| | | | | | |
|---|---|---|---|---|---|
| 5111029312 | GATTAGGGGCCTCCAACTTGGTTTCTGGCAATAGTACAGATCATGATCCTGATCTAAAGC[A/C]GGACCACAGATCTAGACAAAGCCCTCAGATGCTGCCTGGACCACAGACATCAACATGGC | A/C | 5 | 111029312 | 0.988 |
| 5114178292 | TCAAGGTTTTTGTGACTAGGTCAATGTCCAGATTTCTCTTTGCTTACCCTGCAGAGTACC[T/C]TCCTGTACCAGAGAATATAGTGTAGGAGTGAAGGATCCATGTAGATACCAGTTGACTTC | T/C | 5 | 114178292 | 0.942 |
| 5115760857 | ACTTGTTTAAGAAGAGTGCTTCATTCATTTTTCAAAGAAACACTAGGGCATATGTTTATTA[C/G]GTCCAGATACAGAGTGAGATTGGGGGAATGTGTCCCGAGTTATAAAGTGATGTTACTTAGC | C/G | 5 | 115760857 | 0.965 |
| 5117431202 | TAGTGAGCTAACAGGAATGAATACCTTCATGTAGTTGACTGCACAGACATCAGTTAAATCT[T/C]TTGTTTTTGCTGTATCTTTCTTGGTCATCTGTGATCAATATTAGATATTTTAATCTTAAGT | T/C | 5 | 117431202 | 0.912 |
| 5118962726 | CAGTGGGACTAAGAATTAAATATAAGATACTAAAGGTAGTATGAGAAAAATCAGTGCTTTG[T/C]GTGAGACCACATTAAGTAGAATGGTTCAGAGACTAAGATAGGATCCTCGGAACCCTGTGCT | T/C | 5 | 118962726 | 0.838 |
| 5122070525 | AGCCGGGAATAAAGGTGTGAATCACCACAGACTAGCAATACAGTGTAGTTTATGAAACTT[T/C]GAACTTTCTAGAGTTCAAATAATGGGAAACAATCATGGAATTGTGGTTCAAATGGTTAG | T/C | 5 | 122070525 | 0.739 |
| 5123700718 | TTCTGTTTTGTCTGTGTGGATCTTTGTTAGCATCAATCTCCTCTGGCTCTCTTGTCAGTC[T/C]CCTCTTCTACATAGTTTTCTGAGCACCCAGAGGAAGAGTTTGATGAAGAAATTCCATTT | T/C | 5 | 123700718 | 0.971 |
| 5127022967 | CCAAGATATATCAAGCTGAAGAGATTACTATGGAGACAATGAAATCAAAGCTATGGTCAG[A/G]GGACCACATGGGTTAGAAGAGAAGACCTTGAAGTAAGAATGGGGGAAGGGATCTCTCAT | A/G | 5 | 127022967 | 0.95 |
| 5130181490 | GGCCCTGGAGCACCGATTTCCCTACCCTAACAATTAGAAGATGTTTAAGGCAGTTTGGTTT[A/G]TAGAAATCTTAACGTGGACGGTACCCACTGAATAACTACAATGAATCTAATAGAAAATATC | A/G | 5 | 130181490 | 0.922 |
| 5132074162 | GGGGAGCATACAGCGTTGCCTCCCGCCCCCACCCCCTCCAAACCTTTCAACTTTTGGTAT[A/G]CTTAAGCATCTAAACATATTTGTTCACTTAAAACAAACTGAATTCTGAGTCAAATAGGC | A/G | 5 | 132074162 | 0.911 |
| 5136722385 | AAATACAGTAAGGGAAGTGAATATAGTAAAAGACCAGTTACTAGGCAAAGGACAGCACTCT[A/G]ATGTATGAGAACAGATTCAACTTGATTATCTCACTATAGGACAAAGTCACTTAGTGGCTTT | A/G | 5 | 136722385 | 0.907 |
| 5138298219 | GACCTGTTTCCCCTGAGAATTCATTCTGATTGGAAAAAACCAGAAACTCTAGTCCCTGTC[A/T]CCCAGAGACAACTTTTCACCATGGAGTGTCTCCCTCGAGCCTCTCTTCAAGACCTACTG | A/T | 5 | 138298219 | 0.969 |
| 5141430321 | CCTGGGCTCAGCACGTAGTCCAGGTGTGGCTCTCTGTGTTAACCACCGTTTACTGTAAGA[T/C]GCTTCTCTGCTGAGTTGAGCACTGACCTGAGTCCCAGCAAAGTGCATAGAACTAATTTC | T/C | 5 | 141430321 | 0.889 |
| 5142998347 | ACCCACAACACGCAAACCGTTATTGCCCTGGTCCAGACTTCCAACACTGATGTCCTAGAC[T/C]GAGTCCCCTCCTCAGTGAGGCTGCAGTCTAGGGTTGGCTGGTTTTATGTGCTTACTCCA | T/C | 5 | 142998347 | 0.971 |
| 5147654034 | TGGCAGCAGTTGCCCTGCAAGAAATAAAAAGCAACCACACAGGAGATGAGCCAGAGAGTC[T/C]GAGGCTGACAGGGAACACGTGACGGAGACAGAGTTCTGAAAGAAAAGTAGCCAAGCGTG | T/C | 5 | 147654034 | 0.903 |
| 5150773470 | GCCGACCAGGGCAGAAAGTGTGCAGGGACCCACACAGTACAGAATGGAGCGTAGGTCTGTC[C/G]TTAGGAGTGATTTTGCACCCCTAAACCGAGAGGACCTCGGGGTGCGAGTGCTGCAGCGCTC | C/G | 5 | 150773470 | 0.879 |
| 5154056634 | TCCCTCTCTTCATCTCTTGTAGCCCAGGCTGGCCTCAATTTTGCTACATAGCTGAGAACTT[T/C]AACCTTCTGATCCTAGATGATCAGAGGATCATGTGTGCCACCATCATACCTTTCTTTCTTT | T/C | 5 | 154056634 | 0.748 |
| 5155616304 | CAGGACCCAAATAGTGGAAGGAGAGACCAACTTCAGTAAAGTTAACCTCTGACCTCCAAA[A/C]ATGCTCCAAGGCATACCTGCATGGCTGTGTACGCGCACGTGTGTGCGTGACACAATGGT | A/C | 5 | 155616304 | 0.885 |
| 5157190339 | TCCGTCCACCAAATTACAGTCCAGTTCAAAGCAAAATTTCTGTTTGCAAAGCAAAGAACAG[A/T]GCTGTGTCAACAGGGGCTGGGATTCGGTTACAGGCTCATCTCAGGAATGCAGACCCCTGCA | A/T | 5 | 157190339 | 0.837 |
| 5160400750 | CAACAAAAACCAAAAAAAAAAAAAAAAAAACAACCCTCTAGCTTTAGTTTCTGACACTGGC[T/G]GCGTAAAATAAGAATTCTCTAAACCTTTACTTGAAACCTTCCTGAGTGCTCCAAAATACAC | T/G | 5 | 160400750 | 0.86 |
| 5163432237 | AGTCTAACTGGAAAAAAATGTGGAAACATTTAGTTAGAACAGTAGAGCAAGGTATTAAAGA[T/C]CCCTTTAACGGGTTAACTCTGAGGGGAATATGCAAATAATTAGGTCTTTAAACATGCTTTT | T/C | 5 | 163432237 | 0.626 |
| 5165261734 | TATCTCTGAATTATTTAAACTACAGGTCCCCATAACTCTTCCCCTAGATTGATGTCAGTTC[A/C]TACTAACCTAACATCCTGTCTCATCCGCCCCAGAACCTACTCTATACATGGAAGCTTCCCC | A/C | 5 | 165261734 | 0.921 |
| 5167650243 | GTTGCCTCCCCGTCCTGTTTTCAGAGAGAACCCAGGTAGGAGGCTGTTACCATGGTTTAC[T/G]AGGGAGCCAATCAGGATAAGCAGATTTTGTGCAGTGGAATTCTTACTCAAACAGGGAAT | T/G | 5 | 167650243 | 0.91 |
| 5169200076 | CTTGCTCTGGGGGAGGGCCCGAGTCCCAGTGCTCACACCCACAGAGCAGCCCACGATTGTC[A/G]CAAGCCCAGCTCCAGAGGACTTGGCAGGCATGTGGGACACATAGGTGAGTGTAAACAGAAC | A/G | 5 | 169200076 | 0.674 |
| 5171011819 | CCCTTCACAGACATGCCCACAGGCCGGTCAACTCTGACGGTCCTTCCTCGGGACTCTTCTC[A/G]GATAATTCTGGGTTGAGTCATATTGACAATTAAAGATAACTGTCCCAAGCCTCTTCCTGGC | A/G | 5 | 171011819 | 0.985 |
| 5172536318 | CAAGCGCTGGGATTTTGTTGTTTTTTTAATACTTAATTTTATTTTGAAGTGTTGAAGGACC[T/C]TAGAGACTTTTGCCAACCTTACACCCACCGCCTAAGGTTAAGATTAAGCCGAGTACCAGCT | T/C | 5 | 172536318 | 0.727 |
| 6000013290 | TTTCAGGGTCAAGTATGGAGTATTTTCATAACTCTGAAGCACAAACTGGGAAGTCTTAAT[A/C]AAAAAACAGCACAATACATCATTCAACTGCTTAGTCTATGTGCTCTGTTCTTCACTGTC | A/C | 6 | 13290 | 0.936 |
| 6001561442 | TTCTTATGGTACTTCCCTGATCTAGCACATTCTCTTTCTCTGAGGGACTACGTCTAAGTCC[T/C]TACCCGAAGCCCAGGGTCCTGCCTTCATCTGAACTGAGCCTGCAGTGTGCTGCTCTGCTCA | T/C | 6 | 1561442 | 0.95 |
| 6008158299 | AGGGAGAGGTGGGTGTTATCACCCACAGACCAGAGAAGATGCATATTGCCCCCTATGGTT[A/G]TCCATTACTATAATAATCATCAAAAACTACTGATAACTCAGAACACGTGCACTGATTCA | A/G | 6 | 8158299 | 0.853 |
| 6009743133 | TAATTAACTTCAGGATGGACTCTCAGACCCTGGGGTAGCCTAATGGGCCAGGGCACTTTTC[T/G]GTTGGAGTGAATAACTTATCTTGGGCTTCTTGTATCATTGGTGTCATTGGTGTCTTTCCTA | T/G | 6 | 9743133 | 0.993 |
| 6011372152 | CACCTTCATTTTCATCTTTCTGTCTCTTATTCTGATCTGCAATTTCTTGTATCTTCAGTTC[T/C]AGTGTTTCCTCTAGGCCACGTTGCCAAGTCTTAGGTTTCTCTTTCTGTTGTTCATGCTGCT | T/C | 6 | 11372152 | 0.538 |
| 6012883623 | ACACTGGAGGACACTGGTAGGGAGGAGAGTGTGGATTTGAGCCAAGAGAGGGCACAGGAC[A/C]GTGAGCAGTGATCCCTTTCAATCATATCATGTGGGAGGAGTTCTTTTCCTACATCTAGC | A/C | 6 | 12883623 | 0.829 |
| 6014629683 | TTCCCTCTGAATCACTTGGGCAAAAGGCACAGTCCCCTACCCCTCTACATAAAAGTAACC[A/G]GTGCCTTTAGAGCTCTTAAAAGGGAAGGAATCCGGCTTTATTTTATTGGACCAAACTTG | A/G | 6 | 14629683 | 0.921 |
| 6016421220 | CATTTCTAAAAAACCAACATCCTGTTAACATCAGCTGACCACACGCATATAGTGTCCTTG[T/G]CCTGTGTTAATGTTTCACAATCCCCCCTCCCTCTGTTACGCATGTTATGTTATAAATTC | T/G | 6 | 16421220 | 0.706 |
| 6018033419 | ACCCTCTGCCTCTCAGTGTTTTCTACCATCACTTCTGCAATGTTCCTTGGGTCTCATTGG[T/C]GGTGAGGAGATTAATGTAGGTGTCCTGTTGGGGCTGAGTACCCATGTCACGTTTGGGTT | T/C | 6 | 18033419 | 0.953 |
| 6021142260 | TGCCAGGACTGCCACTATGTAGGACTACAGTTGCTTCTTCAACTGTTTAAGCCTCTTCATC[A/G]GTCAGGCTTTCCGTCGTCAGCACCACTGCCATCTGTTGTTCCTGCTCACTGCTATTCCTGA | A/G | 6 | 21142260 | 0.925 |
| 6025496450 | GGGGCCAGGCAGAGTCTGTGTGGTATAACCAGGCTGCAGGAGGGAGTGGATGGAAGCCTC[A/G]GGGCAGTGCTGGGTTTCAGTGCTGAGGCAGGGGCCCTGGTTGGGGAGCCCAGTGCCTGG | A/G | 6 | 25496450 | 0.645 |
| 6032978412 | GTGCTCTTTAGCACTTGTGTAGTGTGCAGACAATTTTTGTTTTAATGATTTTGCTTTGTAG[A/G]CCTTCAGCTACTCTGTAGGTAGACTGCCTCTGGGCATAGAAAAGAATAAAAAAGAGCACAG | A/G | 6 | 32978412 | 0.878 |
| 6036190841 | GGGCCAGGTACAAAATTACTGTTTATCATTATTTCTTGTTCCACTTTGAGACCCGTTGCC[A/G]GGGAAACACCTGTTAGAGAAGCCTGCCCTGTACCCTCTCTGCTTCTCACAGAGTTTGTG | A/G | 6 | 36190841 | 0.718 |
| 6037905008 | TATAAAATCCTTACTTTATCTTGGATTGCAACATAGTTCTGCAATCATATGTGTGTTCTGT[T/C]TGTGGCTACTATGGAGAAGGGCACCTGAAAGACACCAACATACTTCTAAGAACCGTAAAGA | T/C | 6 | 37905008 | 0.878 |
| 6039447989 | TCAGCTACTCGGCTTCCTTACTATGAGCTACAGGTGGGCTGCAACACCCTCCAGGCTGTA[A/T]CATGGGCTCTGGGAATCCACATTCCATCCTCGCATTTAGCAGGGCAAGTGTTTTACATG | A/T | 6 | 39447989 | 0.656 |
| 6041140217 | TTTATTAGCAATTCCCCAGGAGGAGGAGAAAGCGGTAGAAAAGTTCTCATAACATAAACC[A/G]TACAATTATTGAAGGATTCCTTTACCTGTCTGAAGACAGTGATAAAATTGCATTATGAA | A/G | 6 | 41140217 | 0.811 |
| 6044507052 | TTGAAGGGAGAACAAGAGGGAGAAAGGATGAAGAGACCTGAGTCACCAGGCTAAGCAACTC[T/C]CCACTTCTGTTCCCTTCTCTCAGGAGTCAAGGCTTCTCACTATTTCTGGGTTGCATTTGGA | T/C | 6 | 44507052 | 0.924 |
| 6046019027 | AAGCCTACAAAAAAAAATCTCAGACCAAAACCCCAACTGCGAATGAGCCATATCTGAAGGG[A/G]AAACTCACAAAGAAAATACAAAATGTGAAGAATCACAAGGGGACATGTTTTAGGTCATTTT | A/G | 6 | 46019027 | 0.973 |
| 6049571373 | TTCCAGGTCTGTGACAAAGGAGCTTCAGAGCCAATTCAGAAATATTTTTGGGGACCAGTTA[A/T]TTCACCTTAACCCAAACTGTAGATCATGAGTGAGGAAGCTCTTGGATTTAGGTAGACTGGT | A/T | 6 | 49571373 | 0.915 |
| 6051304734 | TGCCTTTTACTCTTGAAATATTTAACATTTAGTCAATGAAGTTGCTTCTCCTAAGTTTAA[T/C]ATTGATATTGTGAAAATAAATGCAGTTCAGATTTCTTATTTCTTAAGATTCATTCTTCC | T/C | 6 | 51304734 | 0.83 |
| 6052974072 | TTCTATATACCACTAGTGTTTTTAGGGGAGAGGTTTTTAAATCCATCCAATTCATAATAG[T/C]CACACATACGAAGGCCCAGAACGAGGAATGAAGTCAAATATGTAAGGGGAGGACTTCTG | T/C | 6 | 52974072 | 0.98 |
| 6054555767 | AATTGAACTTGGTGTATTTTGAGTGGGGGAAGCAAAGGTGGGGGTGGAACTGGAAGGAAT[A/G]GGAAGTCAGTGAGATCATGGTGCATTAGAAGATTCCTAAATAATTAATAAAAATATTAT | A/G | 6 | 54555767 | 0.857 |

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|---|---|---|---|---|---|
| 6060907377 | TAGCAACCAGAGCTATATATGTGACAGTCACGCTGAGCAAGTGAATAACAACTGTTTTCAG[A/G]GGTGACTAGTTGTAATTGATTCTGTAAAACTCCAAACCCCATGCATTCTTTTCTCAATACA | A/G | 6 | 60907377 | 0.789 |
| 6064062891 | ACCACAGTAATCTTAGGTTCTATTAGCTATGCTTTCAGTGATAAATGTTGGAAGAAATTC[A/C]GGGTCCAAATGAAACTGGTAACTATTAGATTTGTAAGGTTCACTTTTCTATTGTCCAGT | A/C | 6 | 64062891 | 0.885 |
| 6067096063 | TCTTAGGTTAATATGTCTGCATGTTTCACATGGATGTGGAGATTGTTTGAAGTGATATTT[A/G]TTAATTCTTGGCTGTTTTTACAACTTATTTACTTCAACTTTTGGATACTACTTGGTCAC | A/G | 6 | 67096063 | 0.738 |
| 6068704582 | GAAGTTTGGACAGGTACTATGTTATTGATTCTCTACCTGTTTAAATTTTAAAAGTTGATGA[A/G]ATATTAGCATCACATAGCAAGATAGATCTGATTGTGTGTGGGGGGGCAGGGTACATGGTGT | A/G | 6 | 68704582 | 0.666 |
| 6070332650 | ATCAGCCCTTTCCTGTATATCGGCTGAATGTTAGTCCATATGAATTTTGACTCAGTGTTTC[T/C]AAATAGTCACATAAGATTATAGTAGGAAGAGACAGTGAGGTTTTTTTTCATAATTTTCAGA | T/C | 6 | 70332650 | 0.638 |
| 6073669372 | CTTCATTTGATGTTTTGAACAAAAAGGAAAGAAGTATAGCGTGAGGGCTGACATTTCACAT[A/C]ATGGATGTTGTTTAACAAGTTTTCACAAGCTGGCCCTGACTGTCAGAAATGAAATGAAACT | A/C | 6 | 73669372 | 0.899 |
| 6076890237 | GAAAAAAGTCTGTCATAGCATGTCCACGATCATTATTGATCTTCAGTGTTACACACATAC[A/G]TACTTCTAGGTAGTGGGCAGTGGGCAGGAGATCTGTCTGCATCAACGGAACTACAAGCA | A/G | 6 | 76890237 | 0.627 |
| 6078607389 | CAGTGGATATTTGGGTCTGTTGAAATTACCCAGGAGCAGAAAAGGAAAGGTCAAATATAAT[A/C]TATCATACATAACAATATTCTCGAATATGTTTCAGTGAGGATATTTTTCTCTGTCGTCACC | A/C | 6 | 78607389 | 0.755 |
| 6080367921 | TTAGAGTTGTTGGCTTTGTTCTGAGGCAGTCAGCTAGCTACTAACTGAACCTGATTTAGC[T/C]GCCATTCTGTCTCCCCATGTGGCTCTCACTGCCTGCTTCTGGTTCCATCCATCTTCTTC | T/C | 6 | 80367921 | 0.789 |
| 6085254123 | TTAAAACATATAATCATATGAAAATATAATTCATAGTACTTAAAAGTCAGAGGTGATATTT[T/C]CTTTCAATGGGTACGCAGCTAACTTTCAACACACAAACACACACACACACACACACACA | T/C | 6 | 85254123 | 0.853 |
| 6086850472 | AATTCTAAATAATCTGTTTTTGACACACATTGTTCTTTAGTCCCACTCTGCGATGACTGG[C/G]TAATTTTCTCCCCTCCCCCATAGCTCACTTGGATGAAGTGGCACAGAAAACTATTTCAG | C/G | 6 | 86850472 | 0.698 |
| 6088424825 | CATCTTGGATAGTATTTTTAAGTCTCCGAAACAAGATTGGCTCTCTTCTAAGGCTCACTAC[A/T]TTAAACTTTATTTTATCCTTTAAATTCAGACCAAACCTCATTTTTCTTTTGTTTACACTAT | A/T | 6 | 88424825 | 0.773 |
| 6091698875 | CATGCTGCGGTGATTTAACAGAGATGAGGCAAATCAAGGCGTTAAGTTACCACTAAAATA[A/G]TTTAAAATAATACCCGTAGTATCCAGTTCACTGAATAAAATTAAAAGGATAGAAACTTG | A/G | 6 | 91698875 | 0.796 |
| 6093557664 | GGAGGCATCAAGTCTGGGACCTCTGCAGGGGCCCATGCCCCACCCCCACCCCCTGTTTAG[A/C]TTGAGTCGGAGACGAGGGTACTCAGGCTCGAAGATGGGAGCTGGTTCATCTTAGCTGGG | A/C | 6 | 93557664 | 0.668 |
| 6095106508 | TTAATCTATTTCTAACCTTAACTGTTTGCCCTTGAACAAATGGTGGTAAAATGTGCTTTT[A/T]ACCTTAAAATCCCAGCAATTATCTTTGCTTCATCATACCCATGTTATGTCAAGAAATGG | A/T | 6 | 95106508 | 0.903 |
| 6096659693 | CACATTTAACATTCTCTTCTAAAACCACTTGAACCAGGTCCCCAGAGGTCAAATGACACTC[A/C]GCACCATGGTCTTCCATGTTCCTGCTAGAATGGCCTATTAAGCTCTAATTAAAGGATTCAA | A/C | 6 | 96659693 | 0.789 |
| 6099761123 | CTCGGGGAGAAGGGCAGGCAGCCCCAGTTATGTGCCAGCAAAGTGCTATAGCACCACAGC[T/C]TAACCCCCGGCACCACAAGAAGTTGCGCCGGGGGCTCAAAGGTAGTGTGTAGTGCTTAT | T/C | 6 | 99761123 | 0.766 |
| 6101338779 | TCAGATGCTCCTAAGAGCAACCTGACTGAAGACTACATGGCAAGGAATTTCTAGAAAACTT[T/C]CCTTAGCCTGTAATTCAAAGACGAGTGTTGTAATTAGACCCACTCATCTTGTGTGAGGTGA | T/C | 6 | 101338779 | 0.905 |
| 6102864807 | CCATTAACCATCTACAACCACATTTAAGTCAAGATGAAATAATATGTAAAAATGTACTGC[T/C]GAGGCTCGCTCACCACGTGTCAAACACCTGATGGCGTAAGGGCTGGTGGCCCCTTCATT | T/C | 6 | 102864807 | 0.785 |
| 6107754298 | CAAGCACGTCATCATGCTCTTTGTTCCTGTGACCCTCTGCATGGTCGTTGTGGTGGCCAC[T/C]ATCAAGTCAGTCAGCTTCTACACCCGGAAGGATGGGCAGCTGTATGTATAAGTGTTTCA | T/C | 6 | 107754298 | 0.951 |
| 6109613591 | TAGAAAGTTTCATCCAAAGGAGAGAAAGTGGGAGAAGGATGAATCGGGAAGTGGAGGCGGA[T/G]ACAGGGGCTGGTGTCAAGCAGGGAAAAAGATGAAAAGTGCTAAGCAGAACAAATGATCATA | T/G | 6 | 109613591 | 0.625 |
| 6114412200 | TAGCTTAGGTGGGCTCAACTCAGATTTGAATAATGTTCTCTGTTCAAATTTAAAGTCTTAG[T/C]TGATCATCTCTGAAAGAGCATAACCTTTTGGCTATATGGCACCCTGGAAGACCAGACTCCT | T/C | 6 | 114412200 | 0.842 |
| 6115919556 | CTGAATCTACTTAAAATTTTACCCATGGGATGCGCACATCATTGCACATATTAGCTTCTC[T/G]ATCCAGCCATTTAAAAGCCTGTATGTTTCTCCCTTTATTCCTGTTATTAGTACTGTTGA | T/G | 6 | 115919556 | 0.957 |
| 6120589080 | TCAAAAGTATACGCGAATGGGTCCATGGCTCCTGGTATTTGTAGCAGAGAATTGCCTTAT[T/C]TAGCATCAATAGGAGGGGAGGGCTTGTTGCTCCAGCGAAGGAGGATGCTAGAGAGAGGA | T/C | 6 | 120589080 | 0.679 |
| 6126772459 | TGGAAACCTGTTCTTACTGCTTTTACACGAGAAGCCACACACGTGTCTGCTGTAAGTTAAC[A/G]GCACTGTGACCTTAAGATTCCACAGGGCTGGGGGGTGGCAATGTCAGAGACCCAACTCCTC | A/G | 6 | 126772459 | 0.823 |
| 6130237987 | TGAGAAACTGGAATCAGCTTCTCTTTCCTTCTCTGACACAGCATAGCAGTTCTTTTTGCCC[A/G]TCTAACTCTATTCATGACACTGATCTATGTGCTTAATAACTCACCTCCCTCATTGTGACTT | A/G | 6 | 130237987 | 0.932 |
| 6131878479 | GGACTGAAAACTTTAATTGCATTAAAACTAAGCATTTCAGAGTGGGGAGAGGGTGCTGGAG[T/G]GATTCTCAACCTTCCTAGTACCATGACTCTTTAATACAGTTCCTCCTGTTATAGTGACCCC | T/G | 6 | 131878479 | 0.553 |
| 6133578383 | CCTGAAGTCACTTAGAGCAGGTATGAAGTTCCCATAGCATTGTGGTAGACTGAGGCTGTCC[A/G]GGTTGGGCACTATACCAATTAAAGGAACTAGTAGGGAACACTGTGAATGGTCCTGGTACAG | A/G | 6 | 133578383 | 0.879 |
| 6136673954 | GTACTAGCGCTGATCCAGGGGGTCAGATCTACTGCCGAGCACTAGCCACACAGAATGTTT[T/C]GGCCTGGGGTAAGAGGTTTCCTTTTCTTTTCAAACAGCCATCTGTGGTAGTATATCCTT | T/C | 6 | 136673954 | 0.914 |
| 6138214721 | ACCAGCAGGGTAAAAAAAAAGGCTAAACAAAGCATTATGAGATAATAAATCTCCCCAAATA[A/T]CCCTGGGACACGGGGTCTGCCCTTAAGTGTGCCTTGAATATTCAGTGAGAATCCTTTGCAG | A/T | 6 | 138214721 | 0.931 |
| 6141283496 | AATGATGACAATGAAAGATGTCTTCAACACTGTGTAAAAGGATGGCATTGTCTGGCAATAA[A/G]AGGAGAGGCTCTTGCACCTGTGATGCCTTGATTCTCTACTGTAGGGGAATGCCAGGATGGT | A/G | 6 | 141283496 | 0.74 |
| 6142802595 | AGTCCCCTGCTGGCTCAGCCCCAGCAAACAAAGCATTAGGCAGCAGCTAAAGGGAGCAGAG[A/C]CTACAACTGGGGCAGTAGAAGCTGTTCCCACTCCCTGCCTGAGTTCTCTCCCCTTGCCCTA | A/C | 6 | 142802595 | 0.656 |
| 6144550712 | CCTAGGGATATTTTGGATTTTTTTTTAGCGCAATTTGAATTTTTCCTGAGTTCTTTCTTGG[T/C]AAATTCATTATTACTATATAGGAAAGTTACTGGGATTTGTATATTAATTTTGAAATCTGCT | T/C | 6 | 144550712 | 0.614 |
| 6146192021 | AACTGCTGAGCCATCTCTCACATTTTTAAACATATTCTTACTGTGCAGCCCAGATTGACTT[C/G]GGACTTCTAACCCTCCAAAATGATTGCTTTCAACAGGTGTTTTTATCCTTTAAAAATGTCA | C/G | 6 | 146192021 | 0.956 |
| 7001590648 | CAGAAATGACAGCTGAGTTTGAGGAACCTAAGACATCTTGCAGCCTGGATCAATTCCAAAG[T/C]AGTATAGCACACAGCCAATAACCCAGAATCTGTTAGACATGGTGACACACTCTCACAGGAG | T/C | 7 | 1590648 | 0.984 |
| 7003226327 | CACTGTGCTTCTGGGAATTTTCCACCTGGTGGACTTGGTGTGTGAACCTCAGTAAATCTT[T/C]GGCAATATTGTAGCACAAATTACTCAAGTCTCTATTTTCTTGTTATATCCCCCAAGTCT | T/C | 7 | 3226327 | 0.812 |
| 7004873961 | TTGGGTTAATACCTATGAATGGGTCTTGTGCTAGTTTTAATTTTAGCTGTTTAGAAAGGTC[T/C]TTATTGATTCTGGTAATAAATGTAACATGTTGTACTCTCACCAGGAGCAAATAAAGTTTTC | T/C | 7 | 4873961 | 0.543 |
| 7008005145 | AGTTTCTACCCTCTCTGAAAAGAAGGAGATAGGGAATGAAGGGAAGGACTGTGTGAGACA[A/G]AGGCCAGGAAGGGTGCAGTGAACAGGATGGTCGCTTGATTTTTGACAAAGGAGTAAAAA | A/G | 7 | 8005145 | 0.667 |
| 7009511628 | ACGGAAGTTTGCAAAGGCTTTACTGCATTGACTGCATTTATAGGGCTTCTCTTCCGTATT[C/G]ATTCTTTCATATGTCTGAAGAAAACTCTTATGTGCAAAGGTACATTGCTTCTTGCCATG | C/G | 7 | 9511628 | 0.754 |
| 7012670072 | GGTAGGGAAGGAATAATTGGAATCCTCTAGGGACAGCAGTCACAAATGCATCCTAACTCC[A/T]TCAATATTCCTAATACTAGACAAGGAGTGTCACCTCAGCTGCTCAAGGCTGCTTTCCAA | A/T | 7 | 12670072 | 0.887 |
| 7024166242 | CAAAGACCAATGGGCTTCACAGAAGGTAACAGGGCAGCAACATTAAGAGTAGATTTAGAAG[A/G]TGTTGAGCCATAAGTACTGGAGGGAAGGGCACGCTAGCAGTAGGAGGCTTGGAAGTGCCCA | A/G | 7 | 24166242 | 0.915 |
| 7031949612 | TATTATTCTTCCTCCTCTTCCCTTTTTCCTTGTTGGCTTATTTTCTGTCGTTTTCTCTGT[T/C]AGGCAAGCACTGTATGTTCAAATGTAAGTGTAAAAAGGGCAGTTACTTGCCAGTTCTAG | T/C | 7 | 31949612 | 0.956 |
| 7033543143 | TCCACTAAGCTTCCCTCTTCCCAGATGATCCTAGTTTGGGTCAAGTCGACAAAACCCTAA[C/G]CAGCACAAACGTCATTAGCCATCAGAAAAGTTTCAAATTAAAACCGTTCTGAGATCCCA | C/G | 7 | 33543143 | 0.815 |
| 7035148996 | AAATACTTAATTATCTGCTTCTAATACAAAATATAATCCCAACTCATAAAATTAACTTCA[A/T]GCCTACAAATATTTACAGTGTGATTGAAGCATGCATGATTGGATATCAAGTCACAGCAA | A/T | 7 | 35148996 | 0.786 |
| 7038377962 | CTCAGTCTCTATAATGTTATTTTTGAGCTTCTTTAGCAGCTGGATTAAGTTAGGCTTCTAC[A/G]CGTCCTTTCTTTTCTTTTTTCTCATTTTACAGTATCAGAATGAGTTATGCAAAATCTTATC | A/G | 7 | 38377962 | 0.669 |
| 7043152083 | GTTGAGTTTTGTGCAGGGTGACAAGTACTACTCTATTTTCTTTCTACTATACGCAGATATC[C/G]AGTTTGACCAGCAGTACTTTTCTTATTTATGTTTGTTTTAGCTATCCTGGATTTTGTGTGC | C/G | 7 | 43152083 | 0.705 |
| 7044716533 | ACAGCGCACAACTACATATTATTATTAGAAACTATTATTCTTACTTTTGTTCACATACAT[A/G]CATGAACTATGGCAAGTTCAAGTGAAATGAGAAGTGGGAAATGAATTTAATCCTGCCTG | A/G | 7 | 44716533 | 0.854 |
| 7046228404 | ACTTGTCCAAAGTTGTTTTATCTAAATTAATCAGTGATGTAAAAATTAAACCAAATGAAT[A/G]GTGCTTTTGAGTTTGGGGATCTGTGGACTATCTAGGTAGTAGACTCAGGAAGGCAGCTC | A/G | 7 | 46228404 | 0.974 |

| | | | | | |
|---|---|---|---|---|---|
| 7047763375 | CTTATTGAGCTTGCCTTTAATTGAAACTTTAACAATCTGTCTAAACATATGTATTTTCAT[A/G]TTTAGAATCAGTGGCTATTAACATACACATAATATTAAGGCTTAAGCATCTTATATGGT | A/G | 7 | 47763375 | 0.659 |
| 7050867822 | GGAAAGACAGAACATTTCCTTGTGGATATTTCTTTAAATGGCTACTGTTCTGTTTTTTTTT[A/T]AAAATAGATTCCAGTGGAAATTTCTCTTATTTGAAGTTTTCTCAGCTCAGAGGACTTCCTA | A/T | 7 | 50867822 | 0.816 |
| 7052808733 | ACATGCAACTGCCAACTGAAACACAAGGTCTCAATTTGTTCAATAGGCCTTCTCATGAAGT[A/C]AGGCTTCAGCTACGGATTAACTCCATAAGCCTGTGTAGCTTCAACTCATTGTATTATTATT | A/C | 7 | 52808733 | 0.917 |
| 7054565301 | TTTGTCTGCGGTGTCCACAGATGGGATAAATGGCAGTGCTGAGACAAGCAGGGATAGCTA[A/C]CTCCAAGGGACACTAAAACTAATGCAGATGGCTAAGGGAAACATAGATTGTCTTGAAAA | A/C | 7 | 54565301 | 0.967 |
| 7061140277 | TTACTCAGAACACATAACTCCAGGGTTATGTTTGTTCTCTTGCAGCCAATCACAGCACAGT[T/C]CAAAAGACCTTGATCTCTAAGAACATTGATCATCGTGATATCCCAGTAGCTAAAACAATAC | T/C | 7 | 61140277 | 0.988 |
| 7064576568 | ACTCAGATTCTCTCCTTAGCTTCCTAGCCTCTAAAAATTGACTTTGAAAATTGAAGCAAAA[A/C]GTTCAGATGTGGGTGTTATATCAGAGGGTTCTGATGCGTCTCAGTTCTGATTGGCTGTCTA | A/C | 7 | 64576568 | 0.787 |
| 7066130885 | AGTAATAGTAATAGTTTTTTATTATCTAGTAATAAAACCCTGCCTAGTGCATGGCCTCTG[T/C]GCTGATCCAGTTACCTCATCTTGGGAGATCTCCCACACCAAATACTCAAGAGTTCTGGA | T/C | 7 | 66130885 | 0.965 |
| 7067766886 | CTGGTTGGTGAGGTTTAGATTGCAGGGGTAAGGGGAATGTCCTGAGAAGGGTGTGCATAGG[T/C]CAGCAGGAATTTCCTTGCCCGTCTCAGCCCTTCTAGCCACTGAGGTGGGAATAACTGCTGT | T/C | 7 | 67766886 | 0.837 |
| 7075273694 | TGCAGTTAAAGGACTCAGCAGCCTGTATTTTATGAACAAAATGGAGGAGATTTCAGTTTGC[T/C]CTGAGGGTTACAGACAGAAGAACTACTGCTTACTCTCTGTTCTGTTGTTGCAAAGAGATGT | T/C | 7 | 75273694 | 0.955 |
| 7078441808 | TAGAATTCTATGTGAAGTGAATATGGTAGATTCCAATACTAGAAAATCATCGACCAATCAC[A/G]GAATCCCAAGTACAGACAAACATTAATGATGTGCCAACAGATATGCAAAATAAGTGATACA | A/G | 7 | 78441808 | 0.83 |
| 7086661510 | TCCTTAAATAAATAAGACTAGTAATAGAATATCTAACAAGAGCCCTCATACAGATATTTT[T/C]TTCAGGAAGTGTAACTTATCTTTATAGCTGAAATTAGATGAAACCCACTGATCAAATTT | T/C | 7 | 86661510 | 0.621 |
| 7088227484 | GTGTACTTACAATGTAATAGACTTGAAAGAGAGGTATATCTGTGCTTGGATCCAAATCTTA[A/G]ATATGATGTTGATCAGAAAAATGACTGTAGCATCAAGTAACAAACCTTATAGTTCAAGAGA | A/G | 7 | 88227484 | 0.912 |
| 7091402105 | CCACTGAAGTGCCAAAATGGGGAATTTTGGTAAGAGATGAAATGTAGTATCTGGTGGTTG[A/G]TAATTGATAAGGAAACTAGAATAGAGTACATTCAATTAGACAGTGACAAATGTCTCTAA | A/G | 7 | 91402105 | 0.728 |
| 7092964847 | CTATGCCAGCAATGCTATAGGAATCGAACCCAGGGCATTTTGCATGCCAGGAAAGCACTCT[T/G]CCACTAAGCTAATCCCCATCCCTTCCATGTATGCCTCCCAAATAGAAATATAAGATACAAA | T/G | 7 | 92964847 | 0.904 |
| 7095066786 | GCCAGAAGCTTTGTAAACTGCCTAGGGTTTGGCCCTAATTTGAGTTTTCCTGATTTCTCCA[A/G]TTTGTATTATTTCTTTGATTCCATGCACCTTCTGTGTTTCCAGTATGGACTATGTTTTGAA | A/G | 7 | 95066786 | 0.9 |
| 7101196778 | ATGGAAAGCAGCACCTTCCTTTTTTGTCCTTAAAAGTTCAACCTAAAGCTACTTCCATTT[T/C]CAGTAGGCCTTGCCCTTGAACTCCAACCACCAGAGAACTGAAATCTCTGCAATTCCCAA | T/C | 7 | 101196778 | 0.993 |
| 7102913634 | CACGTAAGTAATGTATATGTTTGACATGCAGGATAACTGATATATGACACCCCCAAAGGA[A/G]TAGCAAACCACAGGTTTCCTTAGATCTATCCAATCAAGAGTTAGATTAAGAAGGACAGG | A/G | 7 | 102913634 | 0.844 |
| 7104438040 | TGAAGAAAGACTTTCTTCCAAGCTTACTTGTGGACTCTGGGGGTTGAGAGGATCTCATTCC[T/C]GTCTCTGAAGGAGCAAGGACATCTTTAATATTTAGTTATCTGGAAGCTAAAGCTATCCCAG | T/C | 7 | 104438040 | 0.875 |
| 7105956466 | GCATGGCACAGACATGGAGATAGAAAGGCCAGCTCTCACGCACCCTGCAACTGTGGGCTTC[C/G]GTCTTCATAGCCCTCACGCACCCTGCAACTGTGGGCTTCCGTCTTCATTCCCTTCCTGCTA | C/G | 7 | 105956466 | 0.66 |
| 7107555394 | GAAAACAATGCAGGATATTGGCTATGATATTGATTGCCCTGCACAACTTGATGGTAAGGAA[A/G]TATTACAGAAGATATATTTATATATATCATCAAACATGGAGAAATTTGGCTGGTGTCCAAC | A/G | 7 | 107555394 | 0.534 |
| 7110711496 | ACAACTGCACAAATGAACTCATAGCAGCTGTGTTTGCTTGCACAATTTCTATCATGGAGC[A/G]GGGAAGGCTTTATGAATCCCCAACCCCACCCCACACCCCAGCCAGGAGCTACTGTCAAT | A/G | 7 | 110711496 | 0.954 |
| 7115986732 | CGTGTGTGTGTGTGTGTGTGTGCATGGAGATGAGTGAGTTAGTATGTGTGTGCACACACATG[T/C]GATATAAGCTAGAGGCTGCCATCAGCCACCTTCCTTCACCACTCTCTATTTTGCTGTTT | T/C | 7 | 115986732 | 0.805 |
| 7117925849 | ACTGCAGGTTAGCCAACTCCAAGTCCCACCCTACTCAATCTGCTGCTGTCTTCTCTAGAGG[A/G]AAAAGTACACTTCAGGCACTAAAACTATATGGCCTTTAGTAGTTTATCCTACTTCTGACGA | A/G | 7 | 117925849 | 0.942 |
| 7119813204 | CCCCTATGATTCCTTACATAGGCCATTTGGCCATGTGTCATCTTGGCCTCTTGGTCCACT[T/C]CTCTCTTGGTTCTCTTGCCTGTCTTCGTTAAGGTTTTACTGACACGACCCAGGCAACTC | T/C | 7 | 119813204 | 0.866 |
| 7121418726 | AACCGGCTTTTGTATAGGGGCCATCTCTGTGGGGATGCTGGGGAGACAGGGAGGCTGGAGA[A/C]AAGGTGCTGCCACTGAGGACTGCTTCAAAGCTGTAGACTGATGCAAGGAAGAAGGTGTTGC | A/C | 7 | 121418726 | 0.708 |
| 7124933938 | GCTTCGGGAGCTGTCCAGGGTAGATGCGTACCAGCAGGAAGTCTGCGAAAGAGCATAGTC[C/G]GTTCTGGAGGCTTGAGTGGATCTCTACAGCAGCTGAAGGGGCAGGCAGGACCTGGAGGA | C/G | 7 | 124933938 | 0.947 |
| 7128013636 | AGTGAGGTATTCATTTCTTTCATCTTGTCTTTGAAGCCTGAGATTCTTTCTTCCGTGTCTT[T/G]TACTCTCTTGGTGAGAACCACCTGAAGTTTCTGTTTGACTTCCTAAATTTTCTCTTCCAGT | T/G | 7 | 128013636 | 0.775 |
| 7131041216 | GAAGCATTTTTTTGTTATGAAACATTTTTCCGTAAAAATAATTTTTATGGTTCAAAACTC[T/C]AATTTTAATTTGTCATAAAGGAAATTATGTGATCTAATGACTATATTTATTATACTTAC | T/C | 7 | 131041216 | 0.522 |
| 7132553862 | CACAGTCACCAAAACAGCGTGCAGCTCTGCTCTTGCACCATGGCTACTGAGACCTTAAAC[T/G]TGGGCTGGGCTCTGTACCAAACCCCAGGATGGATGTCAGGGGGCACCTGGCTCTTGCTT | T/G | 7 | 132553862 | 0.924 |
| 7134076525 | TCTGAAATCACCTCTGCTCGTTTAGAATAGATTTGATAGCACAGGAAACTTGTACATGAAG[T/C]TTGTATGAAATCTGGGAGCGGAGCACCTCACCGTTTTTCTTTTTTGTTGTTGATGTTTCTA | T/C | 7 | 134076525 | 0.945 |
| 7135617602 | ACAAAGTTCCAACTACTGATGGTTTTCTGTGTCGGTAAGCACGGTCACCAGTGAAGGCCA[T/G]TGTGCCAGGGCCCCTTACGGGTCTCAAGGATCCTCTCCCCCAGAGTTCAGAACAACTCC | T/G | 7 | 135617602 | 0.609 |
| 7138802842 | CATGAACACTGAGCAGGAATGGAGTGCTTTCCATCTTTATCTATAGATACTTACACAGATC[A/G]GCCCTCATATACAGACTCATGTGTACATGGTAATTTTAAGGTTATGCTGTGTGCTGTGTCT | A/G | 7 | 138802842 | 0.587 |
| 7140344560 | TCAACCCCACCTCTTTCTCTTTTCCCCAGCTACTTTATTCACCAATCACAATCAACTGGG[T/G]CACTCAGTGTCTTATGAGCAGACTCACTCGTCTTTGTGGCAAACAGCCTTGGGGGCCCA | T/G | 7 | 140344560 | 0.5 |
| 8000035169 | TGTTTTGTTTGTTTGTTTGTTTGATTGTTTTCTGGTTCATAATGTCTGTAAGCTCCAGTA[T/C]GCCTCTATTTGGTTTTTCTTTGTATAGCCTGACTATTGATGAGAGTGGGTTATTGAAGT | T/C | 8 | 35169 | 0.658 |
| 8001536108 | TCTAAAAAAAACTGCAAGGACAAAGATGGGTGAGAGACTAAGGGAAAGACAGTCCAATGA[T/C]TGGCCCAACGTGGGATCTATCTCGTGGGGCATGTACTGAGGCCTGACACTAATACTGGT | T/C | 8 | 1536108 | 0.637 |
| 8004634330 | TGTCGGGCTCATGTGACTATGGTGAAGTGACTTGATAGCCTACAGAAAAAGGACTCTTCTT[T/G]CCTAAGGGGTTGGGGGGAGGCTCTATCATGATTGGCTGGCTATTTGCCTGCTTTCAGGCTA | T/G | 8 | 4634330 | 0.94 |
| 8006157839 | ATACACAACGTGGGATAGTCAACAGTTTAGCTCTGCCAAAACAGAGTAGAGAAGTCCTTAA[C/G]AGTTTCTTCTTCATTTCAAGGTTTGTCAGATGGTTCTGGAGTGGAAAACTAAAGACAGATG | C/G | 8 | 6157839 | 0.698 |
| 8007676104 | TCTATTCATACAGAGGATCACGTCCTATTCATACAGAGGATCACATCCTATCCATACAGA[T/G]GATCACATCCTATTCATACAGAGGATCACATTCTACTCATACAGAGGATCACATTCTAT | T/G | 8 | 7676104 | 0.672 |
| 8009250989 | TAGAGTATAAGTGTTCTTAACTCTAGGACTTGTTGGTGTGTCAGCTCCATGCGAGCAGTCC[A/G]GGGTACGGAGGTTTAGATTGACCAGCTGCTCTTGCTACAACAACTGACTTCAAATGTAATT | A/G | 8 | 9250989 | 0.921 |
| 8010819817 | GGGGGCAGCCGGTCAGCCTCTCATAAGTATTTGTTTTTTTCCAGTACAAACAACCTCAACG[A/C]GGCCAAATGAGGGCTTTACAGCCCCCAATCTCCATGAAAGTTCTCAAAAACAAACTCAAAT | A/C | 8 | 10819817 | 0.97 |
| 8012459253 | CAGTCTTGTGGACTGAACATCTACTGACAACTCCTGGATTCTTGGACTTTGCATTGGACAG[T/C]CATTGTTATGGTACCCCAGCCCCTTAGTTCTGTTCCGTTAGAGAACCCTAGTACATATAAT | T/C | 8 | 12459253 | 0.753 |
| 8019389163 | TCTTCAGGAATATGAGACCCACAGGTCTCCTTGAGGAACTATAAGCTATAGCTGGTTAAAT[A/G]TTGCTAGAAAAAAGGAAGTCATATTTTTGAGTGATATAATCACTAGCAAATTGCCCTTTCA | A/G | 8 | 19389163 | 0.652 |
| 8021044500 | GACACACATCTGTTGTCCCAGGAATGGCAAGATGGGAGGTGGAGACAGGTGGAGTCACAGA[A/G]GCTTCGGGCCACCCAATCTGACCTACTTGGCAAAATTTCAGGCCTGTGAGAAGCTCTATCT | A/G | 8 | 21044500 | 0.809 |
| 8024523304 | TGCCAGTCTACTCTACCGTGCTTGACCTTAACAGTCATCCTTCCTTCACAGAATAAGTTGT[T/C]CCCTCCTTCTGTGGCCCTCCCCTACCCCCAGCTCAGTAGAGAGCTCCAGATTCATCTGCCC | T/C | 8 | 24523304 | 0.95 |
| 8029283497 | CAAAATGAAGACCATGAAATGTCAAGTCAAAAGGAAGCCAGAGCCCGTCCCAAGTGGCCTC[A/G]TGGGTTTATATCTCCCGTTACACAGATGGTATGCAGGTAAAAAGTGTCCTAGACAGGATTG | A/G | 8 | 29283497 | 0.907 |
| 8030788581 | GTGTGTGTGTGTGTGTGTGTGTGTGTATTTGTGTATGATTTTTCAGATCTCTGTTAATTAACT[A/G]ATCAGATTAGAAAAACACCATGGTAGATTACTGGAGTGGTTTAAAGGAGAAATACCCACCA | A/G | 8 | 30788581 | 0.744 |
| 8032321266 | GCAAGGAGTTGCTGAAGATTGGCAGTTACGGGAAAGGAGAAGAAATCTGGGCGGGACACCG[A/C]GGACCATCCAGCATTCTGTGACTCTGAGCGGGGCAACTAGGACTTGGATTCCTTACTTGGC | A/C | 8 | 32321266 | 0.758 |
| 8038009549 | AAATATGTTTGGTAACTGTCAGAGAGACAGAAAGGATGAGGGCTCTAGAAGGCAGCCAAC[A/G]TGTTATCATAATCATGCACATTACCTACAGGTAGGAGGCAGACTAAGAAAGAGGATTTG | A/G | 8 | 38009549 | 0.992 |

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|---|---|---|---|---|---|
| 8039630834 | CCACAGCCCATCTACCTAACTATAATATACACTACATAGAGGTGGTGGGATATACATTAA[A/G]AATGTGCTAACATTTTGTATTAAGAATTTTAGTTCCAAGTTTGTAATGGAGTGGTGTGA | A/G | 8 | 39630834 | 0.639 |
| 8041550093 | CATGTGATATGCTAAGCAGTCCTAGTATTTCTGTGGAGCCCATGTTGAAAGAAGCCAGTT[C/G]CTTGCAATAGCATTGACATCTTACATTGCCATTTATTTCTATAATTTTTTGATAATGAA | C/G | 8 | 41550093 | 0.883 |
| 8049983558 | CCTCTTATCCCACAGGTCTGCCAAAAACCCTTCCCTCTAGAATGAAGGCAGCCACTTTAAT[A/T]TCATTTCTCCTGTTCTTCCTTTAAAGTGGATCTGAGCATGAGTTCCATAGACCATGGCTAC | A/T | 8 | 49983558 | 0.913 |
| 8051530223 | GGTCCTCAGGTCTTCTTTGCATTTAGCATATGAGTTCCCTCCTTCCCTTGGCTGAGAAGAG[T/C]TGAGAGGGATGTGACCTAGAGATGTAACATCACATAATGGCCAGGTGTCTGCGCCCATGAA | T/C | 8 | 51530223 | 0.883 |
| 8054887505 | TTGAAATCTCAGCACGCCATAGGCTAGAACAGGAGAGTCAGGAGCTCAAATCACTCTCAG[A/G]CACTACTGTGTTTGATGTCATCCAGAGCTACATGAAGCCCTGTCCAACAGGACTTTTTC | A/G | 8 | 54887505 | 0.928 |
| 8059837778 | CAGGAAAACATAACATTCAGTCAGTACTAAAAAGACAAGGCGTAGGTATTGTCTATGTGAC[T/C]GCTGTACTTACCTAAGTTGCTGTATGTTGCGCTGCACGGACTCACGTCTGTAGGATCCGAA | T/C | 8 | 59837778 | 0.871 |
| 8064417055 | ATTATATGAGCACATAATATTAAATCTGGGGCACAATTATGAAGATTTGATTTCAAATGT[A/G]CTGAGCCTCTAGCTAGACTACTGCAACCCAGCAGGATTTCCCACTGGGGCCACATGATC | A/G | 8 | 64417055 | 0.792 |
| 8066103802 | ACTCAAGGACCCACCAGTTACCTCAGTTTCTCAACAAGACTCAAAGGATTGGTTCAGCGTG[T/C]GCCACCAGCTGCACCTATGTCAGCCCGCAGAGGTCAGAGTAGGACAGTGACCCCCTGCCTC | T/C | 8 | 66103802 | 0.777 |
| 8067960675 | ATGCCTGTCTGGATGCTGCCATGCTCTCACCGTGATGAAAAGATGCTGTAAGCCAACCCCG[A/G]TTAAATGTTCTTACAAGAGTTGTCTGAGGTGGGAGTGTTGGAGAGGTGGCTCAGCTGTTAA | A/G | 8 | 67960675 | 0.957 |
| 8072132143 | CCAATCTAGAGCCAGTCCGGTGGAGGCATTTTCTAAATTGAGCTTCCCTCTTCCCAAGTGA[T/C]TCTCCACCATGTCAAGCTGTCATAAAATGAGCCATCAGGCCAACATACGGAGAAGACCGTT | T/C | 8 | 72132143 | 0.542 |
| 8073971857 | CCTCCATGTTTCTTCATCGGTTCCTGCCCCCAGGTTCCTGCCATGACTCCTTTGATGATGG[A/G]CTGCAGTGTGGAACTGTAAGGTGAAATGAACCCTTTTTCCTCCACATTCCTTTTGGCCATG | A/G | 8 | 73971857 | 0.755 |
| 8075515604 | GTGTGTGTGTGTGCGCGCGCGCGCATGCACGCGCACGCTTGCATACTTGTGCACATATGTG[T/C]ACACGTGCTCATGTCCAAGCACATACCTGGTATAGAAGATTCACAGAGAATGTCACTGTGC | T/C | 8 | 75515604 | 0.972 |
| 8077062114 | CTTGGACTTTAAGTCCTGAATTTCATCCTCCTACAATCAATGATATTATCAATTATGTGAA[A/T]AATGTACAAGATCTGCTAATAGAATGCACAGCAGAAAACAAGAGTCTCAGATGCTCTCTGA | A/T | 8 | 77062114 | 0.716 |
| 8080228166 | GGGGAGATGAGCCCTACTAGGTCTCAGATTTTCTAGAGTCAGAGGACTGGCCTGGCCACTG[A/G]AGAGTATCTGTGAAGACACTTTCCGGGCACTCCCTCGGGAGCCTCACCCACCATGCTCAGG | A/G | 8 | 80228166 | 0.946 |
| 8081834042 | TAAAAAATGACCTTATCTATGATAAGAACACATACCATGATTGTTGGACATAAACAAATCA[A/T]GATTCAGTTGAACTGGAAGGTCTCTTTCTGGTGCTATGAAGGCTGCTGGAGAAGAAATGTC | A/T | 8 | 81834042 | 0.91 |
| 8083476331 | TCTATGGGCACTTTACACACATGATACACAGATATACATATGGGAGAAGGCCCATGCATGT[T/C]AAGTAAAAATAAGTATTGGGGGAAAAAAGAAAAACTCTCATCTCAGTGTCTGACAAGTGCT | T/C | 8 | 83476331 | 0.961 |
| 8085387993 | AAGGCAACTGGTAGTTCTACAGGAATCAGAACAACCAGCATGGCAGGATACCCATAATGGC[A/G]CCAAAGCGGCGTTAATACCTTGGTGGTAACCAACAGTTCTCTAACCGGACTCAAAGGCTGC | A/G | 8 | 85387993 | 0.819 |
| 8086960225 | CTGCTATGAGGTCTAAAACATCTTTAGCCATCTAAAGATGTTCAAAGAAAACTGTTGAGGT[A/T]ACGGAAATTAGAAAGTCTCCAATTTATATGGTAAATAGTTAAAACTGAATCTGAGCTTTCC | A/T | 8 | 86960225 | 0.852 |
| 8088545231 | CACCCAAAATTTATATTAAAACTGCAGCAGGGTTACAGTCTCTAAGCCAAATCAGAGACA[T/C]ACCCACACCAAAGTGTGTGGAAAAAGGCTTTCAAAGTCAAAAAAAGCATTTACTCCACT | T/C | 8 | 88545231 | 0.899 |
| 8091656605 | TTTTTAAACTGATTAGGGGAAAAGCATCTACATAAATGGCAATGCTACAACTACTCTGAAA[A/T]ATTCAGAGCTCCCCAGACATCAGTGAGGGGTCAGTGTAAGCAAAGACAGGCAAAGAACAGA | A/T | 8 | 91656605 | 0.979 |
| 8096468057 | GAATTTCTTATAAAAACAATAGATGATGTTGTGTGGATGGAGCAGAAGTGGGCAAAAGAA[A/G]AATAGGGGAAGTGGAACGAATATGATTAGAATACATTGTATAAAAGTCTCAAAAAACTA | A/G | 8 | 96468057 | 0.948 |
| 8101253044 | GAACTCACAGCTTTACCAGGTTGGTTCATTATACTTTGCTTCTCTTTCTGAATATACTTA[T/C]TGTATTGTATATTCTACTAGTGGCTGTATATTAGCAATAATGGCACTGAAAATGAATCG | T/C | 8 | 101253044 | 0.505 |
| 8104337188 | GTCCCCCGTCCCCACATCTGCTCCACCATTTGTTTTTAGTATTCTCGAAAGCCATTTTGTT[T/C]GTGTGAGATAAAATCTTAAAGTGGTTTTAATCTGCATTTCTTTAATGGCTAAGGTTGCCGA | T/C | 8 | 104337188 | 0.704 |
| 8109079791 | AGTCCTTTTTTTAGCCAGATCACCTACAGATCGCCTCACAGAATGTAGTTATGTGGGAGC[T/C]CTCGGCCCATGGTTGATCCACTCCCACTGTTCCTCAGCTTCACTACTTTGGCTCCTTCT | T/C | 8 | 109079791 | 0.951 |
| 8110621346 | CAAATTACCTTTAGAAGCTTAAAAACTCTTCATATGTCTTAGATCACGCAGTAGTAGAAT[A/G]TGTGCCGTTTTACCTAGGGAGGCTGAGCGCATACCAGCAACACTGGAAACCTTATTGGG | A/G | 8 | 110621346 | 0.987 |
| 8112131352 | TTCTTCCAAAGCAGGCACACTGTTATCCTGTTTCTGTAATGTGCACAATATGGGCCTGGA[T/C]GCATATGGATGAGCACTCTGTGCCTTTGCTGCAGTGCTCTGACTGCAGAGATGTGACAG | T/C | 8 | 112131352 | 0.932 |
| 8113672002 | CACCACACTTGGCTACTTTGGTAATTTCTTAAAATGTTAAACATACATTTACCGTATGGCC[A/T]GGCAACCCTGCCCCTAAGTATCTACATCTACACAAGAAAAAATTAAAGCAATGTCCACATC | A/T | 8 | 113672002 | 1 |
| 8116787492 | TGGATTTTCTAGTTTCTGCAAAGTGTATGCTGATTGGCGTCATGACGCCTTAGGGAAGTT[T/G]CGGGCTGGCTTTGTGTGTGTGGTATGTGAGGGACCACCGGATGACATTGCTTCATGGTG | T/G | 8 | 116787492 | 0.786 |
| 8118338566 | GACACACGAGCAGCAAGTGTGCAGTAAGATACTGCTGAAGAGCACTCGATTCTTCCAGAC[A/G]TTCCACTACCAACCTGTTTCAACCCCACTTAGTCAACCCAACTCAGGCTGCACAACCGC | A/G | 8 | 118338566 | 0.882 |
| 8120093696 | TGGACCACAAGCAACTTATATAGATTGAAAAATACCAACCTGAAAAGTTGTGACGTACAGC[A/G]CCCATTTACATAAAATTCCTGTAATAAATTATAGTGGTGAAGGGTCACAGAGATACTGATC | A/G | 8 | 120093696 | 0.904 |
| 8121605051 | CACTCCACTACTTATGTCTGGCTCAGTTCCCACAAGCAGGCAGAACCCCAAGATCAAAAC[T/C]ACAGAGGAGTTCACGTGACCTGTGCACCTACAACTTACCACGGGACTCCAAATAGTTCT | T/C | 8 | 121605051 | 0.869 |
| 8123189500 | ATTTAGAAGTTTCTATAGAACACTTTGTAATGTTGAGACTGGTCCCTCAAGGAAGGCATG[A/G]TGGGAGGACCCTGAGGCAGGTAGTCACAGGTGTCCACAGTATCCTAGGCTCTTAGGATG | A/G | 8 | 123189500 | 0.625 |
| 8124822775 | GGACCCCCTGCCATGAGCTATCGAGAGCCCCCAGCCAGGTGGGTTTAATCTGCAGCCCTC[C/G]CCTGTACACTCTTCCTACATAAAGCTTCCAGAAGCAGCCCTGGAGGAGAGTTCAGCCAT | C/G | 8 | 124822775 | 0.974 |
| 8126447368 | ACTTTAATGGGAAAGGATGTCCTTGTCTAAGACCCTAAGATGTAGTCAGTCTTACTTTTTC[T/C]CCCTCATTAAAACTATTTCTGATTTGGGCTTAATGGTTTTTTTATTAAGATTTATTTATTT | T/C | 8 | 126447368 | 0.764 |
| 8127969315 | AGCCTTTCATTACTGCAAAGCAACCCTAGAGTTCGCTGGGCCACTTGCAGATGCAGCTGAC[T/C]CAGCACGGGAGCTGAGCTGTGGTCAGCTTGCATTCATGTCAGGGCACTGCACAGCCAAACC | T/C | 8 | 127969315 | 0.738 |
| 9000007599 | TAATATACAAATTGATAGTACATTTGCCTAAGAACTTCTAAGGAATATACTTTGCAATGTT[A/G]GGTTTAGCAATTTTGCAAACAAGAGGAGAAAGTTAAAGTTGGAGTGTACTGTTCATCCATC | A/G | 9 | 7599 | 0.924 |
| 9004638687 | AAACTCTGATAGCTGTAAGAGTATGGGATTATATGTTCTACTCCTCTATTCTGTCCCACTC[A/G]TCAGTGTGTCTGTTTGTATCAGTGCCATGCTGTGTTATGATAGTGCTGTGGCACGACTTGC | A/G | 9 | 4638687 | 0.949 |
| 9006153383 | ACTTCCGGAAAGGCGGTGTGCTGGTGAACGCCGTCTTCCAGCTTGGCATGGCCAACGGTAC[A/G]GAATGCTTTACCTCTTTTCTTGTTCCGGTGATCTTGGCTCTTCTTCCCAGCGTCCTCCATC | A/G | 9 | 6153383 | 0.977 |
| 9007696760 | CATACATCAGAACTCGTAGAAGACTGTAGACCATCTCAATCACCCTCCTTGTTATACAAA[A/G]AGGAAATCTAGCCCAGAAAGGAGTGACCTTGTGCAGTTGAGAAAGCTGAGAGGGTCCCA | A/G | 9 | 7696760 | 0.956 |
| 9009290725 | TAGACAGGAAAAAAACTGGTACTGAAAGTGACTTGTCCTCAAACACACAAAGGCCCAGGGT[T/C]AAGCAGGAAGGGAAACTGATTGTATACTAATCCTCTTGTATTCCCTTCCCCCTTTTCCTGT | T/C | 9 | 9290725 | 0.872 |
| 9010824989 | TGACCGGGTGTCTCTGCCAGCATCCCTGACCTAGTCTCTGTACCCTCACCTGGAAGCAGGC[A/G]GCAGCATGATCCTCTCCGGGTGACTTCTGCTTCACACCTCCAGTCCCCTGACAATGTCACA | A/G | 9 | 10824989 | 0.664 |
| 9012529501 | GTGGGTGCAGGGAATTCCAACCCAAGTCCTCATGCTTTCAAAGAAAGCGCTCTTAGCCAC[A/G]GAGCTACCCTCCTGCCCCAGAGGTATTTCATTTAATAAAAGTTGTGTAGACATAGGGAG | A/G | 9 | 12529501 | 0.716 |
| 9014275270 | CATTGAAACAAATATATATTTTAGTAACCCCTTTTTTTCCATCAGAGTGAATCTAAAATC[T/C]GAAACTGCAGGTGGCTAACGATCTGTTTGAGATTACAACATGTGAATAATAACATAATA | T/C | 9 | 14275270 | 0.989 |
| 9018112709 | GAATCATGGTTCTTACAGCTGGGGAACATCTGGAGGAAACAAAGTGTGCCCCCAAAGCTCA[A/G]GAAGTATCAAATGCTGAAGTAGTCAGTTGAAGGGCCTGTTTTTTGTTTTGTCTTGTTTTGT | A/G | 9 | 18112709 | 0.977 |
| 9019698843 | GGTGCTGGGAATTGAACCTAGGTCTTTGACTGTTCTAAGTGCACCATCACCAAGGAGTACT[T/C]CCAGCCTCTAATGATACTGCCCCTGACTTTAGAGGTAGCAGAGAGGAACTGGAAGCTATCG | T/C | 9 | 19698843 | 0.888 |
| 9022924893 | CCATATAATTAATGCTTATCGGGGCGAATCACTTTTCAAAACGAAAGTCTTATCCACCCAC[A/G]GTGACTACCTGGCTCGAACGACCAGCTCACACAAGAGTTAGTGAACAAGATTGGGTGGAGT | A/G | 9 | 22924893 | 0.886 |
| 9024499905 | CAGTTTTATTACTGTTTCCCAGCATAATGACACAAGAAGTTTCAATAGCCGGTAGTCATT[A/G]CCTGTCAATTTCTAGTCTCATTCATTGCATTCGGGGAGACTTCCTGTCACATAGATGTA | A/G | 9 | 24499905 | 0.876 |
| 9026201841 | AAACTGCCATTTAGATGTAATCTAAAATAAAAGAATAAAGAAAAGATCAGAAACACAAAA[T/G]TACTGTGATTATTGTGCTAGTGTTCACTCTAACTTAACTTTAGAGATTGCCTAGAAACC | T/G | 9 | 26201841 | 0.763 |

| | | | | |
|---|---|---|---|---|
| 9028315173 | TTACAACAATAGTTTGTTCTCTTTGTTTTTTATATATAAATTAGTGTCTTTAACCGCTAA[C/G]GATCCTGTAAGACAGCACTTTTTCCTTTATTCTTCTGAGAGCTTATCTCTTAATTGTCC | C/G | 9 | 28315173 | 0.876 |
| 9035235062 | CTTTGCCGCTGGGAAGCTGTGTGACCCTGAGGCAGGTTGTCTGACTTCTCTGAACCTCGGG[T/C]GTGACATCCGTAAGGCGTGTGCAAATGTTCAGCCCCAGGTAGCGCAGGAGAGATGGGCTTC | T/C | 9 | 35235062 | 0.872 |
| 9038814990 | GTCTTTTTTGCCAGTGAGGATGCATCTGTCTCTTTGAGGACTTCCTGTGTTCCAAGCAAGC[A/G]CTCTGCCACTGAATTACACCCAGCCTGAGTCTTAGGTCTGAGGCTGCTTACCTCAGCCTCA | A/G | 9 | 38814990 | 0.842 |
| 9041986839 | GGGGAAACTTGGGAAGATCTGGCTTTGGACCTTGGCTGGGAAAGTGTTCCTTCAGTCCTTC[A/G]GGCCTCGCACTTTGCAGACTGCTGGATAGCTAGAATGGCTGACTTGTTCAAGGTTCTCTAC | A/G | 9 | 41986839 | 0.938 |
| 9046897982 | CACAGGGAAAGGTTAACAACCTGACCTGAGTGTTTTCGAAAGTCTTTGCATTTTCCTCAG[A/T]GTTGCCCATCTGAACCCCAACGTTCATTCCAAACCAAAAAATTGGAAGGGCATCGTTTT | A/T | 9 | 46897982 | 0.941 |
| 9053618889 | TTCTAAGACAGCCAGGGCTTCATAACAAAATGAAAATAATAATCTGGAGGGTGACAGAAG[A/T]AATCACAGGACATCGACCTCTCTTCCACAGGCCTACAGTACAAACATGAGCACATACGT | A/T | 9 | 53618889 | 0.926 |
| 9055129164 | AAACTATAGTTTAAATTAGCTCTCACTCTTCATATGATATTTCAGTCCTCGGCTTCGCCC[A/G]TGTTTTCCAACCAACCAGGATTAGTACCATTTTCATGCTTATATTGTAACAGGTTTGGC | A/G | 9 | 55129164 | 0.774 |
| 9056661667 | TCTTTATGATGCAAAGTCATAATGCTCAAATGTCAAAAACCATGTCAAAACATGAAGTTGA[T/C]CTCATTACACTATGTTCAATTAAGACGAGGTTCTTTTCTTAAAGGTTTATTGTTTTATATG | T/C | 9 | 56661667 | 0.858 |
| 9059744869 | GACAGGTGGAAGACAGCATCTCTGGACATTACCCTTTACCACTCTCCAACTTACTGCCTTG[A/G]GACGGTCTCATTCGCACGGACCTGGAAGCACGTTTTTAGCCAGATTGCCTGGCCATCCTGC | A/G | 9 | 59744869 | 0.92 |
| 9062839938 | TTTTTATTTGGCTGCTTGTTTTTTAACCCTGATGTATGCCTACGAACACCTGGGGACTCTC[A/T]TTCTTTTGGGGAGAAATAAGCTGGCATATATTTTATGTTCAGAAGGTACTTTTGCTTAAAT | A/T | 9 | 62839938 | 0.94 |
| 9067629682 | ATTTGTAATGAGTTGTCATTTTGAACTGTGAAATACAGAACCACTGTGGAGAGCTAATGC[A/G]CAAAAATAGCAAGATAAAATTACAAGCAGGACTATGTCTTAAATCTTTGAAAAAAACCC | A/G | 9 | 67629682 | 0.908 |
| 9069300117 | GCCAGTGTGATACTCCTCTTATTTTCAAGGATACAGATATCAGTGTGAATCTTCACTTTTC[C/G]CTCTGAGTGTTTTGAGCGTCTTTGGAGAATTAGTCGCGTGTGAGATGCTCACAGACATCGT | C/G | 9 | 69300117 | 0.944 |
| 9070857309 | TCCCCTGAGTTGTGAGCCATCATAAATGCCTCCTCCCGTGTGTATTTTAGTTCTAGTGAT[A/G]TAAAAATAGTTATCCTCAAGTTAGTGTGTAGGCTGTGTCTTCAAGAAGTCATTCTACTG | A/G | 9 | 70857309 | 0.732 |
| 9072613889 | ATATGAACACTGCAAAATGAATCAAGACACAAACTAGGTTGTACCATCCCATTCCCGCCTC[T/G]CTGGAGAGATGAAGAATGCTAGTTTCTTAAAAGAGAAAAGTGTTTTGAAGTTGTAGAGAGC | T/G | 9 | 72613889 | 0.963 |
| 9074172087 | TCCCTGTATTATTTTACAGAAGTTTCACACAAGGTAGAGGGTGGAGCTCAGGCCTCCACGT[T/C]ATAAAAATATCTCCCTGTATTATTTTACAGAAGTTTCACACAAGGTAGAGGGTGGAGCTCA | T/C | 9 | 74172087 | 0.741 |
| 9079064675 | TGTCCTACTACTGATGGCCAGCCTTGAGCTCTCGGTTGACATTTTATCCCAGAGACCATA[A/G]GAGCACAACCTTTAGAATCAGATCTGCTGTTAAGTGACAGAGATGTCTTTGGCAAGCTA | A/G | 9 | 79064675 | 0.908 |
| 9086630595 | ACACTGACTTTACAATGGAGGCCGAGGTGACTCCAGCCCCTCTATACTTAGAGCTCTGGGT[C/G]ACCTTCGACTGAGAGTTTGGACTTGGCATGAGGGTCAGACCTATTTGTTATCACTAAGCTA | C/G | 9 | 86630595 | 0.94 |
| 9090103431 | CTGCATGTGAGCCTAGCAAATGCCTTAAAACACACAGCCACCACCGCAGCAAGGGGCAAGG[T/C]GCTTCCCTCAGCCTAAGAGATGCTTGCACTTCTGTGGCAGTCATTCTTGACCCTGACCCCA | T/C | 9 | 90103431 | 0.811 |
| 9091773328 | TGTGTAAACATTGTTCCCTAATTGTTCCTCAATTGGTCAATAAAGCAAGTTGATCAGACA[A/G]TGACTGAACAGGAGAGCAAATAGGGCTGGACTTTCTCCTAGACAGAGGAGGGTGCAGGT | A/G | 9 | 91773328 | 0.969 |
| 9098131050 | TCCAATGTATTCTACAGATGTGGTAGAAATGAGCACGCTTGTTTTCAGGAAACACTTCCTA[A/G]TCATGCTAATTTATGCTTTTCACAGTCAACGTTTTGCTTTACAATTTTGTCCTGAACAACA | A/G | 9 | 98131050 | 0.931 |
| 9099767344 | TCCTACATATTTCAGTAAGTAAACAGGGTGATTATAATGTCCTTCAACCACCGAGTCCTT[T/C]CTAATTTTGACTTGTATCCTTGTCCTGCTATTGGTTTCGTTATTTTCGCACATACATGA | T/C | 9 | 99767344 | 0.985 |
| 9104399314 | TCCGGGCTTTTAGAGAGAAAGAGCAGAGCCAGATGTGAACAATGCCCTCCTTCTTAAGCAG[A/G]TTCATGGAGAATCTAAGTTGTACCCAGATCCCCAGCTGTGAGGCGCACCACGACTGCGATG | A/G | 9 | 104399314 | 0.981 |
| 9105972844 | TTATCAGGCAGATCTCTGTGGATCGCAGAACCAACACCAAGGAGAAAGAAATCAGTAGAA[T/C]GGGTTGTCTTTCCAGGAGATCTCGGGCATTGACTGCATCTCAGCCTGTTTAGGAGGTCA | T/C | 9 | 105972844 | 0.968 |
| 9107605440 | CTATGAAATAAAAAAGATATTTTTATATAAGAGATATTTTTAGATTTTCAGCAGCAGAAAG[A/G]AAATGTTTCTATCCCACAAGGAAGGAAACAGGAGGGACGTGATGTAGGATCAGACCAAAGC | A/G | 9 | 107605440 | 0.919 |
| 9109154182 | AATAATCCAAAAAGAGACATCTGTTTCCAAGTGGTATATTTTGATCTTCAATTCAAAATAC[T/C]TTCCTCATATATACGGGATTTCAGAAAACATCATACCAACATAATTGTGAGTTAAACTGTG | T/C | 9 | 109154182 | 0.76 |
| 9110891808 | CCAAAGGTCCCAGGGTTCTGATCCTAACACCTCAACCTGTTATGATCTGCATCTATTGCT[T/C]CTTTCCCCAATATATTCACTTTTAGGCTGTGCCTCATAATTTTTGATGTATTATGCTGC | T/C | 9 | 110891808 | 0.883 |
| 9112476703 | TGAGAGAAAGGATGACTGATTCTTCCCTAAAGCCATAGAATGGTAAGAGCCCAGGTGCAA[A/C]CTGAAGCCTGTGTATGATTTAGCAAGAAGATCATTTGTTCCTCTCCACGGGAACAGGGC | A/C | 9 | 112476703 | 0.971 |
| 10000138483 | GATCTATCAAGATATAAGTCTAATAGGCTTCCAGGAGGCATTCCAGGGAGATTCCTTGGGT[T/C]TCAGAATAACCTGACTACATTTTGACAAATTTGTAAGCCAGCTGGCAGCCACTTAGAAACA | T/C | 10 | 138483 | 0.991 |
| 10006775353 | CCTCTTCAGGTTTCCCAAGCCAAAATGGCCCCAAATCCAAACCTCCCAGTGGGTTTTGTG[C/G]GGTCAAGGTGCTCTGAACACATGAGCATGGAATGGAGGCACAAACCGGTAGTCTCAGGC | C/G | 10 | 6775353 | 0.918 |
| 10008363675 | AGGCTGACGGGCCAGCTTGGGGCACCGGGAGCCTGCTTGTCCCTGCCTCCTCAGCACTGGG[A/G]TTACAAAAGCATACCACTATGTCCCCACTTTCTGTGTGGATCCTGTGATCAAGTTCAAGCC | A/G | 10 | 8363675 | 0.783 |
| 10009957612 | AAGGCACCTGGGAGAACTTTGTACCATGCAGGGGTCTAGAAGTCAAACATCACAGAAAGA[A/C]TTTGGGGCTGGAAAACCTGCTAAGTGTTGTGCTTCCCGCTCAATTATTAAAGTTGATTT | A/C | 10 | 9957612 | 0.973 |
| 10011516717 | GGCCTAGGACGTTTGTAGGCCAAGGTTATTGCTTAGAAAGAGAGCGCTCGTCTCCATGCAC[A/C]AGGCTCTGGGCTCAGTCTATGCCTGTATGAGGACTTCTTGGGAATCTCTAGTTAAATCCTA | A/C | 10 | 11516717 | 0.804 |
| 10014700063 | GCAGTCGAGGGAGGCTTCTGTGACTCCCCCCTCCCCAACTCCCAGTTTTCCTTAAGGCACC[A/G]GGCATCTGGGAGAAGGGCCTGACCCACATTCCTCAATGCTGCTGGCCCCAGCAGCTCACTC | A/G | 10 | 14700063 | 0.811 |
| 10017759555 | GCCCCTTCAAGGTGCTAATGGCTTCAAGATGGGGTTACCCCTTCTGCCTGATCCATGGCTC[A/G]CGGCCCACTTAATGTTGGGGGGCAGGCCATCTGCCACAGCTGCAGAGGTTCTTTGCTTCTT | A/G | 10 | 17759555 | 0.61 |
| 10020870209 | ATGAACACACACATGTGGGAACACATATTACTACCCATACCTTGAAACAAGAAAGAGAATA[A/C]TACTAAAAAAACATAAATACATTCAAATGGGCTTTTTAAAGAAAGAAAGGGGAAAGTTCGG | A/C | 10 | 20870209 | 0.744 |
| 10027170584 | CATTTTGCTTCACTGAATTATAAAAGCAATACATTCTTATTAAAAAAAAACAGTAAGGAAG[A/G]GGCAATCAAAAGATAAATGGCAGAAATAGGCTGTAAAGTGGCATCTTCAATCCCATTTCCC | A/G | 10 | 27170584 | 0.849 |
| 10028719102 | GCTGCAGTTTTGGTGAAGCGACTGAAACGCGCTCTGCCTTCCACATTCCTCATAGCTTACT[A/G]CAGAGCTCCTCCCCAAATCCACAGTTCACAATGGGAGACCAATTTGTCTCCCTGGGACCTC | A/G | 10 | 28719102 | 0.976 |
| 10030374109 | TAAGGCACTTCCAAAGTTAAAGGACCTTGCAGAGAAGCAGGATAAAAATGACAGCAGCAG[A/G]AATGGGAGATGGGCAGTTAAGGGCATTTGCTGTTCTTGCAAAGGACCTGACCCGTGTTA | A/G | 10 | 30374109 | 0.818 |
| 10031907156 | AAAAAAAAAGAGCTTCAGTCCAGTTCTCTATTCAAGGACTTCTAGTTTTATGGAATTTATT[A/T]TTATAAGGCAATTCTGTATACATATATCTTCTAAGTCAAAGTTCTCTAAGTTCAAAGTGTG | A/T | 10 | 31907156 | 0.537 |
| 10033524496 | TGTAGTAGGATCCATACAATTCCCTGGAGTTACAATATTGGTACCTACAAAACAAGGCAA[A/G]ATCTATATTACCTCGGGTTCCATCTTGAATATACATAGGGCACAGGGAAGGAATTGATT | A/G | 10 | 33524496 | 0.888 |
| 10038246551 | GCTAAGCCAGAATAGAAATAACCAATTAATTTCCCCTTTGAAAACAATTCCACGATGTTCC[A/G]TTTTCCGTGCCAGCCTTCCTCTGGCACATTTGTTTTCTGGTCTCAGAGGTAAGCGTGCACG | A/G | 10 | 38246551 | 0.916 |
| 10039818446 | ATGTGGTAGAACTGAGTTCAACCTGTCTTGTCTTTTACCAGATTTTTCATTTAAATACAT[A/G]GAACACATTATTTTAAGCATATGTCGGGCTTTGGGTTGTTTTGTCTTATGATGCGGGAG | A/G | 10 | 39818446 | 0.829 |
| 10041439179 | TGTGAAACCTTTAGGAGGCAGGCTCTAACTCCCCATTTCTCCCTCCGCCTGACTCTCTGG[A/G]GTTTGCCCTCATGGCTCTTGCTGTGCTGCACCGTCCACCCAGGTGGAATTTGAACTCTT | A/G | 10 | 41439179 | 0.662 |
| 10044705113 | GTGTATATATTTTACATAAATCTGACTATTTCATTGGTTTTCCTTTACAGGCACAACAGTT[A/G]TATAAGAATGTTGGTCTGTTTTTATAATGTGACGTAGTTTAATGACAATTTTGAAATAGGG | A/G | 10 | 44705113 | 0.71 |
| 10046241978 | CCCAGTGGCCACAGCAGGTTGGAACTCACTCTCCTTCCTCTCCTCCACTGTGGTCTCTCCT[A/G]TCTCACACTCAGCCCTGTAGCAGTCTTCTTGAAGGTACCCCTCCTCTGACTACAACTGTCT | A/G | 10 | 46241978 | 0.836 |
| 10047776989 | AGGTTCTTATTGCTCTAAACAGCCACAAGTACAGCGGGCTGAGATTCTAGGAGCAGTATA[C/G]TTAGTTTCCCTTCCTGTGGAATCTGGACCTGGAATGTCTCCCGAAGCCCATGTGTGAAA | C/G | 10 | 47776989 | 0.943 |
| 10055969848 | TTTGCTGATTGTAGTGAGGCAGGTGAGTGCCCCGGGACTCCCGTGAGGTTTGGGGCTAATT[T/C]ACAGCTTTTGTAATTAGTGCACTCTTCATGGGCATGCGCTGTATACACACACACCCCTCCC | T/C | 10 | 55969848 | 0.992 |
| 10064286854 | GGGACCAGATGCACAGGTACCACCCCCCACCTCCCGACACTGAGCCTGGGTTCTCCACATC[T/C]CCACTCACTTAGCTCCTCGGAGAGAGGCGGGAAGTCATAGATGTGCTCACAGGTGTTCTTG | T/C | 10 | 64286854 | 0.737 |

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|---|---|---|---|---|---|
| 10065987410 | CACCATCAGGATTATTGGGAAAGGCAAACAAGACACAAGGTGAAAACTGCAGAAGGTACAG[T/C]TTGGCTTTGAAGAACAGAGAGAGGGGGGGGGTGGGCCTCGAAGACCCAGGCAGGCCTGAGA | T/C | 10 | 65987410 | 0.935 |
| 10067577050 | TATATTTTGAGGTAGAGCCTCATTATATACGCAAGGTTGGACTTGAACTCAAGATCCTCC[A/T]GTTTATGCCTCTCTGGTGATGGAACGGCATGAGCTACTGTACCTGACTGATCCTGTATA | A/T | 10 | 67577050 | 0.642 |
| 10069114925 | CCTCTTGCTCCCCTCTTGCTATAGCCTTGATGCTTAATTGCAAGGGTCCAAAAGTTTCATC[A/G]TTAGCAAAAATAATTATTCTTTCAGCTCCCTCTTTTGTTCTCACTGGCCTCTGTCTTTTTC | A/G | 10 | 69114925 | 0.969 |
| 10070676395 | GGTATCTTGCAGAGCTTCAGGGCCACTGCACCTCACACAGCTAGGATTCCCACTGTACCAT[T/C]GTCTCTTGGGAGTATGGTAGGTGTGTTTGTCTCCGTCTCTCCTGCAGAGGTGCTGGCTCTT | T/C | 10 | 70676395 | 0.922 |
| 10072264375 | TCGGTATTACCTGTGGAATGAATGCTATCCACCAGGGTCTTCACTGATGCTAGGAAAACAC[T/G]TATGCATACCTGTTTCATGTAGTATAACTACATGTTTCTACACGTCCTGAAGGAGGTTATC | T/G | 10 | 72264375 | 0.924 |
| 10077287817 | GAAACAGATAGATGGGCTGGAGTTGGCAGCTGACTTAGAGGGAAGGAGGAAGGGGGAGAGT[A/G]GAGAGAAAAGTATGAGGAACAGGCAAACTTGTCAAACTCCTTTTTCATCCCTCTTCCGCCT | A/G | 10 | 77287817 | 0.966 |
| 10078860043 | GCAAATCCTAGTTATTTTTAGAGTACCTTAACACACCCTTTGAAATCGATTCGTAGTAGA[T/C]GGTAAGCTTAAGAGGTTGATGGTTCTGAAGAATGGAGGAATAAGAGAACAGACTGAGGC | T/C | 10 | 78860043 | 0.92 |
| 10080464456 | TTATTCCGATTCAGGTTTTGCTTGAAAGCAGTGATTGACAGGACAAGATGATGTTTGATAA[T/C]GATAAACAATAAGATACTTTCTCTATTTCCTCATGTCTCTCTCCTTACTAGACAGTCTCAT | T/C | 10 | 80464456 | 0.621 |
| 10081985153 | GATTTCTCTCATAAGGACACTAATTGTAAAGATTCAGTCTATGTGAGTATGACCTAATGAA[A/C]CCTCAAAGGTGCTACTGTGACCATCATACTAGGCACGAGTACATTAATACAGACATTTGGA | A/C | 10 | 81985153 | 0.937 |
| 10085150354 | GCCCCACCCAAACGTCAGATCATCTTGGAATGCAGGCTGAAGTGAACCTTTGACCTCTGAA[T/C]GCTGAACTCTGGAGAAGATAGATAATGGCATGAAGATTTCCCAGCTCCACAACCTCTGCCA | T/C | 10 | 85150354 | 0.819 |
| 10086714378 | GGGAACGAGTGTGGAGACACAACACATGCTTCTAACCCACATCTGCCCTCAAGTCAAATGT[A/G]GAAAGGAAGTTCTGGGAAAGGAGGAGTAGTGTGCCTGACCGCCTGAGGCCATCAGGTGCCA | A/G | 10 | 86714378 | 0.866 |
| 10088241830 | ATGTCTCACCAGCCCCTGACACTTGTTTGTAGTACGTCAGAAGCGATTAACAGAAGTTCTG[T/G]GCGTATTAGCTTTGCTAAAGTTTATAAATATGTGGTTTTGGCGGGATTTGTATTGAGAGTT | T/G | 10 | 88241830 | 0.876 |
| 10089766892 | TTCGATCCCCAGCTCCGAAAAAAAAAAAAAAAAAAAGTTCATCTGCACATACATATTCTCTT[T/C]GGAATACGGAACACTTCCCCACATCAGAAACAGGAGGAAGATTTCTAGGGGAACGCCTGAT | T/C | 10 | 89766892 | 0.989 |
| 10091419662 | CTGACCGTTGCTCATCACCAGCTGCTGCTTTGGTCTTCCCGGACTCTCCATTCTTTGTATC[T/C]GCTGCTCGCTCTGCAATCAGCTCAACCTCTAACCTATTAGGATCAGAGTGACTTGCCAACT | T/C | 10 | 91419662 | 0.941 |
| 10094502019 | GAGGTTTTTGACTGTTGTTTATCAAAAGGAGGTGCACTGGTTTAGAATTCTATAGACATT[A/G]AGTCTACATTAACCACTTGATATATTATCAAGTTGACAAAAGTATTTTATTTCCTCTGC | A/G | 10 | 94502019 | 0.578 |
| 10099943591 | TGCGCGTTGCGTGTTCAGAACCCAGGCTACAGAGACGCCGCCCCGTGCAGCTCAGGTGAGC[A/G]CCACCAGAAACCAATCCGTTTCTTTTCGTTTTCGGCTTTGATTTTGAATTGACTTCATAAT | A/G | 10 | 99943591 | 0.76 |
| 10101611833 | TGCATATGTGTACAGGTTTGAGTATATGTTCTCACATGTGTGCGTGCATATGATCTGGGCA[A/G]GCATGTATATATGTTCAGGATCCTCTGATTGTATCCCTCAAGCAACGGAATTAAAGCTATC | A/G | 10 | 101611833 | 0.961 |
| 10104629819 | TGAACCCCGATTTTCATGTCTGTTAGACAAGCACTCTATCATTCTACATCTGAGCTGTAGT[T/C]CTAGCCCTTATTTTGCTTTTACTCTTTTTTTAATTTATCTTTGTGTGTGTGTGAGTGCACA | T/C | 10 | 104629819 | 0.766 |
| 10106193291 | TGGTTTCATTCTTCTGTCTCCTCCCTTCCCAAATACTCTTTCTTGGTGCAGTAAGTACAGG[T/G]GGCAGCTCAGGTTAAAATGGTCAGCAGGAACATGTGCTGGCCGGCCCCTTCTCAAGACCTA | T/G | 10 | 106193291 | 0.806 |
| 10107819766 | TTTCACAGAGCAGGCAAGAGGCAGAGGTTGGCACTGTAGATAGTAAATGAATAACCAGCCA[A/G]TTCCCACCTCAGCAACAGGAAGTGCTGGTCATGGGTATATAGTGCATGTTGTCAGATCTCC | A/G | 10 | 107819766 | 0.958 |
| 10109399893 | CTGCAAATGACAGTCTTCTGAGAGTGTGACACTGCCTTTGCTGTTCCTGCTGTGTGACTT[A/G]CCATCTCCCCCCTTATCTGGCCCTCACCCTCCAGAGTATCGAGTGTGAGGAAGGGGGGA | A/G | 10 | 109399893 | 0.834 |
| 11000889960 | TTTTAATCTTTCTCTAACACCAACTCATGATAGTGACTTGGGTGCCTAGGGCAAGTGAATT[A/T]TGCCTTCTGGCATATAAATGAATGCATCAGGAAAAAATAAATGTGGATACATTAGGCAATA | A/T | 11 | 889960 | 0.965 |
| 11007329190 | AGAAATACCCAATTTAATAAAGATGAAATAAAAAATCACATTTTGGTCTTCTGGAAGTAGA[T/G]CCACAGCAGGTTGTGAACAGCTAGATTTGGGAACTAGAGCCTGATCTCAGATTTTCCTTTT | T/G | 11 | 7329190 | 0.993 |
| 11009165141 | GGTTGGAACTTGGATCTCATGCTGTGTTCGTCAGTTACCGTGTATGCTTTTGTATCTGTCT[C/G]TCTTTAATCATTTCTTCACATCACTTGCTGTAGAGCTGTTCCGTCTAAACAGAATAAATAT | C/G | 11 | 9165141 | 0.846 |
| 11010882373 | AATTAATTTTGAATGGATAAGTGAAAATGTTATCCAACAAATACACAGTGGAGGTCTTAA[A/G]ATGACTTGATAATTTTCTACTCACTCACTGTTCTTCTTAAGATAGTTTGGGATTTGGTT | A/G | 11 | 10882373 | 0.733 |
| 11012641195 | CACAGAGGCAGGCAGGCGGGTAGATAGACAGACAGGATGGAGTCCGGTTTCTCAACTTGG[T/C]CATATGAGATTAATCAAGATAAAGTTATAAATACTTAAAGTCTTAAGAAGAGAACCAGA | T/C | 11 | 12641195 | 0.69 |
| 11017619785 | GGTCATTAAAGGAAATTGTAAGCCATCTGACATTACGCTTATCACCCATGCCCTGCCTCG[T/C]GGTGTTGAGAAATACACAGCTTGAGGGTGGGTGAATTGGAGTCAGTCTTTTGATGTGAG | T/C | 11 | 17619785 | 0.639 |
| 11019203719 | AGGTTCCCAATATCCATATCATCCTGTCTCTGACTGCAGCCACCATTAAACAAGCAACTTT[T/G]CTTCAACACTAGAGCGTATGTACTTTAATTCAGAATATGGATAACATGGTCAGTTTGGACA | T/G | 11 | 19203719 | 0.962 |
| 11022388395 | TAATAGTAATTTGGAAATATTGGAGGGAGGTAGATTAACCACATGATAGTTAGGAAGTAG[T/C]TCAGTCATTGAGCTCTTTCTGCCATATCAAACTATAAAGTCTCTAAGTGAGGTTTGTTG | T/C | 11 | 22388395 | 0.939 |
| 11024052265 | NNNNNNNNNNNNNNNNNNNCATCCGTGTGACCATGAGGTAAATGACCATTTCTCTACAGTG[T/C]GCTGTGTGGCTGAGCTGTAGCACCTGGTAAGTATGCAATGCATTTCCAACGTGACTTACGG | T/C | 11 | 24052265 | 0.985 |
| 11025582611 | TGATGAAGAGAGACATTATGTTTATGCAAATACTCCTCCCCTGCCTCTCTCTCCTAGACTT[A/T]TTCCCTGCCTACCCTTCCTTTGTATCCAATAAAGGGCTTCGCCTTATCCTGGACATGCCTT | A/T | 11 | 25582611 | 0.724 |
| 11030346235 | TGTAACATGTGTCCTTGTGGTATGGTGGTGTAAGGGTTCAAAAATCGCCAAAGGAAGACCC[T/C]AGATTTAGATATTATGCAAAGACAAAGAACATTTATTCTGCAGAAATACCAGCATTCAGGG | T/C | 11 | 30346235 | 0.795 |
| 11031854195 | TCGTGGGCGTACTGCATTTTACCTTCACGGTGACTCTGATGTGGCTTTGTCTTATTTCAA[C/G]TGAAATGCTTAATTTACCACAAGGGTAGGCACTCAAGGGGGAGCGTTAATTGACAGTAA | C/G | 11 | 31854195 | 0.92 |
| 11033435569 | AATGTTTACCTCAAAATATAAATATCGGAGCTGGTGTTAATGACTGCAGGTTCACTCACAC[T/C]CCTACTTTGAAAAACCTGAGTGTGTCACCAACTCAGGATTAACCATCACTGATTTGGGGTA | T/C | 11 | 33435569 | 0.946 |
| 11034966294 | ATGGCTCTAACCTCACTCATTTGCTGTCATAAATTTAGGGCCAGGGAGTTAGTCTTCGGG[T/G]TAGTGAAGCGTGACTTCTGATTTTATGCATATATAGTCAGCCTTCCCACTATGAGAGCT | T/G | 11 | 34966294 | 0.944 |
| 11036509230 | CCTTCTAAATTATTTATGTTTGTTTCTATGGGTTTGTGCTGCTCAATTAAATTTTGACTTG[T/C]GAATTAGTTAACTTTCAGCTGTATTCTAGGGAGTGTTCTTTCCCATCATAACAACCACTTG | T/C | 11 | 36509230 | 0.821 |
| 11038526316 | TTTTTTTTATAAATCCAATACCCCCACGGAGGCTAGCAGACTCTCACGTTGAGTGAATTAA[T/C]TCCATCTGTTTGCTTTCCTCTTGCTGTGGTCAGCTGTGCTGAAAGAGTCAGCATTTTAACA | T/C | 11 | 38526316 | 0.985 |
| 11040166875 | CTTCTAACATTTGCTTCAGTTCCATAGATGTCATTACTATTCATAAAAGGCAATAACAAT[A/G]TAATATATAGAGAAGGGTTACACAATAGATCATTTTTACAGCAAGTGTTCATGATGGAA | A/G | 11 | 40166875 | 0.546 |
| 11045566388 | TGTGTTAGCAAAGTGGCAGGGAAAAGCAACAAGACAACTCTTGTTCTATTCGTTGTTCCTG[T/C]GTAAGTAAGGAGACAAGACTGGCACTAGCTTTTATGGTAAAACTCTCACAGGATACTTTTA | T/C | 11 | 45566388 | 0.894 |
| 11049064419 | TGTCATTACTGATTTTAGTATCACTAATTACAGCACGGCCATCTGCAATCTATCATCAAC[T/C]TGATTTGGGCTTTAAAACTACATAATTGACAAAACAACAAAAACAACAAAAACAACCTC | T/C | 11 | 49064419 | 0.979 |
| 11051063125 | ATCATAATTCACAACATATATGTTCATAACATGAACACATACTCTACACATAATCCCTGAG[A/G]CTGAGCTGATATTAATTCCTGTACAGGTTGTGTTTAAACCAATAGAAGCTTATTAAAAAGA | A/G | 11 | 51063125 | 0.814 |
| 11056214836 | GGGTGAGAATCTCAGGTATGCACATTCCATTCCCATTTTCCACACCACTGAAACCAAGGGC[T/C]GAAAATGCTGACCAGCGCATTCTGAACTGAAACAACTCAGACACCCACAACAAAGTAACCT | T/C | 11 | 56214836 | 0.788 |
| 11058986195 | AAATGTCTTTAAATAATTAATTACAAGAGTCAATACACTTAGTATTGAAGGGTTATAAGAT[T/C]TCCATGTCACAAATACATTAGATGAATTCAGAGTGGCTATTGGATATCCAGAAAACAAAAT | T/C | 11 | 58986195 | 0.744 |
| 11062684008 | TAGCTCCTCTTTGGCTCTGTGCCAAGGTGAGAATTGCATGCTAACCCACTGAAGCCAGGG[T/G]CATCTATAGTAAAGCTACAGCAGTACCTCAAGATAAGAAAGCAAGATGTCTCATGGAAA | T/G | 11 | 62684008 | 0.903 |
| 11064270722 | AGTGTGGGTCTGTACCACAGCACCTGAGCTCATGCGCATTTGTGAGCCTGTGGGACTTTG[C/G]TGATACAAGGTACCAGTTCTCTGTTACAGGAAGTGTGGTGGGAGATGCAGGTCAGGGCT | C/G | 11 | 64270722 | 0.995 |
| 11065981687 | CTCATGGGATAGATCCCCAGTTGGGCCAGTCACTGGTTGGCCATTCATTGCTTCAGTGTC[T/C]GCTCTATTTTTCCCCTGTAATTCTTTTAGACAGGAGCACTTTGGGGTCAAAATTTTGTG | T/C | 11 | 65981687 | 0.736 |
| 11067508537 | GAGTCCTCTGGAAGGGCTCTTGACCATCTAGCCATCTCTCCAGCCTAGGACTACTTAAAAA[A/G]CAAACAAACACAAACAAACACAATGAAGGAAAAGATTGTGTGTATGTGTGTGTGTGTGTGT | A/G | 11 | 67508537 | 0.742 |
| 11075571033 | GACAGGAGCCTGATATAGTTGTCTATTAAGAGGCACTGCTAGAGTCTTACAAATAAAGAGG[T/C]TAGTACTTTTAGCCAACCATATAACTGAGAAGAGCATCCCCATTGGAGGAGTTAGAGAAAA | T/C | 11 | 75571033 | 0.606 |

| | | | | | |
|---|---|---|---|---|---|
| 11080261983 | TCATGGCTGGAAGACACTCATCCTGGGCTTTTGTGGAGAGGACCCAACAGTCAGATTCTA[T/C]CACATCTAAAACTAAGTAGTAGATGGTGGCAGTTTCCTAAGGGTAACAAGGAAGGGACA | T/C | 11 | 80261983 | 0.724 |
| 11081846340 | GTGGCCTAGAAAGATGTGCTGGGGTCCAGGCCGTAGAAGGTGCTGTTTTCCATCAGGTTT[A/G]GAGCAGCAGGGCCTCTGTCTGCCTTGTCTGCCACTGTATCTGCAGTAAGGAGGCCTGGC | A/G | 11 | 81846340 | 0.863 |
| 11083407429 | GCTGTTACTTATACCTAGGGGTATCTGAACAACCAGTTCACCAGCATGTTAAAAAATATAG[C/G]AGTAACCAGGATTTTCTCATTACAAAGAACTTTTCCCAGTTTCTCCTACCCGCTTGCTTCC | C/G | 11 | 83407429 | 0.813 |
| 12000092958 | AAAATTGACAATATGAAAACATCTGGCTAGCAAATAACTTATTGTTGAATAGTAAGTGCTT[T/C]TGATAGAACGTAGCTGATTTGAAGTAATAGTCTATAATAGTGAGGGCATACCAGCCTGAGA | T/C | 12 | 92958 | 0.597 |
| 12001618778 | GGGTGACACCAGTCCCTATGCTGGGCTCTGGAATGTTTGAGAGTAAAGAAATCTTGCTGA[C/G]CAAAAGTTAAGCAAGTAGGCAGCATGGACATTCTCTGCTCTTGATAGTCATCTAAGTTC | C/G | 12 | 1618778 | 0.781 |
| 12003229231 | GACGGTGGACAGTACACTGCAAATCTGTAAGAAGAACGAACAGAGAGAAGCATAGTGAGG[T/C]GATTTCCTAACTACTGTCAGCACCAGCGCGGAGGTCTTCCACAGTGCTGCTCTGCGCTG | T/C | 12 | 3229231 | 0.932 |
| 12006393572 | AGTGTGTTTTGTTAACGTTTCCTCCCTGAAGGCTGAGCGCTTGGTGAACAGCTGTCCGCTC[A/G]CACCTGTTGGGCTGCTTTACACCGCAGCCTGAGAGGAGCGCATGCCAGGCTAATTGCATTT | A/G | 12 | 6393572 | 0.805 |
| 12008120463 | AAAAAAAGACCCGCAAAGAGGTCAAGATCCACAGGTTGAGAGTTGATGCACTACAGGCTC[A/G]CAGACTTGAACACTTAGCTCTAGCTAGCTGGTGGTGCCATTTAGGGGTGGGGTTATAAA | A/G | 12 | 8120463 | 0.965 |
| 12012794920 | TTAAAATAAAATTTAAAACAGATAAATAAATTTAAGAGAAACAAAACGACACATGAAGGC[T/C]GCTTCTATATAGCTGTGCACAGCACGCAGGAGTATTCATCGTCAGATAAACCGTTAGAC | T/C | 12 | 12794920 | 0.959 |
| 12015944442 | CTTGCTGGCCACCAATCTAACGTAACTTGGGGAACACCTACCCAGTAAGAGATCCTGTCT[T/C]AGAAGACAAGGTGGATGATTCCTAAGGAAAGACACTAGTGCAGGCACATGCATGCACAC | T/C | 12 | 15944442 | 0.757 |
| 12017543910 | CTGGAAATGCAACATGACTTATTTCTTATTGCATTTATTTTTGTAACAAGGTCTTGTTGT[A/G]TAGCTCTGGCTGGTCTTGAATGGAGATCTGCTTGCCTGTTCCTTACATGCTGGAGTTAA | A/G | 12 | 17543910 | 0.996 |
| 12022724423 | TGGCGGTGGAGGGGACGCCCAGAAGATCATAGAGAGCGTTGCGTGAATAAGTCCTCACTCG[T/C]GAGCACAAGCCCGTGGCCGAACTTTGAGGCAAGCCCTGGACCTGCCACAATCTCCGTAGGG | T/C | 12 | 22724423 | 0.824 |
| 12025836114 | CCAGCCAGCCAAGGCTTAGTGACAACCTGTCTTAATACAAAACAGAAAGGCAAGCTCGCCT[A/C]GTATGAAGGCACACATCTGCAATCCCAGCATTCCACAGTGGAAGATAAGAGAAACGGAAGG | A/C | 12 | 25836114 | 0.534 |
| 12027351891 | TGGATGCCTGTCATCTCCGCCGAGATGAAGGCTGAGGCAAGAGGATCCAGGCCAGCCCAAA[T/C]TACATAGCCAAACCCAATCTCAAACAACCGAACTGATAACAAGTAGTAGTAGTAGTAGTAG | T/C | 12 | 27351891 | 0.848 |
| 12032286665 | TTTTTTGTATCTTCTGGAAATGTACTCTCCATATACTATTTTTATTACATTTCTTTGTGTT[T/C]GGATGTATGTGGACCACGATTTGTATGTCCCACAGTGGAGGAGTTAGTTTTAAGGAGCTAG | T/C | 12 | 32286665 | 0.733 |
| 12033820507 | CTTGTGAAACAAGAATGACACTGGGACAACTTTCAGAGCTCTGGTAGGAAGACAGTTGCT[T/C]TTTTGGTTAACATCGCCTCTGTCACATCCACAAAATTCACCTTCTCCAAATCCAGCTTC | T/C | 12 | 33820507 | 0.94 |
| 12035529975 | CCTGACTCCAGCCTGCTGGCTGCAGGGGAACTTCACACCTTCCCCTGCTGGACTGCTGGTC[C/G]CTACCGTGCTGGTTCTCTTCTTGGTTGACCTCCAGCTGCTCCTGCTGCTCTGCTCTCCCGC | C/G | 12 | 35529975 | 0.766 |
| 12037049230 | GACACTACACCGAGAAGCCTTGTACACACATGAATTCATCTACTTACACAGTCACCTTACA[T/C]GAGGTAGGTACTTACCAGTAACCCTGTTCAGATAAACCACTGACACAGAGAGATCAAGGAA | T/C | 12 | 37049230 | 0.717 |
| 12041773251 | CACCAGGCCGGGAGAGACTATAGGGTAGGAAAGGAGCTGTGTTTGATGAGGAGGAAAAGTC[A/G]ATGCAGCTGAAATATGGGAAAAGAGGAATGGACTAACCTGGGAGAGGCTGGGGAAATAAAC | A/G | 12 | 41773251 | 0.937 |
| 12043298723 | AAAACAAGGCCTCTAATGAATTAGCTGTGAGATGAAATGTATGAGAAGCCCAGAGACATC[A/G]AGGGTCCTTTTCAAGGTCACACAGCAAGGCAAGAATAGGGCTCTATTGGGCACGTAAAA | A/G | 12 | 43298723 | 0.953 |
| 12045115666 | ACACATCTATGTCCCTGAACACTGAGTCCAGAGCAGGACACAGTGACGTGCTCCATGTCT[A/G]CCTGTGAGAGGGATAGATAGAAGGGACAGGAGACAGACACACGTAGGACAGTTGTCATC | A/G | 12 | 45115666 | 0.994 |
| 12046643613 | TCAAAACGAGGGCTAGCACACTGACAGCTGTCACTACAGACACACAGCCTCTGACTCCATC[T/C]GTCTTCTGTGACTGACGACTACCTATGAATGAAGGAACTCACCAATAATAAAGTCAGCTTA | T/C | 12 | 46643613 | 0.959 |
| 13004993693 | GAGAGCAGAGAATAATTATTACAAGGCTTTGAGCATTGCATCCAGTAAAGAGTTTGGAGAC[A/G]AGACCAAAAAAGAACTAGGGAGTGCTAAAGCACACATAGGAGCTCTGTGTATACTCAGATT | A/G | 13 | 4993693 | 0.94 |
| 13008708707 | GCTGACAGTTGTTAAATTTACTTAAACAGCCAGAACATACTACAGAAGGGCAGCCTAGTTT[T/C]TTTTGCTAGGAATTTTATATTCTTATAGTAAAAATCAACTTCCAAATATTCTCTTAGTCTC | T/C | 13 | 8708707 | 0.794 |
| 13010273719 | CTTGATGTTCATTAAAGAAAAAATCTACAAAGATGACATCTCAATTATAATATCTATGCC[A/C]TCCATACAAAGGTACCCATATCCATAAAAGAAACATTATTAAATTTTAAATTGCCCACT | A/C | 13 | 10273719 | 0.518 |
| 13014933245 | TAGCCCCAGATAATTTGTTCTGTTTCTCGTACCAGGGCTTGTTACCCATAGGTTGAGCAGG[A/T]CTTAATTCCAATTATATGATACTGTTTACTGCCAATATATGAGTGCCGCAATTGTACTCAC | A/T | 13 | 14933245 | 0.83 |
| 13016609621 | TGGAGGCATAAGTCCTTTCCTGTATTCTCTTGGAATGGTGATTTCATCCCTGGAAGCTCTG[A/G]GGGTTGTGGTTAGTTGATATTGTGTTCTTCTTATGTGGTTGCAAAGCCCTTCAGATATCTT | A/G | 13 | 16609621 | 0.523 |
| 13018411493 | TTTAGGGCTACTTCTACGTTGCCTGTCATAGTATCTGGTCTTGTTGAAGTTCATGATGGTA[A/G]AAATATTTGAAATCTTCCTTAATCAGATAACAATACCCTGATTTTACAGAAGAAGAAGGCG | A/G | 13 | 18411493 | 0.901 |
| 13023383719 | TCCACTGTCTTTTGAATCAGGCAATTAATACTGAGATACTGTGCATTTAAAGACAGTGATC[A/T]GAATCCTGATTCTTGTAAAAAATGTTATACTTTGGGGTATAACTTTAAAATTGGAGCACTT | A/T | 13 | 23383719 | 0.781 |
| 13026804728 | TAACAGATTTTAATATTCATTTTTTGTTCTGTCCATTTAGTGCTTTGGTTATCATGAGGCA[A/T]GTGTATTTTCTTTTTGGTCCAATCTGTTTGGTGTTCTATATGTTCCTTGTGCATTTATAGT | A/T | 13 | 26804728 | 0.695 |
| 13036488082 | GAAACAGCCCATCTACTTAAATTATACTTTCTTAAACTTTGATTTATTGTCGATTTTAGGA[A/G]CAGAAGCTACAGATACTTAAGCTTCTTAAGCTTTTCCCTTTCACAAAGCTATGAGATATGG | A/G | 13 | 36488082 | 0.724 |
| 13039921157 | TGGAACTGGGTTTGCAGGTCAGAAATATCCAGGTGTTTAAGAACAGTTGGGTTTCTTAAGC[T/C]GAAGAGCTGTGATGAGAAGACAAAAAGTTACATTCCCCAGAGACTCCTCTATACGGTTGCC | T/C | 13 | 39921157 | 0.905 |
| 13041625844 | TACAAACAAGTTAATTTCAGTTTCAGTATCTTGTTCTTTGAATGGGGTGATAAAAATCTA[T/C]AGTCTTGCTCCTTGGGTCCTCATAGCCTTTGTGATTTGCTTGTGTGCACAGAATTGGTA | T/C | 13 | 41625844 | 0.962 |
| 13043391300 | TTTCCCTTTTCTTTTTACTCAATACTGTACTGTAAGTCTTCCAACACATAAAAGGTTTTAA[A/G]GTATCGTAAAATTGTGTATATCTTACTGGTCAGTGGAACCTGGATCTTTCTATAGTTGAGC | A/G | 13 | 43391300 | 0.652 |
| 13051499112 | AAACATTTGAGAACTCCTTCAGAATCTGAATTTGAAATAAAATGTGGGAAAGGATTTCTCA[A/G]TCAATTAAATATTTATCTTAATAAGCCTGGTAAAAGAGATTGTGAATCAAAACTAAAGTAA | A/G | 13 | 51499112 | 0.739 |
| 13053045095 | TTGAATCTAAAAAGACAACATTTGAAATTTTGAGAGATCAAGTTAAAGTACTGGTTCAAGA[T/G]GAGCCAATAAAAGTACAGTGCTAAATGCAAAATCAAAACTTTAGTGATTTTTGTCTATAGA | T/G | 13 | 53045095 | 0.844 |
| 13057797660 | TTCTGGAGAATCTCACAGCCCAAACAGCTTGCCTTTTGAGGCTTGGGCATATGCTTCAGG[T/G]ACTCTGTAGCCTGCTTTGTATGAATTCTGTGGCTCCCTTCCCTCTGCCAAGACCAGCTG | T/G | 13 | 57797660 | 0.857 |
| 13064090867 | AAGAGTGTAATTTTCAAGCTTACATCTGTCGAGAAAAACTGAATGCAGAAATACGTGTAC[T/C]GGGAATTATAAACCGCTCTTAGCATCCCTTTTACGGAGCATGAATGGCGCAGTTTGAAT | T/C | 13 | 64090867 | 0.928 |
| 13067234922 | TCCATTCTTGCTCCGGATTGGCTCCCCCAGTCGCATGGCTTTGCGACCCCACACCTGGCT[A/G]CTTTCTCACCACCATCCTGCTAAGAGCCTTTCCTCAGGTAAACTTTTTAAAAACTAAAAGC | A/G | 13 | 67234922 | 0.708 |
| 13068987423 | GTGGGGAGGTATTGAAGGACCCCTTTCCTCCCTGAAACTACATTTTATCATAGGAGAGGAA[A/G]CATGATTCTCAAGAATAAATAGCATATGAATTGCCTGGTCCTCATCAGCTTCTGAAGTCAC | A/G | 13 | 68987423 | 0.712 |
| 13070520624 | TTTTTTTTTTTTTAAATTAAGGGCTCCATGCAGGCAACATGGAGGGCTGGTGATGAACTCT[T/C]GACTCAGCATCCTGAATCGCTTTCATTTCCAAATAAAAGACCCAGGGGAGTAGGCCACTTA | T/C | 13 | 70520624 | 0.797 |
| 13073623100 | GATTTCTGCTCATTTGGAACTTATCTGTATAACACCTGTTACCAAGCTCTAAGGACCATT[T/C]AAAATCTCATCCGAGAGCACAGTGGTGATGTGATTAGTGTCCTACATAGTATTCTCTTT | T/C | 13 | 73623100 | 0.966 |
| 13075145314 | ATGTAGTTGTGTCTTTCTTCCTCTTTGTATGATTGCTTCCCTAAAGCCCAATATTACTAG[C/G]ATGAATTTGGGGACCAGGCTTCTAGCACCAGAACTTTTGGGAGACACATTCACTATAAC | C/G | 13 | 75145314 | 0.99 |
| 13076714709 | AGCCAGACACGGTGGTGTTTACCCATAGTCTCAGCACTGGGAGATGAGAGAGGAGAATCC[A/G]GAAGGCTTGGTAGGCAGCCAGTCTAGTCAGCCATTGAGCTCTGGGTTCAGTGAGAGACT | A/G | 13 | 76714709 | 0.549 |
| 13078283339 | TGTGCTGAGATAGATGTTCTCCGCCCTGTGTTAATTGGATTCACAGGTAACAGTAAAGAGA[T/C]GGATACTTCCCTTTTTGCATTTAACAGATGAGTGTAGTTGATATGGCAAAGTAAATATTAA | T/C | 13 | 78283339 | 0.912 |
| 13079883630 | AGCGACATTAACTTTTCTATAGCAGTCCTGGTGTCCAGGACGTGGTCTAACTCCCTGTGG[T/C]GGCTGTACTGGTGTCTAGAGCACTGGTCCTTGCAGAGCTATACTGGCTGTGCTCTGGAT | T/C | 13 | 79883630 | 0.966 |
| 13081709022 | TTGTGGAAGTGCAGTCTCACTCTCCAGATTCGTAATCCACCTGTCAACACCCTATCTTCTG[C/G]ATTCTTGCTCCAGCTTGTCACTCAGAATAGACAATCCTAGCTCCATCTTCATGTACTACTA | C/G | 13 | 81709022 | 0.966 |
| 13083620119 | CAGTGCCGCAGCCCCCTGAAAAGCCGACAGGGAGTAGGGACAATCTAGCGCCCTCCCTCC[A/G]GAGGAAATCATTTGCTGCAGGGCCAGAAAACTCTGGAAAGAGCTGGTCACATTGTACCC | A/G | 13 | 83620119 | 0.836 |

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|---|---|---|---|---|---|
| 13087054272 | AAAGTGTCTATTCTTTATTAAATTCTAGACTGGTAAATTCTTTTACTCTCAAGCCTTGGAC[T/G]AGTTCCTATCAAGCCTTGGACAAGTTCCTACTAGAAACATATGTTTGATGTTCATTCTCTT | T/G | 13 | 87054272 | 0.902 |
| 13088649999 | GCTCTCGACACAATGATCGATAGGAAGAGAAAGTTTGAGGCCATTAAATAAAAACACATTC[T/C]GGATTCTCTTTATTTTAATGAAAACGAAATATACCTATATCTTCACATGGGAAGACAAATC | T/C | 13 | 88649999 | 0.854 |
| 13095577311 | TAGCATACGCAGTGAGGTTTTTACTATATAGAATTTTCAGACATGTTATTATCTTTTTTTT[A/T]AATTTGTGGTCAAATCTGTGAGACTCAGTTCAGAGGCTTTACTGGAACACTGAGGGTTTTC | A/T | 13 | 95577311 | 0.849 |
| 13097326077 | CCTTTCTACAGACTTTCCCAGACAGCCTGGTCTCCACATGGGTCTTCTTGGCAAGAGCAGA[T/C]GAGCCATTCAGTGCCTGCCATGGATGGCACAGCACGGAGCAGATGGGGACAGACTGCAAAC | T/C | 13 | 97326077 | 0.824 |
| 13104581568 | CAAAGTCTATGACAAAGTGTTTTACCGTGTTCTTGGGCGGTCCAAGCATCCCTTCCAATAC[T/G]TTGGCAAAAGCAAGCTGTGTTCAACCACAGTGCTGTTGATAGGTATGACATATCCTATGAA | T/G | 13 | 104581568 | 0.79 |
| 14000060332 | GAACATATGAGTCTCTGCAATCACACAGATCGGATTTAAAATAAATGGGAAAACAAAACAA[A/T]TGAAAAGACAACAAGCATACTTTGAAATTTTTCTCAGATTTATTTTTTCCGAATTGAAGAT | A/T | 14 | 60332 | 0.572 |
| 14001569186 | GGCAGATGGGATGCTTCAGAGCTGGCTGAACAAGGGTATTGCCCAAGCACTTCCACAGAG[C/G]TCTGTGACACTGAGGTACCAGTGAGGTAAGAAGATATCATCAGCAAGGTGAGAGGGCCT | C/G | 14 | 1569186 | 0.916 |
| 14006164102 | TGCTCCTTCTCTTTGAGTTGTGGTCTCTTACTGAGACTGAAGATTCCTGATGCCGGTAGG[A/T]CTGCTGCAGAATGAGCTCCATGGATCATCAGGTGTCCCACCCATTATGGACATGGACCC | A/T | 14 | 6164102 | 0.821 |
| 14007721627 | CAAAACAGCATCTGCTAGGGGAGGGGTATGTTTGCATGCCGGAAGGGGCGATTCCCCCAGG[A/G]ACTGAGAGTGCTCTCTCTCTGTCATTGTCTAGCGCATCTGCAGCTAGTACTACGGCTTCAT | A/G | 14 | 7721627 | 0.852 |
| 14009423933 | TTGGTGGAGAGGAGGAAGCATTCAGAGGCGACCAGTCTGCCAGATAGCCACAGCATTGATG[A/G]AAAAGAGGAAGAGTGGCTCTGAATGAAAGCCTTCTGCCATACACACTTCCTCATTAAATG | A/G | 14 | 9423933 | 0.914 |
| 14010936357 | TTTTTAAAAACAAATCTGGAAAAAACGTGCACTAACATTTGCACAGACAAGTGTTTTTAC[T/G]CTTCCATTAATAAAAAAATGTGGACTTAAGGAAATCTGTTAATTTAAATAGAACTGCAG | T/G | 14 | 10936357 | 0.866 |
| 14012622412 | TCAAAAAATATATTGCTCTTTCTAAACCTCTTGGTCTGTAATCATGAATGCTACCATTTC[A/G]TGGCACCTTTCTTTAAGGCTTGTATCAGATTTCAGGGGCTTCAAATAATTTCTGTTAGT | A/G | 14 | 12622412 | 0.981 |
| 14014207213 | AAAGATGGCATTCCATTGTGCGATTGTACCATTACTTAATTGTCCATACATGTGTACATAC[A/G]TGTGGAAGCCATAAGACAACATGAGGTGTCATTTTCAGGAACACCTCCTTTGGGACAGATT | A/G | 14 | 14207213 | 0.932 |
| 14015762319 | CTAATCATCTGTAGAAAGGAAAGGACACTGTAAGAGTAGTCTTCTTGCAAGGTTCCCACAT[T/G]GGAGTCCCTGTGTAAGGGAATAGAGTGACTTATAGCAGGGACAGAGTTCATTCTGCATGGA | T/G | 14 | 15762319 | 0.967 |
| 14017380668 | TTAGACACCACACAGTGAATACTTTTTCCATGCAGCAAGCTGGCTGCTCCAGCACAAGACC[A/G]AGAGAACCAGTCAGGAGCTTCTGTCCTCTGTTCAGAAAAATATGGGCTTCCCCAGATCTCT | A/G | 14 | 17380668 | 0.903 |
| 14020494696 | AAAAATGAAGACAGAACCCAAAGACAAACAAAAGCAGGAGAGAAAGTGGGCAAGGAGAGG[A/G]ATAGCTGAGGCCCCAGTCATGATCGGTCATATGTGTCCTAAGGCCCCTCTAAGAAGGTT | A/G | 14 | 20494696 | 0.751 |
| 14022100230 | AAGTTCGTGGAAAACTCTGCAAGTGAAAGTGATAAATCATTTATTGATAAAAAATTGGAG[A/C]GGCACAATGATTTTATTTTGCTGTTATTACCATGTGATTATAATCATTAAACTAATAGT | A/C | 14 | 22100230 | 0.909 |
| 14025264109 | CTGTATTGGAATTTAATTATATAAATGAATCAGTGGGATAGAAAAAAAAGCCCAGAAGTA[T/G]GTCTGAATGCACTGACTCTGTTAGTGGTTTTTGCCACAAAGCAGTGACTTTTCTTGGTA | T/G | 14 | 25264109 | 0.913 |
| 14028439601 | TGATAGTAGAAAAAGTGTAGTCGTCCTGGCTTCTATTAGCACAGTAGAAGAAAGTTCTTT[T/C]TAAACTGTAAGGTGCTGAAGGGTTCCATCATTGCTTTGCTCTGATGTGATTTCTGGGAA | T/C | 14 | 28439601 | 0.912 |
| 14030319736 | TTATCCCAAGATCTGTTGCCTATCTGGAGAATATGTTTTCTATCAGGGCTGTCTTGTTTGG[T/C]CTCAGTGATACAGGATGTGCCAAGCCCTGCAGAAACTTGTTGTAGGGGGATAACCAAGGGT | T/C | 14 | 30319736 | 0.905 |
| 14033491220 | AGGAATTTACATTGCTGAGATACGATATCCAGTGTACTTGGACTATGCATTTCCTACATGA[T/G]ATAGGCAATAAAAATATATACTGAGTGGTGATAAGTTCTGTGAGAATCTGAGGATTACAAT | T/G | 14 | 33491220 | 0.806 |
| 14035022703 | AATGTGCACGTTTCTCGGCACACACAACACATCTACCGTCTTCGTTAGGATTTCTACTGC[T/C]GTGATAAGACACCATGACTATAAGAAACTTGTGGATAAAGGGGTTGATTTTTGTCCTAC | T/C | 14 | 35022703 | 0.519 |
| 14036554401 | AAGTGCTGAGAAATGGTTCTCTGACCCGGAGCTGGGGTTGAGGAGTTTGGCGGTCACTGA[A/G]CTCTGCCTCAGCTCAGACCTCATCTGGCTTCATCCCGCTCACCCTTCCTTCGCCTGTGA | A/G | 14 | 36554401 | 0.77 |
| 14038119728 | CTCCCTGGGGCTGTTTGACCCCCTGTCAGTTTCTATCTCGGTGTGTTTAGGACAAGGCTC[A/G]GAGTCCATCAAGTCCCGGGCGCTCCTGCTCAGTATGTGGCCTTCAGGAGGAGCTGGGCT | A/G | 14 | 38119728 | 0.876 |
| 14039687344 | AGAAAGAAATAGTGAATATTGTTGAGAATAATAGGCTTTGAGATAATATGATATGGTATGG[A/T]AAACCATAAATTTAACAGCCTACCTTCCTCAACTACAGAAATTAAAACATATCATTAAAAG | A/T | 14 | 39687344 | 0.797 |
| 14047726412 | ATTTTCAGAGGAAGTTGTTTTGTCATTTCCTACATTGACTTACATTTGGTGCAGAAACAAT[A/T]GAGCCTGAGGAAGCGGGGGTGAATCCTCATAAAGATTCTGTAAGGAATCAGATCCATTGTG | A/T | 14 | 47726412 | 0.883 |
| 14049720566 | AAAAACAAAAATACCTTGTGGGTGCTGGTATTAAAGGCATGTATTAACTCTGCCAGCTTT[A/T]AGGTATTTCCAAAAAAAGCAAACAAACAAACAAACAAACAGCCTTATTACAGTTGCAGC | A/T | 14 | 49720566 | 0.715 |
| 14051659098 | TGAACACACCTTTTAGGGCCAGAGAGTGGAATGTGGTAGCAATATTTGGAGGTGTGAACT[T/G]GTTATAGTAGATGTAGCTTTGTTAAGTAGGTGTGGCATTGTGGATCTGGGCTTTAAAAC | T/G | 14 | 51659098 | 0.659 |
| 14054243535 | CAAACCAAAGCAGGGAATATCATTCTCAGAAACATCGAGGATAATGTTTGACTACATCTAG[A/G]CATCATGGACCAGTTAAGCCAACACATGAAATTAAACATCACAGTGTTGCAACCATTCCAG | A/G | 14 | 54243535 | 0.859 |
| 14057388340 | CAGCCCTTAATGCACATATTATATTCATGTATAAAATATTTGAATTTTAATTCATTCATC[A/T]GTGTACCATTATAGGTACTTTTGTGCATTCAGAATGTAAAATATAGAATATATTTATAT | A/T | 14 | 57388340 | 0.708 |
| 14059067499 | CTGAGAAGAAAACACTGAGAACTATATCTAAATAAAAATGTGTTACCTCTTTGATACCTGT[A/G]TTATTACTGTTTTTTAATAATCATGAGACTTGTTGCCTAGGTATCACTTATGGACAAAATT | A/G | 14 | 59067499 | 0.648 |
| 14064271419 | AGATAATGCTTGAGACACTATTCTCTCTTTTTCCTTTTTTGATTTATGCTCCTGACCTGT[A/T]TGCCAAGAGAGAAGGAAAATCAGGAATAACAAACAGATATCTTATGTAACAGGCTGAAA | A/T | 14 | 64271419 | 0.819 |
| 14065908860 | ATAAACTTTTTCTCCCTCCAATTGTTTTTCATCAGGGTTTTTCATTATCACAATAGGAAA[T/C]GTAACTGACACAGCTTTGAGCTGAAATGTAGGATAGCCCTCCTTTTTGGTGGTCATGCT | T/C | 14 | 65908860 | 0.925 |
| 14067446669 | GGAGATAGAATACAAGTTCACCCAAAGGGCAACTTTTAGATTTCCCTTGTTTTTTCATCC[A/C]TAACAAGAGACTAACATCCTGGAGTTCAGTCATATTGTGATATTGACTTTACTTTATAT | A/C | 14 | 67446669 | 0.889 |
| 14069100564 | TCTAAAACAGAAACATTCTGCAGGAAAACTGCCCATAAATAGCCTATGTGAGTGAGATAGC[T/G]TCCTTTCAGATATGTTTCAAGTTGAATGGTTTTGTCTTCATAGTANCTTGGTGCACNCTGA | T/G | 14 | 69100564 | 0.823 |
| 14074797749 | ACATTAGCACAACTTCAAAAGTCCCATAGGCTATACTAGTCTCAGCAATATTAAAAGTTCA[A/G]AGTTCAAAGTCTTCTTAAATTCATCCAATAATTTAAACATAATCCTCTATCAAATCAAACT | A/G | 14 | 74797749 | 0.615 |
| 14078060932 | GTTTATGTGATGGTGGATGTGAATGCAAATACCTTATGAACCAGGGATTAAATAACTTTT[T/G]GGGGGAAAGAATGCCCAGAAAGGGAAGCTCATTGGCCTAACACTATCTAGATGCCTCAT | T/G | 14 | 78060932 | 0.671 |
| 14079645175 | GACTTGAGGGTGACAGAGCTCTGGGTAGAAGGCAGAGCATAAGCAAATAGTTGGGGGAGCA[A/G]GTGGATGGCACCAGGAAACCTTGGCGCCCAGGCTGAGATGCCCCTACATGGGAGGCTGCTG | A/G | 14 | 79645175 | 0.804 |
| 14084841644 | GGGAACTGGTTTTTCACTCACCTCTAAGCAGTATTCTTGCTAGGTTTAGGGATCCGGCTTC[T/C]TAGACAGCTTAGACCTCAAAGGAGTATCGGTCTGGGCTCACATCTTCACTCACTTGCTTAA | T/C | 14 | 84841644 | 0.962 |
| 14086540454 | CTGTTGGGAGCAGCGTACCCAAGCTTACCCCAGTGCTGCTGCGCCCGGCTCACCAGGAAGG[A/G]TCTCATCTGGATAAGGCGTGTGGCATAAATATGGGCGTACTGTCGGTTAAAGCTGCGCTCT | A/G | 14 | 86540454 | 0.809 |
| 14088308546 | GAAAGAAAGGACCAGGGCTGGAGAAATGCTCTGCAGTTAGGAACACTTACTGGTATTCCA[T/C]GTCAGTTCCCAGCAGCTCACAGCCTTCTGTAGTTCCAGGAGATTGGGTGCCTCTAGACA | T/C | 14 | 88308546 | 0.763 |
| 14089819261 | CTCAGTAGTATGTATTGTTATTATATGCCAATAAAATCATAGAATAATGAATTGTGAAATA[A/C]TGACAAGTCAGGTGTGCCAATCACATATAATCACAGTAGCCGCAGGTACCACTATTGGGTG | A/C | 14 | 89819261 | 0.911 |
| 14092879829 | AAATAAGACATGCTGTCTTCTCATAACCACTAAAGCAAAGTCCTGCCTTTATGAGGTTTCT[T/G]TTTTAAATGGAGACAATAGATACCCACAGACATATTATACAGTTTGCTCATTTACAATTAA | T/G | 14 | 92879829 | 0.773 |
| 14094448681 | GCCAGAGTTAAGTCCTATACATTGGAGACCTTTCATCTTATCCCATTGTTTTTAAGCATTG[A/C]TTTTACAGAGGCCTCTCATATCATGAATTAAGTTGGTTATGCTTATATTTACTTGTGGCTG | A/C | 14 | 94448681 | 0.874 |
| 14096038202 | AGGGCCTGCCACTTCTGTGAGCGTGTGAGACGGTGTTCCTAGTTGTATCAGAACTATTTGG[A/G]GTTCAGCTATCTCTGTAATTCTGTGATGCTGTCATCCTGAGGTCCTGTGTGTGTCAGAGCT | A/G | 14 | 96038202 | 0.781 |
| 14104354286 | GAAATTACATACAGGTGGTTGTAATGTATTTGCTAGGAAGACTGGAATTTGATTTCAACA[T/G]TCATTCCCAGAAGCCAACAGTTAGTTGCCTATAACTCTAGGTCCAGGGTATATAGTAAA | T/G | 14 | 104354286 | 0.972 |
| 14109129876 | AGAAATCATCAAGATGTAAGCTAATGAGTTTTCTTGCAGAGGAAATAAACACTGGAAATA[A/C]GGAACAATGTCACATTGGGTGAAGTATATTTAAAATTAAATGTAATCGATTCCAGTGAG | A/C | 14 | 109129876 | 0.989 |
| 15000027190 | AGGGATAATTAAACAACTGATCTACTGCCTCTACCCCATCATGGGCTGAGATTGCAGACG[A/G]GTGTCACCACAGCTAACTTGACACAGGTGCTGTACAGCTCTGAATCTGGGGCCTCGTGT | A/G | 15 | 27190 | 0.937 |

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|---|---|---|---|---|---|
| 15003160721 | GAGAGCCGTGTGGGGGAGGGATGACTTAGGAGACATGTAATGGAGGTAAAATAAAGACCCA[A/G]GAAACCAGAGGACCACGGGGAGAGGGACACAGGAAAAGGCTGAAGGTGGACACTGTGGCAG | A/G | 15 | 3160721 | 0.972 |
| 15004801074 | ATGTCCTAGAGATTTACCACCACTGCTTTTTTTCTTTAATAAAGTTGGGGAAGTAAAAGG[A/C]TTTGTTGTGCTTTGCTTTGAATTAGTGTATTCCGTTTCTATGATTATTGTGCATCCTTT | A/C | 15 | 4801074 | 0.91 |
| 15006564128 | CATGGTCAAGCTTTTTTCTCGAGTGACTATTCAAACTTGATATTTTATAACTCACTTTCA[A/G]ATTTGAGCCTGACATCTTAAGCGAGATTCTTAAACATAAGTCATGTGCTTAGAGAAACA | A/G | 15 | 6564128 | 0.805 |
| 15010453477 | GAAATGTAAAAGAAGTCACCTAATTATTTTCCTGGAATGGATCCATAAGAGTGTAAATGTT[T/C]TTTGCAGATGTGAGGACACCCACGCTTGACAAAGTGGTGGATGTCTGCCTGATTGCTCTGA | T/C | 15 | 10453477 | 0.991 |
| 15011989650 | AATGTCATACAGAATCAAGTTTGGCCTTGTTACTACCACCAATGTCAACCAGATAACACTT[C/G]ACCAGGATATGTGTAGTGTACACCCTTGAGCAAGAACATGTGACCTCCTAAGCCATACGAA | C/G | 15 | 11989650 | 0.946 |
| 15016761941 | GCCAAAACTATGTTACACAACTTTTGGTATATTGATTTTCACTTGACTATCAGACATGTAG[A/G]TAAATAAAGAAGGAAAAAGAGAGCTTTTAGCTGGTTACCTGGAATTTGTAAGCATTGCCAC | A/G | 15 | 16761941 | 0.763 |
| 15018306647 | TATTTTTGACTTGAGTTCTCAGTGGCCGGAACAATTTTAAAAATTAACCACCCTGGAAGC[A/G]CCCACTTAGTCAGGAATCACTGGGATCCATTTTGTTCTCCTTTACTAGAAGTCAGGTAG | A/G | 15 | 18306647 | 0.957 |
| 15020021035 | GTGTCAAGAAAAACTATGCTTACTCTAAAACAGAAGTCTGAGGATGAACAGTCTACAGATA[T/C]AGTGACCTCCTGACAGAGCAAGAAAGCGATCTTTAAGCTGAACTCAGCTCAGTCCCTGTTC | T/C | 15 | 20021035 | 0.619 |
| 15021614352 | ATGGCGGTTTCAGCCAGAGTAGACGCTAGAACTTCTTGTCCAGGAAGAGAATGGACGTTGA[A/G]GGAAAGCAATGCCTAACAGTTGGACATACCCTGTGTCCTGCCCATATCTCTCTTATCTCTC | A/G | 15 | 21614352 | 0.926 |
| 15023183146 | GGAGCACACACTGCTGCTCGTTCAGAAGACAAAAATTCGATACCCAGCATCCACATCGGGC[A/G]ACTCACAACTGTGTGCTACACCAGTTCTAGAGCACCCAACGCAAAGCCTCTGGCCTCTGCT | A/G | 15 | 23183146 | 0.789 |
| 15024877509 | TTTTTAAAAAAGCATTTTAAAATAATCATTGCATTTAACCTTATAGGAATCTTCTACAAGT[A/G]TACAGATAGCCAGAATATTGTTTAAGGCCTAGACGATGCCATTCTAATTGCTGTAGAAATG | A/G | 15 | 24877509 | 0.748 |
| 15029215322 | AGATTTAATATTTTCGTGTTTTTGGAAATCTTGATTTTTTTCCTCCTTCTGTTGTTTTGAT[A/T]AAGCTTTATTGTTCTTGATAACAACACGAACTGGAACATCAGCCTACGGAACTGTGTTTCA | A/T | 15 | 29215322 | 0.638 |
| 15031761885 | AATTTATGTTCCTGGCTTTGAAACTGATTATTTGGCTGCCTTCCTGTGCCCCTTTCCATAT[A/T]CTGCCTTTAGGTAGGGATATCTATCCCATGCTGTTAGCCTCACTACCCCCGACCAATCACC | A/T | 15 | 31761885 | 0.733 |
| 15033388004 | TGGGCACAGCCACTGCTTTTTAGATCACTTCAGTGGGCCAGTTCAAGGTCAGCCCCTTTGC[A/T]TTGGTAGCACTGTATACATCTCTGAATGCGTCACTGTGATATGTCTCAGCCCTGTCTTGAT | A/T | 15 | 33388004 | 0.986 |
| 15039297389 | ACGAGAAAGACTCAGAAGCTACTATTGGAGGTTTTTTAGTCACCTGAATCACATGGTCAC[A/G]CAATTAGCCACTGGGAATTGTCCCTAGCATTGAGAGGAAAAGAAGTAAATATTAAAAAA | A/G | 15 | 39297389 | 0.859 |
| 15040996673 | GAGACAGACATTGCACATAGGCAAATGACAGTTTGTAAATGTAAAAGGGGAAACCTGTGTA[A/G]GCATAAACTTTTCAACCTACTTTAATAAGAGTTCAATATCCCCTTCAATCACCACCCATCA | A/G | 15 | 40996673 | 0.71 |
| 15042940968 | ATCCCATCCCCAAGTGTTGGCCTCGTGAGAGCACCGCCAGCCCCATGCATCATGCTGATG[A/G]GCTGAAGTGGGTATTTGGGGGCAGAGAGCTCAAGGAAAGAGTTTAGTTTTTCTGTTTCT | A/G | 15 | 42940968 | 0.794 |
| 15044492765 | ACAGAGCACAGTGTCGGGGACTTTAACACACCAAGCAGAAGGAATGACTGACTTAACAGT[A/G]ATTCTCTAAGCATCAGCCACATTTAGGAGCCCGGACGTCCAGAGCAGAAGCCACTGCTC | A/G | 15 | 44492765 | 0.9 |
| 15048583778 | AATCTAAGTGATACAAATACAAGTGCTATTGTCTGGTCATCCTGATCACACAGTTCCACTG[T/C]GGAAAAGTCTCTGGAATCTACATGCCCCGTATTTAAGTTTTTTGACTCACCACTCTGAGTA | T/C | 15 | 48583778 | 0.654 |
| 15050563324 | CTAAGGGTGGCTGATAAATGAGACCAAAACTTAAGGGTTTGCAAAAGACCACTGTTCTCTA[T/C]CTCCTCTCTGTTCAAATGCACCCCACACAGGGCAGGAGGCTGATCACCAGACACACACCTG | T/C | 15 | 50563324 | 0.923 |
| 15054562452 | TTTTAGACCATGCCCAGATACAGTTTTGTGCTGCTTAATGTTTAGCTGCTTCTGCTCCTTG[A/G]AGACACCTGGAATGTTCCTGTTCAGTGAAACTTTAAGACAAAAGCAATTTCAACGAAATAC | A/G | 15 | 54562452 | 0.903 |
| 15056136431 | CAAGACAATCCACTTCCTCTGGGCTGCAGCTGCCACATTCATAAAACCAGGGGGGTAGCCT[A/G]GGCTACTCTTCAAACCCTTGTTTTGTTTATATCACTACCTCTCAGAGAGATTGTGCAGGTT | A/G | 15 | 56136431 | 0.977 |
| 15059253615 | TAGCAGTTATGTCTCCTTTTCCAGTCTTTTAATTTCGTTTTGTTTGTTCACCAGCTTACAG[T/G]GTAGCTGGCGCCCTCGTGGCATTTTCTTGATTGCTGTATTTATGACACCTTTCGTTTTTTT | T/G | 15 | 59253615 | 0.883 |
| 15060888797 | TGTACACACACATGTTTTGGTCAAAAATCAACTATTTCCAGTTTGGAATTGGCTTGCATAG[A/G]GACAATAGAGGATTAGTACAAAGACGAGGGAATCTTTTGCTTTTTCTGTATCTTTACTTCC | A/G | 15 | 60888797 | 0.956 |
| 15073521957 | TTGGGGCTAAATTTCTATAGCCTGACCAAAAGTGATATGAGTGCATTTGTGATCATGATCA[C/G]ATTAAGAAATTAGGCTACACATGGACAGATCCATGGCTCCAGTTGCATATGTAGCAGAGGT | C/G | 15 | 73521957 | 0.981 |
| 15079820106 | GAATAAAGCAGAGAGAGCCTTTGGCCAGAAGGTATCATGATAGTGTTCAAAGGATAGTGTG[T/C]TCTCCTCGCTCTTTTAAGCTTTATAAGACCATGTGGTCTTGAATTACTACCTCTTGCTAGA | T/C | 15 | 79820106 | 0.817 |
| 15081552396 | AATATAGGTGAAAATTAAATTTCGCTATGGCTGCCAGCTTTGAGTGTGCTCTTTACGGAAC[A/G]TAAACAAGCAGAGCTGTTTATGACATGGCAGATGAACAAATATGTACAGAAATAATATCAC | A/G | 15 | 81552396 | 0.947 |
| 15084753970 | AGTATTTTAAAGACTTTCCAATGCTTATGAGCACAACACTTTGTTTTCTGGTATTTCCCCC[A/C]CAGAAAACATCACTTACAGTTTTGAATGAGCCAGACCATCTCTATTTTGTGTTTGAATTTA | A/C | 15 | 84753970 | 0.962 |
| 15089805308 | GTATCAAATTATGCATCTTTGGAATGAGTTGTATGATTCTGTTTGGTTCTAATAATTGCT[C/G]TTGCATTGACTTGAATTCCAGAAAAACTCATCAACTGATCTTTCACTTTGGATTAATAC | C/G | 15 | 89805308 | 0.967 |
| 15091387257 | TACACTATCCAAATATGATAAAGGTGTGAAATTACATTACGAAATATATTCACAGCAAAAC[A/G]AAAAAATAAAACGACTAGATTGATTTAAGCGTTTTTATCGGATAACACACTTAACATTTTT | A/G | 15 | 91387257 | 0.725 |
| 15094560146 | ATTACTGAGGGACATAAGTTGATGGAGACATCTGTTTAGGTCTTTGTTGTTCCAAGGTCTC[A/G]CAGGCTCTGTACAATGTCTGAATGTATGTCTGCCATACTCTGTGGGAAGATGCTTTTCTGA | A/G | 15 | 94560146 | 0.934 |
| 15100784346 | ATATACAGTAATAACTGGCTTGGGAAGATATGATTACTGGTGGAATAGTGGCACAAACAT[A/C]ATAAGATTGTCCTCATTGGTTCATTTCCTCCATGGAAATAACAATGCTTTGTCCATACA | A/C | 15 | 100784346 | 0.862 |
| 15107141928 | TTCCCCAGCAGGGAAAGGCAAGAGGCTGGGCTGCCCTGTGGCCACCACTGTTTTCTTCTTT[T/C]CTTTTCACAGAAAATGGTTTTCCCTGCTATAGCACTGGCTAATAAGAGAAGACTTCACACA | T/C | 15 | 107141928 | 0.942 |
| 16002097566 | AAGTTCTACATTTGAGAGAAAATTTTCAGTATTTGGCCTCGTTTCCTTTCCCTCTTACTG[T/G]CTTCTTATTCTCCTCCGCCTTTCTGTAGTCTCCTTTCTCCACATTTCTATTGTATATCA | T/G | 16 | 2097566 | 0.916 |
| 16003714855 | CCCTGCCAGGTTACTGTAACTGAGGCACAGGGAAGACAGCCTGTCTGTTTCTGAAGGACC[C/G]CTGTCAGCAGTATTAGGAATATCCCCTTGGAGAGAGAGTGACAAAGATTCAGATCTTCC | C/G | 16 | 3714855 | 0.984 |
| 16006905481 | GAAAGAAAAGTAAATAAATTAGACTGTGGCTGTAGCTCGGGTGGACTATTCACCCAGCAT[T/G]CATGAGACTTTGAATCCCAGCACTAAAAAAATAAAATTGATGAAGGTGATCTTATGAGC | T/G | 16 | 6905481 | 0.901 |
| 16008429540 | TTTCCTCCTTCAACCTGAAACCATGGCGGGGCCAAGCCTGACCATGGATCTTCCATGGAG[T/C]GCTCATCCTCCTGGTCAGAGCCTAATGTGACCTCATGTGGTCCTCACCCTCTCCTGCAG | T/C | 16 | 8429540 | 0.787 |
| 16011475486 | TTTGAGCTTTCTGTCTGCATAGATCTATTCATTAAGGAATTCTTGACTAATACTAGACTC[A/G]TTTAGCTTCTTGGCTTAACACAGTAACATTGAAACTTGCCAATTGTAGCTTGAATTAGC | A/G | 16 | 11475486 | 0.59 |
| 16013144600 | CCACTTAATTTTTGTCAAATGGAACCAAGCTTATAAAAGTTAGGCTGAGGGAATTTGTGCT[A/C]CAGGAGCACTCATCATCTTAATCAATTTCCACTCAAAGTGCACACTTGCTCAACTTGGAAT | A/C | 16 | 13144600 | 0.964 |
| 16014682846 | AAATATCCACCTCTTTAACCTGATTCTGAATTAAGGACTTAGATGGAAGAGAGGAATTGAA[A/G]TTAACTAACCTGTGTCATTTCCATAACCAGCTACTGGACACATTCACAGCAATAAGGAAAA | A/G | 16 | 14682846 | 0.901 |
| 16017852571 | GTTGGGCCTCAGCCCCTGCTGCCTGCTCTATGGGAAAACTTTCACCCTCTGATTCCAGCC[T/C]GGGGTTGCCTCTTACTGACTGAAAGCAGTGAGAGACACCAGAAACCCTGCCTGAGAATG | T/C | 16 | 17852571 | 0.886 |
| 16019450680 | CTGTAATGGGATCTAATACCCTCTTCTGGTGTGTCTGAAGATAGTGTAGATAATTTTTTTT[A/T]AAAAAAAGGCTAATGGATACAGCCCATGGGATGGTGTTCTCCTGATTGACTCCTAGGAGAA | A/T | 16 | 19450680 | 0.726 |
| 16021150350 | GGGATTCCCTGTCACCACCTCCTGCCTCATCATCAGTGCCCCAGGATTCAGATGCACTTG[A/G]GATCATCAGACTTCATGTGGATTCTGAGAATCCAACCTTCATTCTCACAGACTCATGGC | A/G | 16 | 21150350 | 0.685 |
| 16023115819 | ATTTCTGCTGGACAGCGAGCTGAGTGTCGCTAATTCTCTTAAGGTACTCTCTTCTTTCTCA[A/G]CCTCCTGTCAGCTGTAGAGCCCGAGAATTTGGTCAAGTCTGGTGTTTGAAGCAGGTTAATA | A/G | 16 | 23115819 | 0.933 |
| 16028357587 | GTGGAGAGAAAGAGGAGTCAAGTTTGAAAAGAAGTCAAGGGTCCTAGAAAAGGGAACTAT[C/G]GATCTACTATTAGTATAGGAAAAGGAACTATAGATGGCATAAATTTTGGATAATGAATA | C/G | 16 | 28357587 | 0.695 |
| 16030342160 | TTGCATCCAAAACTGTGAGATTGATTCTGACCAGAGTGGAAATTGAGACCTGTATCTCTA[T/C]GTTCAATAACTATATCCTTCCAGAGATTACAAACCTAGGACCTGCAACCCCTTTGCTTT | T/C | 16 | 30342160 | 0.718 |
| 16032474356 | AATATTTCTACTGTCTTGCTATTGAAACAACGTTGTGAGCGCTTTAAATTTCTCAAACCAG[A/T]TTCGTCTGTTATACTTGGCGCTTAGTCATCGTCGTACACAGCAGGACCTGATTAAGAAGGC | A/T | 16 | 32474356 | 0.894 |
| 16041701263 | GGGCCTAGCTTCAGCTGATTTGGAAGCGTCCTCCCTGAGTACTAGCTTTCATCAAAAGAA[T/C]GATCTGCTTACTTAGCTGCAGTTCTGTTTTAATTAACTAACAGAAACAAGTACAGCATT | T/C | 16 | 41701263 | 0.902 |

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|---|---|---|---|---|---|
| 16043608855 | GTAAAATATTAGGCATTTCTTCCTTTGCTTTTGTAACCTTTTTATGTATCCAGATTCAAC[A/G]AGATGCTCCCAAGATATTTTTTAAATATTTTAAAGAAATATGCATTAGCCAACAATTTT | A/G | 16 | 43608855 | 0.773 |
| 16045256020 | GACCTTGATGTGTTTTAGATATCTGCTGGGTGTTTTTAAAGTGAAACTAAGTTTGAAAGG[T/C]GTTTGATAGGTAAACCTCAACTTAAGGAACACACACATGGTATTTCAACATCTGTAAAT | T/C | 16 | 45256020 | 0.726 |
| 16048477219 | ATAAAAGCATCCGGAGCCTTAATTATCACCTGGATTTGTTATATCCTGCATACTTTTAAAG[A/G]AAGTTCCTTGAAGTATTTTTATTTTCTGTGTGTGTGTGTGTGCATGAACATGTGAGTGTAT | A/G | 16 | 48477219 | 0.637 |
| 16053321660 | TGTGTCTTTCTTGTTAAAGCTGGGCTGGTGATCAGGGTGATAATTTCTTGTACCCATTTTT[T/G]CACCCAGCTTCCTAATATGATTTAATAAAAATCGTTAATGAGTAGGGGTTCCCCCTGAGGG | T/G | 16 | 53321660 | 0.502 |
| 16055002540 | CAAAATCAAAACCACTTTAGGATTTCCATTTATATTTGTGCAATTAAAACACGACTAGTG[A/G]ATGGTTGTTGGTAATTGCCAACCTGACGACTCCAGAGTCTCCTGGGGATACGGGTCAGA | A/G | 16 | 55002540 | 0.886 |
| 16057142447 | AGGTTCCTTTGGCTAAGAGCTCAGTTGAATGCTTTCGATATTGAATTTATGCAAAGATAG[T/C]CTGTGCCTATTTTTGAAACTGGATCATTAAAGCCTCTAAGTACTTATTCCATTCTCTTT | T/C | 16 | 57142447 | 0.941 |
| 16058682220 | TCACGTTATCCTCCAATAGTAGTCTCTCCACTAGTACTATTGAATTTGCTAGTCCTTTGT[A/G]TAACAAACTTCTGGAGATCATTTGTTCATTAAAAATGTAGTCTTATCTTTCTTTGGAAT | A/G | 16 | 58682220 | 0.861 |
| 16060330064 | AAGGTTGAGCATTTTGAGCCTTTGCAGACGGCTGAACTCGTCGGGCAGAGCCTGTAGCCC[A/G]TTGTTGTCTAACATGAGGCTCTCCAAACTGGCCAGCTCACAGAAGCCGCTGGGCAGAGT | A/G | 16 | 60330064 | 0.897 |
| 16063605256 | GTCTCATTTCCCTCTCTTAGACCACTTTGTGTCTGTGTGACACAATGAGTTTTATCAGAGC[A/C]ACTTGCAAAATCATGGGTAAGAATTTGTCTTTAGGACTATGGATAGTTTGCCAGTGACTAA | A/C | 16 | 63605256 | 0.91 |
| 16066926357 | CCTTTCCCTCTTACACATTCCATACCCTTCATTTTGTCTGCATTTTTAGTGTTTTCATTA[A/C]TATATGATAAGGAGTTCTTTTTCTTATCCTATTGGGTGTTCTTTAAGCGCCTCATACTG | A/C | 16 | 66926357 | 0.703 |
| 16070106379 | TTGGTTTTTATTGGTAGAATAAGTGTGCGACCTCCTGTTAACCGTGTGACCTCATTGTTG[A/G]TGAACTGGACAGGAGTGTCCCCAGCTAGCCTCGATTTCAATTCTGGATCTTCTCTGGCC | A/G | 16 | 70106379 | 0.908 |
| 16071658140 | CACACTGGTACAGAAAGACAATACTACTAATGCAGCAGAGAATTGTAATTGTTTAGGGGCA[T/C]GTATGTCTCCACATGACCTCTTTAATGTCTATAATAGACAGGCATGTGCATCCCATAGCAT | T/C | 16 | 71658140 | 0.932 |
| 16073178584 | GAAGCAGTTGAGTGCATTTAACCAGAATCATCCCCTCGATGCTTCCTGTCAGTGATTTCTC[A/G]CCTGCTGGCCTCCACTCTGTTCCTTAGTTATAAAGTCCCCATTTGCCTTCATTGTAGTTGG | A/G | 16 | 73178584 | 0.931 |
| 16074693199 | AAAAAAGCAGGGAATTGCTCCACGAGCCTGTCTTTCCAGGCCTTCACCATGTAGAGACAC[A/G]CTGGCTCATTGACCTGCCCATTTTCTTACTTAGACCTGGAAGAGCAGAACCTGACATAG | A/G | 16 | 74693199 | 0.887 |
| 16076230619 | AGCCATGGATGACCCCAGTTTCTACCTCCTGAGGGCTACAGTCTTTAAGTGAGTGCCACCA[T/G]GCCTAGTTTATGCTGTGCTAGAGAATCAAGCCCAGGGCCTTGTGTGTGCTGGGTTTGCACT | T/G | 16 | 76230619 | 0.953 |
| 16078170106 | CCATGGCATTGTGACCATGAGTGACAATATCCTTGCACATTTCTTCTAACAAGGTATCCT[T/C]ACCCATACCCTAAATATCAGGCAGGGTTCCTGAAGATTGAGCAAAAGACAACTGCCAAT | T/C | 16 | 78170106 | 0.828 |
| 16079970671 | CATGATTTTCAGTTGTATACACGGGGCCACGTATCAAACAGCTGTCGATGAGCCAGGCATC[A/G]TACCGAGCTCCTCTAACAAGCATTAATTTGAATTTGAACCATTACCTCTCTTTTCTGATCA | A/G | 16 | 79970671 | 0.827 |
| 16083135970 | CAGGTGACAGGCGGGCCTCACTGGGAGACCTGTTTCTCCATGAACACCGTATCATCCTACT[T/C]TCTAATACAGTTGCTTCCTGAGCAGATGTGCGAGCTCACTTATGGTTTTTTTGTGGCATAC | T/C | 16 | 83135970 | 0.939 |
| 16084722774 | TTTTTGTTTCATCTCCTTTGATACTATCCCTGCCCTGCTGAAGGCCAGTGCCCCCTGAGAG[A/G]CCTCCCATTCTGTAGACTCTCTCTTTTATCTGTACAATGTGGAATTTCCCACAGATAATAT | A/G | 16 | 84722774 | 0.842 |
| 16086483770 | AACTAATGAAGTCTCTATTCCAGGTAAGGAGTTGGTGAACCGGGCTTTGTAGCTGACAAAC[A/G]CGTTGACACGAGGTCTCTTGTTGGGTTTGGGGAATACCTGCACATTCGATGTGATGTCAGC | A/G | 16 | 86483770 | 0.946 |
| 16090046133 | TTCTGCTAACTCATGCTGAATAATAACTGTCATCAGTGGAATACCCACTGCTTTAGGGTCT[T/C]GGTTAGAGATCACTCACATAGTATCTTACAGATTCTTTTCAGTATCCCTAAAGGCATTTGT | T/C | 16 | 90046133 | 0.807 |
| 17000144919 | CCATTTTAACTATGAACTTGAGCTAAGCAGGTCCCCAAATATCCACCATCTTAAACTGAG[A/C]ATGCTCAGGAAAGTGTTTCCCTATATACATATCTATAGGTTCTCCAAGAAAAATCTCCA | A/C | 17 | 144919 | 0.924 |
| 17009834035 | GTGTGTGTGTGTGTGTGTGTGCTCATGTATGATATGTATGAATTCAGGTGTGTTCAAGCCA[A/G]GACAAGCATAAGGCAGTCAGAGGACAAGTGGAGACACCCTCCACCCTGTTCGCCCTGGAAT | A/G | 17 | 9834035 | 0.842 |
| 17011614563 | AGATATGGGTCTTCGTCTCGGGTTGTTTTTGGACCCTTTCTTCAAATCAATTGTATTGTT[A/G]GTGCATAGCAGACCCTGGACTCATCTGAGTAACCTGAGTCCTTTTTCAAGATTGTTTAG | A/G | 17 | 11614563 | 0.973 |
| 17020929127 | GCATGACCACTTGAGTCTGGATCCCGGAGACACGTGCAGAAAGCTGGGAATGGTGATGTG[T/C]GCCTGGAAGCCCAGAGCTGGGGAGGAAGCACAGGGATCCGATCCACGGGGCTTGCAGGT | T/C | 17 | 20929127 | 0.698 |
| 17022486161 | TCAGATTTGTGGCAGTCAATTTTTATTGTCAACCAACAGGACTTAGAATCATCTAGGAGA[T/C]ATACCTCTGTGTGTATCTATGAGAGCATTTCTCAAGAGACTTAACTGAGGAGGGAACAC | T/C | 17 | 22486161 | 0.701 |
| 17024009487 | TGAATTCATATTGCCTTTTGGAGTAAATGCCAACAAGAGTATGATTCTGGCACACAATTG[A/G]ATAAGACTGTAATTTTTCAGCCCAAACTTCCTATAGTATCAGTGACATACATCTTTCTG | A/G | 17 | 24009487 | 0.906 |
| 17027239725 | ACGTGTGCTTCACTTTCTCCGAGAGATGGGGTGATGCAGAGTGTACACATTGGGGTGTTGG[T/C]GTCTCAGAACTAATTAGTGGAGGTTTCACAAGGCCTACACACAGCCCTTATAATATTAGTA | T/C | 17 | 27239725 | 0.985 |
| 17028801656 | TCCTCATCCCCAGGAGGCTGAGTTTTCAAGAAGCTTAGTTTTGTTAGAAGTCATAAAGAGA[A/G]TTGAATTTGATTTCATCTAATTTATTTTGGGCACCTAGGAAACAAATTGGAGTTGCCCAGA | A/G | 17 | 28801656 | 0.601 |
| 17031881962 | ATGTAGGTGCTAGGGTTTGAAATCCAGTCCTCCGTGAACACAGTCCATGCTAAATCTCTGA[A/G]CCATCTATCCAGCCCATAAAAATAAGATTTAGAACCAACACATGGATTACAAATGAAAAGA | A/G | 17 | 31881962 | 0.911 |
| 17035082716 | AAGGCCAAGACTATCTGGTCTTTATTGAAAACTTCAAAAACAAGACTCTTGACCTTGCACA[A/G]ATAAGACCCAGCCTTGACAATAGAGTCCCATCTGTGATACTTTGGCAAGTCCCAGTAACCA | A/G | 17 | 35082716 | 0.898 |
| 17036686836 | ACACACACACACACACACGGTCTGGAGAGGATAAGTTCCTTGAATTCATCTACTTCATTTA[T/C]CTTTTAATCCTGTTAAAGGTCCAGTCACTTAAAGGAATTGAGTTACTGTTGTTGTTGTTGT | T/C | 17 | 36686836 | 0.867 |
| 17038219495 | AGAGGACAAGACATGGTAGCCTAGAAATCCAGACATTGCAGAACAAATTAGGGCCAAGTTA[A/C]GCCAACTACCTATTCCTATCCATAGCCATTCACAGTATGGAACCTGGGCGATCAGTCTCAC | A/C | 17 | 38219495 | 0.965 |
| 17039826041 | AGGTTTGGGAGCTTGAAGGAATAGCTCGGTGGGTTCGCACATAGGTACCATATCTGAAGCC[A/G]CAGTTCCTAGCCACAGATCCCCTCCCTTCCTTCATTGTCCCTCAGAAGCTTGTGAAGATTC | A/G | 17 | 39826041 | 0.998 |
| 17050250384 | CCTTCATCTCTATCATGTAACAATAAAAGTGTCTGAAGTTTTGTGTTTGTGGCCAGGTAA[T/C]TAAAGTGATGGACTCTGGGTTATTGGGCTTTTTCAGCAGCAGATTCGATTCCTACACAT | T/C | 17 | 50250384 | 0.962 |
| 17053549720 | TGTAGTCATTAACATTAACAGAGAGGACATTCCAGTAAAATGTGTAATATGGACATAATG[A/T]GAAATATGCATTTTATTATACAAACGAGCCTTAGGCCCAGGCAGCCATCAACACTCTTG | A/T | 17 | 53549720 | 0.548 |
| 17057521811 | CAAAGGGATAATTCCATCAGAGTAGGAAAGCAGGACATCAAGCAGCAGGTATAGTGTCCA[A/G]TGCAGAAGGCCAAGATGTCACATCCTCATTCACAAGCACAAAGCAGAGAAAACCGAAAG | A/G | 17 | 57521811 | 0.787 |
| 17059039727 | ACCAATCAGAATGGCTAAGATCAAAAATTCAAGGGATAGAACTTGCTGGTGAGGATGGGG[A/G]AAAAGGGAAACACTCCTCCATGGCTAGACTGTATAATGACTGTGGAAATTAATCTGGCA | A/G | 17 | 59039727 | 0.631 |
| 17060674272 | GAACCTGGAGTTAAGTCTTAATATCTAGGACTACTTAAAGTTACCTATTACTGTTATTCAG[T/C]TTATTTTCCTAAGAATCCTGTGAAGTGTAGCTATTATTTCTGTCATATACAGGAGGAACTG | T/C | 17 | 60674272 | 0.626 |
| 17068613889 | TCCTTCATTTTCATGCAAATTTATTATGTTTACTCTAAAAAATTCATATGGGGTGGTGGA[T/C]GGAACTGGGCAATTCGTAGGGAGCCCAGGAGGCTCTAGAATCCCCCAGTTACTTCCTTC | T/C | 17 | 68613889 | 0.727 |
| 17070447867 | GAGGCTACATAAACACACATAGGTGCACATGAATAAATAGACAAGGGCTGGAGAGATTGGT[A/C]AGTGGTCAAGATCACTGTCTTGTCTTCCAGAGGTCATGAGTTCAAATCCCAGCAATCACAT | A/C | 17 | 70447867 | 0.821 |
| 17072003151 | TGTAATCAACAAAGAGAAAGGAGGGCTCAACAAAGTCTAAGTCTTTACAGACTAATGCCA[T/C]CCCTACCCCAAGTGCTGGGGCCTCATAGCCCAGGCCTTGAACTCTTCTTGATCATTCTG | T/C | 17 | 72003151 | 0.932 |
| 17076739165 | TAATGGAAGGTTGCGATTTTGAATTCCCCATTATTTTCTAGTTAAAGTGGAAATATAAAG[T/G]GATGCCAATATACATATTGGAAATTCAGTTGAACATATTGTCACCTATGGATTCCCTTT | T/G | 17 | 76739165 | 0.663 |
| 17078245200 | CAGATCCAAGGGGGTGGTGAGGCCTGGCTTTGAACTTTGTCTTAGGCTCTTGGCCTTGCGT[A/G]CTGAGCACATCCGTTGCCTCCCACAGTATAAGATACCCCGTCATAGTGTGCGGCAGGGATA | A/G | 17 | 78245200 | 0.703 |
| 17083276274 | TGGATGTGAGGAAGGTAAGGCTTCTGTAGTTTAGGAGTGAGGGGATTTGGGCAAATAGGT[A/G]GGGTTACAGGAGCAGAACGCCATAGCAAGTTGGTCCTAACAACTTCGGGAAACTAAGAC | A/G | 17 | 83276274 | 0.789 |
| 17084867100 | AGTTAAGATTGCTTGGTCCTATGATTTCAGGCAAATAATTTCACTCAAACAGTGTGAGAG[A/G]AAGCAACTGATTCCTTCTCTACAATGTCAACCTTTGACTTGGGAATCTCAACTCCGAAA | A/G | 17 | 84867100 | 0.874 |
| 17086412600 | CCATGTGTAAAGTTTTCCGTGTAAAAATGATCTTAAATGCCAGAGTCAACCTTCCCTAAC[T/C]TCATGGTGAGCGTCGGCAGACAGAGAGGATAGAGCAAGGGCGGGTCACTCTCTGATGAC | T/C | 17 | 86412600 | 0.832 |
| 17088072070 | TGTGTCATCCACCCAGCCAAGAGTATTTATGAACAGCTGTTAACTGACGAGGAAAAGGAC[A/G]CTTGCTTCGGATCACATTGAGGAATAGCTCATGTGAATCGCATTTATTGATCAGGACTT | A/G | 17 | 88072070 | 0.954 |

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|---|---|---|---|---|---|
| 17089629824 | GATATCTTTAGCGTGACATGAAAAAGTGAAAATGATGTTCAGAAAGGATACATTGAACTT[T/C]GCTAAAAGTAAAAGACATTTAATTGTTGAAAGATACTACCAACAGGTTGAGAAGGCAAT | T/C | 17 | 89629824 | 0.731 |
| 18003818313 | GTGCTCTATGGAGCTGTGGGAACACAAGCAGCTGCTTGCATAAAGGCTTTGATTCAGTCA[T/C]AAATTAAGCAAGAAGGAGGCTGATTTAGTTCTACGGTGTTGAGGTTGAAGTTCAGTGCA | T/C | 18 | 3818313 | 0.896 |
| 18006935933 | GCTCAAGGTTTTGGAGGAATAAGCCCATCATGGTTGGGAAGGCATGATGGTGAGAGTGAC[T/C]TGGGGCTGCTTACACTGTATTGGCAGGAAGCAGCAGGACTCCAAGAACCAGGGCAGGGA | T/C | 18 | 6935933 | 0.794 |
| 18010837308 | TGAAGGGAAGTAAAATTTTAATTTTCTCAATAGAATTTTATTTGGTGTTTATTGTTGTTC[A/G]GTGAGTAATGTAGCTACATTTAACCAATTTGGTTTCAACTTTAACTAATATTAATTAAT | A/G | 18 | 10837308 | 0.714 |
| 18012366935 | AATCTTCCTAAGAAGGGTAGTTACGTTGAATATTGACATAGCATAGTCTTTTACTGTACAT[T/C]CAATTGTTTACACACTGTGCTCTTGATGGATGGAATTCTATCCCAATCAACCCAGGATTAA | T/C | 18 | 12366935 | 0.837 |
| 18013887135 | GGACAATTTGAATTTTTTTTCCTCTTTGGTTAATTGGTCTATTAGGAGATAATTCTATGT[C/G]GACCCATATATAACAAAGTGGCTAAAATAAATTCAATGTATAAAGCATAATGTTGCTTA | C/G | 18 | 13887135 | 0.727 |
| 18015474943 | CTGTGTACAGGATATCTTGGTTGGTACCTTGAAAGACATGAGGGTGATTCAGATTTAAAG[T/G]TTTACCTTAAGAAACTTGCAGGCAACCATAAGAAACCTGTTATAGATGACATATTGGAA | T/G | 18 | 15474943 | 0.924 |
| 18017045165 | AAACTGGAAGGCTTTTTTTTTAATTACTTATTTTGTTGTTTTTAATTCTCTAGAACACA[T/C]TGTATATATTTGGATGGTAAAGTATAAAAATGCACAACTATTTCTTTTTCAAAGATGTC | T/C | 18 | 17045165 | 0.543 |
| 18020212418 | AGCACTTCCCTCCTTACTCCCTGATTTTGGTATTCGGGGTACAGTAGATGCTCAATCTAC[T/C]TACGTGTCCTAAGAGGAAGAAGAAAGAGGTCTTGCTTTACTTTCTTGATAGCCTAGGAA | T/C | 18 | 20212418 | 0.873 |
| 18021940656 | CTGGAGGAAAAGAGGTGGTCCCTCGATTTTCCAGCCAGACAGTCTTTACTGAGATTTATTT[A/G]ATCGGGAACATAGATTGAAATATATTCACAGAGAAATACTCAGAAATTAGGGAAATCACAA | A/G | 18 | 21940656 | 0.752 |
| 18023488446 | TGAAAGAGAGTGAGGCATGGAGAGGTCCTGGAGAGAGAGCTTAACAGTTCCTTAAGTGAAG[A/G]ACAGGAGGAGAGCTTAATGTGGTTGATCGAAAGTATGGGAAACGGTGACACAACTGGAGTT | A/G | 18 | 23488446 | 0.96 |
| 18024995574 | AAATGGCAAACTAGGTCTGGACAGAGATGAACAATGAACCACAATGAGATTTTACAAGGTC[A/G]TGGGATAGAAATTAGTCATCCAGATGGGTCTGCTGAGATCCAAGGCCATGGCATCTTCATG | A/G | 18 | 24995574 | 0.908 |
| 18028487492 | TGTTTTAGGAGACCAGGCTGTTTTGTGAATAAAACTGAATGCATGTTTGTGTCATGATAA[A/C]ACTACTGGCTTCTTGCTCTTGGGTTTTGGAGGGCTGGCTTGGGACTAGGGCTGGGCTGG | A/C | 18 | 28487492 | 0.813 |
| 18032253306 | AAAGTCGGCTATGGGAAGAGTCCACTTCTCTAACCCTTCAGTTCCCAGCCCTGCAGTAAGC[A/G]GAGGCTCTGCAGCCTTCAGCGTGGGAGTGCGGAGCTCAAGACCAGGCTTCTCTATTGTGCC | A/G | 18 | 32253306 | 0.673 |
| 18033919873 | GGCATTGCAATCCTCTGCAGTTCCTTCAGTCGTTCCTCTAGTTTTCCATATTGGCCCCCAA[T/C]CTCAGTGCAGTGGTTGGCTATAAGTTTCTGCATCTGTCTCAGTCAGTTCCTGGTAGAACCT | T/C | 18 | 33919873 | 0.612 |
| 18042542433 | GCATCTCTTCATGCATCTTCAACCGACTTTGTCATAAGCAACATCAGACTATTTCCGTTCA[A/G]AGTGTGATTTCTGTCTTTACAGACAGGGTTAAAAAGATGCTTCTGTGATGGAGTACTACCT | A/G | 18 | 42542433 | 0.862 |
| 18044256339 | CCCTTTTCTTAATAGCTTCCTGTACTGTTCAATAAAATCTGGAGCATACACAAACAGACA[T/C]GGACATGGGAACAGACAAATTCACAAGATAGCATTCAGGCATGCATGGGTACAGATTCA | T/C | 18 | 44256339 | 0.943 |
| 18047721977 | ATTGACTTGATATAAAATGTGTCATTTATTAAGTCCTTCCTGTGTGACTTTTAAATTCCA[T/C]GTTGAAAATGCTATTTAGTGTTAAAACTTTATTAGACACCAAAACACAGCTATTTTCCA | T/C | 18 | 47721977 | 0.901 |
| 18049435104 | TCTCTTCATTTTGCCAATTTTCTTTTCTGTGCAGAAGTTTTCCAATTCCATGTAGTCTCCG[T/C]TGTCAGTTTTTGGAGTTTTTTCCAAAATATTCTCAGTGATGTAGGTGTCTTGAAATGTTTT | T/C | 18 | 49435104 | 0.952 |
| 18051039405 | CAGCTCTTTCTTGAAAGCCTTTGTCTTACTTCCCAGAAGCACACACGTACGATCTAGTAG[T/C]CTTTGCTATTAGAGTAGAAGTGCCAAGATAAATGCTGTAGGAATGAATATAGATTGCCA | T/C | 18 | 51039405 | 0.885 |
| 18052589887 | ATGGGATGCAAGACAGTACAAAGTAGATGAACAGAAAAAAAGATGATTGGGAATGAGGTAA[A/G]TGGGGTTTTGGCTCTCAGGTAGTAGGGCTCAATTATTTAACTCCTTCATATAGCCAAGAAA | A/G | 18 | 52589887 | 0.959 |
| 18055800448 | CGCACGGTGTGGTCCGCAGCATTCCCATTCAGCTCACAGCTGAAAACTGCGTGACGTATGA[T/C]TTACACAGAGCCCGAGTGAGCACGTTTGTAGTCCTAGGTAATGTTGTTAATGCCTGGAAGC | T/C | 18 | 55800448 | 0.853 |
| 18060832258 | TATATAAACATAATACGCCCTCTTTGAAAAAGCCCCGAACTGCTCTGGGTGAGGTACCTAC[A/G]CCTCTGTCCATTACTAATCAACGTGTACATGGCTATGGCCGAAGTGGAAATGTTCGTTATA | A/G | 18 | 60832258 | 0.961 |
| 18063882170 | GTTGGGTCGTTCTCAGAAAATGTTTTGATGTTGCTGTAGTCATTTCTTTGGTCCACGTTGG[T/C]GTGATTTGGGGGGTACATTTTTTTAAAAGTCATCAGTAAAGATCTGCCTCAGCTGAAGTCT | T/C | 18 | 63882170 | 0.829 |
| 18065423483 | GTATCTACAACCTTATGCCTCAAACCTTTTGTGGTTCTTTCATGTAACAAGTGGGACTTC[A/G]TAATACGATTAGGGAGCTTGGAAAAAATTATGTTCTGGGCAAGTAGAGTGCATCACAAA | A/G | 18 | 65423483 | 0.896 |
| 18067006147 | CCCATTCCACTGTTGAAAAGAAATATGTGCATGAATAGCTTTGCCTTTCTAAAAGTCTTA[T/C]GAAGCTATCTCCACTTTTTTAAAATCTGTTTATTCGTCTTTAAGTGTTTCACATCAGGG | T/C | 18 | 67006147 | 0.774 |
| 18073132804 | AGCCTCTGAACCATTTCTCAAACCTCTACCCCCTCTTCTTGTCTGGTACCCCAGCCCATG[A/G]ACAGTGCCCACACTTAGGAGTCTGCTGCTTCAGGTGCTTCTCTCTGGAAACCTTCCAAC | A/G | 18 | 73132804 | 0.859 |
| 18074697767 | GGAAGTAGGTCAGGCCAGCATGGTCCGGTTAGAAGAGCTCAGTATCGACCCCGCTAGAGTG[A/C]AGAAAGCTCATCAAGAAAAAATTCCAGATCTCCATGTCAATGTCTCAGAGCAAGGACAGGC | A/C | 18 | 74697767 | 0.994 |
| 18076353386 | AGTTTGATCTCAGTAGCATGGTTTAGTTATTAAACGTCTGTGCTCCCACTACTTGACTATC[T/C]CTTCAGACGCCATTCTTCCTATGGTCCTTTAGTCCATAATTCTACTTTACTCTTCTACATA | T/C | 18 | 76353386 | 0.971 |
| 18077866227 | ATGAAATCTGACCTACTTTTTGTCTGTTTTCGACATCATTCTAGATACAAAGAAATAATC[A/G]GCTTGCTAAGTAATTCCTGCTGTTTCCCCCTCTGTACCTTCCCCTCTTGCTCTGTCTGG | A/G | 18 | 77866227 | 0.775 |
| 18080901061 | TGCGGATTATATTAACCAGCCAACTGAGTTTTATAAACTCTGGGATCCAGTTCTGCATCAC[A/G]TTTTATAAAATGCTTTCTTTTACTATGCATATTTAGAAATACAATGAATGTGACAAACACA | A/G | 18 | 80901061 | 0.876 |
| 18082458087 | TTATACTTTCACAGTGCATTCTGGCTGGGAAGGTTGTGTTGGTTTCTCAGGAAGGATGTGA[A/G]TGAATGTTATTTTCAGTTATCGATCAATTTTGCAAGGGCTAATTGTCCATAGAAGTTGCTT | A/G | 18 | 82458087 | 0.951 |
| 18083991780 | GCAAGAGGCCTTCAGCATAGGGAGGTGCAGTGCTGCTTTTGTTTGCTAATTCCAGTTCCCA[A/G]TCTGACTCCTCTGTCTGCAGGAAAGGAGGTAGGCCCCTTTCTTTTCTGTTGATTCCATTTC | A/G | 18 | 83991780 | 0.904 |
| 19001746598 | AATCAAAATGTTTCTTTATGAGAAGGCAGCTTATCAAGAACCACACTATTTCATCAATCC[A/G]TACTCATCAGGAATAATTCAGTGGGTCCCCAATCCACTGCAAAAGCTACCTGGTACATA | A/G | 19 | 1746598 | 0.889 |
| 19003281882 | AGGTTGATGAGTGTAACTTATTTTACAATCATTCATGATTTGAAGTGGAAAGGCCTGACCA[A/G]TGGTAACTAAGGAAAAGTGGAGGGATTCAATGAAAATATGAAATCATAAAATTTTAGATAA | A/G | 19 | 3281882 | 0.981 |
| 19004905218 | TGAGAAAGAATGGAAATTAGGTATTTCTCAATAAGTTAGATTCAGCTCCTTCACATGAGTG[A/G]CCTCGGTAACCTATACTTGTATCCAAACCACTTGTTCTTGCAGAAACTACTCCTCATCTAT | A/G | 19 | 4905218 | 0.937 |
| 19010030870 | GTGTTGCAGGTGAAGTGAAAGAACCTTATTTGCACATGGGATTTCCTTAGCTAATCTAAG[A/G]GTATCTGATAAAAACTAAAAAGATACATTTACTTAAAATGAAGTAGAAAACTTTATACC | A/G | 19 | 10030870 | 0.645 |
| 19018014929 | CTCACTGCTCTGACAAAATATTTGGGAAGAAGTGACTTAAGGTAGAAAGGGTTTGTTTGGG[T/C]GCAGAGTTCGAGAGTACAGTCCACCACGGTATTGAGAAGGCATTAACATTGTGAGGTAATT | T/C | 19 | 18014929 | 0.556 |
| 19026469417 | AGAATTGTACACTGGCCTTCATGCAGAAACTGTGGCATGTATGAACACAGGAAAATAAATT[A/T]AAAAAAATCAGAATTCAAAATATCAAGCAAATTTCCCACAGGATTATGGATACTATGAGCT | A/T | 19 | 26469417 | 0.841 |
| 19032800853 | CGCCAGAGACCAAGGCCCAAGGCAGGGAGCAAAAGCAGAGAAGGCTGAAGGGCTAAAGCC[A/G]TAATTAGAAAACATCTTTTCACGTGGAAAGCTAACAAGGAGGAGGGAAACCCTGGGGCA | A/G | 19 | 32800853 | 0.986 |
| 19036121822 | TCAAGGTCAGCCACACATTTGTCAGGCTTTCCCTTAGTATCGCTTGCCTTGTGCTGACAAA[A/G]GCATCCCTGCTGGCCCGCAGCAGAGAAGACCCCGCCTGGGGTGAGGACACCACAGTAGCAA | A/G | 19 | 36121822 | 0.631 |
| 19037837962 | GGGCCATAACATAGGGACATACCTGGCCTTTGTTCCGTTCCTCATCTTCCCAGGTTAACAT[T/G]TCAGAACTTTGTAAGGGGTTTTGAGATTTTCTAATACCTTGAAAATGGGTAATGGAGGCTC | T/G | 19 | 37837962 | 0.815 |
| 19040876227 | GGCCTTGAACTCAGAGCTTACTCTGCCTCTGCCTCTCAAGCACAGGGGTCACTGCCCTGCT[A/C]TTTTTTTTGGGGGGGGAGACATCCACTTGGCCTGACTCCTCAGAATCTCGAGTGTTGGGGT | A/C | 19 | 40876227 | 0.565 |
| 19042542340 | AGGAGAGGAGACACACAATGTTTGAGAGGCTGTGAAGAAGTGGGTTTTATACTCACTACGG[A/G]GCAGCAATTTAAATTGGCCCAGCCTTGCTGAAGATGATCTTTATATTAGTTTACAAATCTG | A/G | 19 | 42542340 | 0.688 |
| 19045796278 | TACTTTATTTTGTTTTGGTTTTGATTATACAAAGTCATCAGAATGGGCTTAGGCTGGCCTC[A/G]GTGCTTCCTCTCACAAATCCTGTGATGACAGACATGTACTAGCATGTCCAGGTCATACAGT | A/G | 19 | 45796278 | 0.872 |
| 19047315592 | GAGCTCTGCCATTGGATACCCTCTCCCAGGAGTTAGCTCTCAGAGTAACAGCCATTTCTCA[T/C]GTCATAGTTGGAGCTGGCCTACTTAAATGGAAGACTTGGGTAGTCAATAGTAGTCAAAAGA | T/C | 19 | 47315592 | 0.918 |
| 19049284552 | TTCTGTGTGCTGTGTAAACAGCGCACGTTGTTGTCCTGGTGAGCTTGTCTTTTAGCAGGCC[T/C]GCATCACGGGCAGTGTCCTAGTTAGCTTTGTCATTGTGTCAACTTGACACAGCCTAAAGCC | T/C | 19 | 49284552 | 0.713 |
| 19054238555 | AGTTGATTATAGAGTCCGTACCACAGTACACCCTTGTGAGGAAGAGTTGTGCGTTCAGATC[A/G]ATCTAACATGGTGACTGTGGAAAGAGAAACCACCCCTGCCACTAATCCTCCACCTGCAGAA | A/G | 19 | 54238555 | 0.932 |

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|---|---|---|---|---|---|
| 20000047516 | TCAACGGATTGTTCTACTATATTGTATGTGAACTCCGTCTTCTTATTAGAACATCTTTCCT[C/G]TCCTTTCCTCTGTACTTCTAACTTGTGTGTTTTTAGCCTCTGAAGGTCAGCCTCAGGGTGC | C/G | 20 | 47516 | 0.749 |
| 20001565758 | TCAGCGAGTCCCCAGGGAGAGGGTCAGGAGCAGTCACTAAACTCTACTGGGTACTAATTT[T/C]CTGACTTTAAAAGGAATGGGGAGATGAACTCTCAAGCTGTCTCTTTTTAAAAGCGTGTA | T/C | 20 | 1565758 | 0.862 |
| 20003130757 | AGTTCAGACTCCTCCAGCCCTGAAGCCCATTTCTACCCTTTCGGATGCTAGGTCCTGAAA[T/C]GCAGGAGCAAGAGAGGTTGACGCCTACAGATTCACAGGTCATGCTCCGGGAAGAAAAGC | T/C | 20 | 3130757 | 0.873 |
| 20004715045 | ACCACAGAGGTGGGGCTAAGAGCAATGGCTGCTCTTGCAGGGACCATGAGTTAGGTTTCC[A/G]GCACCCACCTGTGGTTCATAATTGAAATGGAAACTTCTAGTTTCTTTGGAAAGTCGGTT | A/G | 20 | 4715045 | 0.937 |
| 20007904736 | AGTGGACGGTTAATGATCCTTCTGAGCAGATTGTTTATGTGAATGAAGCCCTTCAGAGCCC[A/G]CGCCTCCCTCTCTGCTGGTTTTTGCCCGTGTGCTCAGCTCAGTTGAGGAGTGTGTGAACCC | A/G | 20 | 7904736 | 0.731 |
| 20009465495 | CACATACACACACAGAGAGGGGGGGGGAAGACCCCTCCTTGCTACATCACACTACAGACA[A/T]GTATGCACACAAACTTTTGAAAGATATTATATACATTCCTATCAAGTGTGATGGGATAG | A/T | 20 | 9465495 | 0.907 |
| 20012527514 | AAACATTTACCATAAATTAGTTCAGAAAAAGAGATGGGGGGGGGATTTCTTTTACTCCTA[A/T]ATATACTCCAAGTTTTTGTAATTGCCAGGTATGATCTGTTGTCTATTCCCACAAAGCCCAA | A/T | 20 | 12527514 | 0.973 |
| 20014310650 | AGAAGCTGAAACCCTGGAGCCCTATCAACTCTTTCAAGGGTAAGTGGAGGGAAAGGGAGCC[A/G]CCTTCTTCAGGCAGAATGCAATCCATCATTATGAACTTACCGGCAGCTTGTTCACCAGGGA | A/G | 20 | 14310650 | 0.726 |
| 20016047305 | CCCTGAAGCTTGTTGAGCCGAGCTGCTTTATGGAAGGATAGAAGGACGATCCAAAAGGCC[T/C]GGTTGCTAGTGGGAGGTTTTCTAGCCAGAAGGTCGCCCCTCCTGGCTCCATAGAGCCCC | T/C | 20 | 16047305 | 0.951 |
| 20017608327 | CGTTATGAATTATTACCACGCAGCACCAAGCCTTCTGCGTACTCTGCATTTGCTGCACTG[T/G]TGGCTCTGCATAAAATACAGAGATATTGGTATGAGCCTGTCTATCGGTCCTCTGGACAC | T/G | 20 | 17608327 | 0.988 |
| 20019324306 | TAGGTCTTTCCAATCCCACTTAATTTTGGTTAGAGAGTGTGGCTTGAAAGAGCAGCGGCT[A/G]TGCTCTAAGGTTACAGGGCCAAGTGCTACCTCATGCCGCCTTCCCCTTTACCCAGCATG | A/G | 20 | 19324306 | 0.82 |
| 20020963417 | GAAACTAAATGTTCATTTAAAATATTGAAATAGATTTTAAGCGTATTAGAGGGCAGGCTGG[A/G]AGAGGTCAGCTCTCACAACCATGCCCACTTCTAAAAAGGGTTTTGAACTGTCTAGGTTATT | A/G | 20 | 20963417 | 0.849 |
| 20022594060 | TTAGCCATTTCCCAGGCAGTGCTGAAAATTTGCCCTTATCTTCCCAGAATTCCATTAGATT[T/C]TGTGCCTCCCAAAATGAAATGGTGTCTGTGGCTGAGAAGGTAAAGCGTTAGATAAAAGCTT | T/C | 20 | 22594060 | 0.974 |
| 20025197576 | GCCTCAACCACAAGGCAATCCTCCTGTGTAGCATCTGAAAGCCAGAGTTAAACAAGTGCCC[A/G]TGTCATCCATCTTGGGAGAAACCCTTTAAGTGCCCATCAATACAGGACTGGCTAATTAACC | A/G | 20 | 25197576 | 0.892 |
| 20026707550 | TCCCAAAGCTCACCTCAAGTCACATGCTTTCTTCAGCAAGGCTGCGTTTCACAACCTTCCT[A/G]CACAGCTCTACCAACCCCACCAGGGACCGAGTGCTCGAATATCTGAGCCAGTGGGTATCAC | A/G | 20 | 26707550 | 0.812 |
| 20028878254 | GGATGACCCTGACCATCTGATCTTCCTGCCTCTGCCTACTGAGGACCCTCAGTTTACTCG[T/C]GCTGAGGAATGCAATCATGGCCCCTTGCACCTTAGCAGGTAGTCTTCCAATCAGCTGCC | T/C | 20 | 28878254 | 0.954 |
| 20031071864 | ATGACTCACAACCATCTGCAACTCAGGTTGTGTTTCAGAGGATCTCACCCCCTCCTCTGAC[T/C]TCCGAAGGCACCGAATATACAAGGTGTATACACAGCATACACGCAAAGCACTCACCCACGT | T/C | 20 | 31071864 | 0.806 |
| 20032653341 | AGTTCCTGTTGAGTTTCGAAGCCAGTCAGCAGTAACTGCCCATTCTATTCTACAAAGTCTC[T/C]TCAACCTCCCTGCCACTGGCCATCCCCCCATCGGCATACCTTGGGCACAAAGGCTACGGAA | T/C | 20 | 32653341 | 0.963 |
| 20034235827 | CCTTAAAGCCATGAACTGCCTCTTTTCACTGGAATCTGCCCTGGGGAGCCATGGACAAGG[T/C]CTTTGCCTATAGAGATGTTGTCTAATCTCCCATAGAAGGACTCTCCACGTTCCCACCAA | T/C | 20 | 34235827 | 0.558 |
| 20035793807 | CCTCTTGTTAACTTACAGTAAGGAATAAACTCCAACATGAGTTTGGGAAGAATAGTTATA[A/G]CTCTCAGAGTTGTTCATTTTTCATATAACTACTGGACACCGATCTGCCGCTGGAGTTCC | A/G | 20 | 35793807 | 0.808 |
| 20037370145 | GTGGATATGCCACCACTCCAGGTATTATACCTAAGTGCTGGAGATCTAAACTCAGGTTTA[T/C]ACACTGTTCCCTGGTCAGCTAGACACAGACTGAGCAGCAGCTGACTCCCAGACTCAGCA | T/C | 20 | 37370145 | 0.663 |
| 20040509529 | TAATAAAGTCTTCATCGCCCACAGCCATCATGGCCAAAGGGTTACATGTGCTTCTCTTCTG[A/G]TCACACTATGCATTGTGAACATTTGTGTTCTTCATTGTTTGCTTTATTTTCACTGAAAACT | A/G | 20 | 40509529 | 0.918 |
| 20042016047 | GAGGTACTAAATATACCACATTTGAATTTTTATCGCCTTGTTTTAGTCTTGCCATAAATC[T/C]ATTCAGTCTTTGAAAAGTTTCTTGGTTGAATTACTTCTCTAGTAACCTCTTTTCCTCTT | T/C | 20 | 42016047 | 0.916 |
| 20043563914 | TGGTTGGGTTTTAGCACCCAGATACTGGAAGGAGGGAAGTGGGAGTATTGACACCCTTGAG[A/G]GTCTCTCTTAACTGGCAGTGACCTTGGAGGGCAGAACAGTTCTTACTGGGAACCCTCCTCA | A/G | 20 | 43563914 | 0.919 |
| 20045068619 | TGCTGTGGTGAAATCAAATCATCCGATACATGAAACATAGTTACAATAGCGCTTGGTACA[T/C]AGTAGACACCTGGTCAACAAGAGCTACTGTAGCATTGTCCTTAACCGGCGCATGCGCGA | T/C | 20 | 45068619 | 0.915 |
| 20046634456 | TCACTGGGGAGTTGCCACCACAAAGCAACCTCACACACCCAAAACCGGAAAAGCGTTTCC[A/G]GGAACGCTCCAAGAGCAACACACCGAGCGCCTTTCTGGAGCAGTAAGAACAGAGTCGCC | A/G | 20 | 46634456 | 0.761 |
| 20048250172 | TCTCTCTACAACTTTCTGTAAAACTGTACATTCCGAGACGGACACGGTTAATTAGAAAAC[T/C]GAGACTAGGACAACAATCTCCCATGCATGGGGTGGAAAGAAATGAAGATGGCACAACTC | T/C | 20 | 48250172 | 0.904 |
| 20049799754 | TTCTTACCATAGAATCATAATGTGGGCATTAATATAATTCTTATAAATGGAGAAATTCAGA[T/C]TTAGGTGTATGAAAGATGGGTATTAAATAATTTGTTCATGAACATGGAGAAAATTGATATG | T/C | 20 | 49799754 | 0.686 |
| 20051345604 | CTTTGGACAGTAGGATAGAAGGGAGGTCAAAGAGTTTGAGAACCTTTATTAAAACTAGGAT[T/G]TTAAAAATCTAAGCATACAGAAGCATTTTTTTGACATACTGGTACCAGTTCCTTTATATAT | T/G | 20 | 51345604 | 0.525 |
| 20052872439 | AGAATTATAGCAAACGTTATAATGAAGTCTCTAAGCAGTTTCTAAGAAACAGCAGATATCC[A/G]CACAGACTAGAATACCCAGAAAATTTTTCAATAACTTTAGATGGAGAAAAGAAAATATTCA | A/G | 20 | 52872439 | 0.689 |
| 20054465630 | TCTCTGGCATGGATTCTCTTTGCTGGTCTTTGTTGGGCTTCACTGATGATGCTTTGGAATT[C/G]ATTCAACTTTCTTTCTTCTCTGGTATTCATTTGTCCTAACTTTGTAGAGAAAAATGCACCA | C/G | 20 | 54465630 | 0.967 |

**Supplementary table 6.** SNPs (n=894) selected for linkage analysis.

| Marker Name | Sequence | Nucleotide_Variant | Chromosome |
|---|---|---|---|
| Rn34_1146593376 | CTATGCAGTAAGAAAAAAAGAAAGAAGAAAATCCTATTTTTGTCGAAGGGGACTTTGAGAT[A/G]GAAGGTGTTCTTTTCAACTGTATCAAAGCCAGCACAATGTTTTAAGATGCTAAGACAAAAA | A/G | 1 |
| Rn34_1148739042 | CTGAGACCCAAGAAGCTAGTTGAGTTGAAAATTCTCCATTGCCTTGAAGAACAGTACTAAA[A/G]TATCTTCAGCTTTTCTAATGCTTTAGCCTGTGTTTTACTATATCTGCTTCTGAAAAACTGT | A/G | 1 |
| Rn34_1173205180 | CCCATTGCTCATTAGAGGACATATTTGTATTAGATGAGGCTGGGTGGGGGCCTTGCTTGT[A/C]CTCCCACTACCTAAACCAGTAAGGAAGCTCAGGAGTCAAAGGAAGTAGCTGAGGCTGCC | A/C | 1 |
| Rn34_1211246657 | TGAAAGGATTTACAAGCAAGAGGCTGGTGAGACTCTGCAATACCAGGCGTCTACCGTAAGA[A/G]GGAGCTGCGGGAGGCTTTTCGATTCAACAGGGACAATTAAACTTTGTTGGTTTGGAACTGC | A/G | 1 |

**Supplementary table 7.** SNPs within the QTL region, selected for Taqman genotyping.