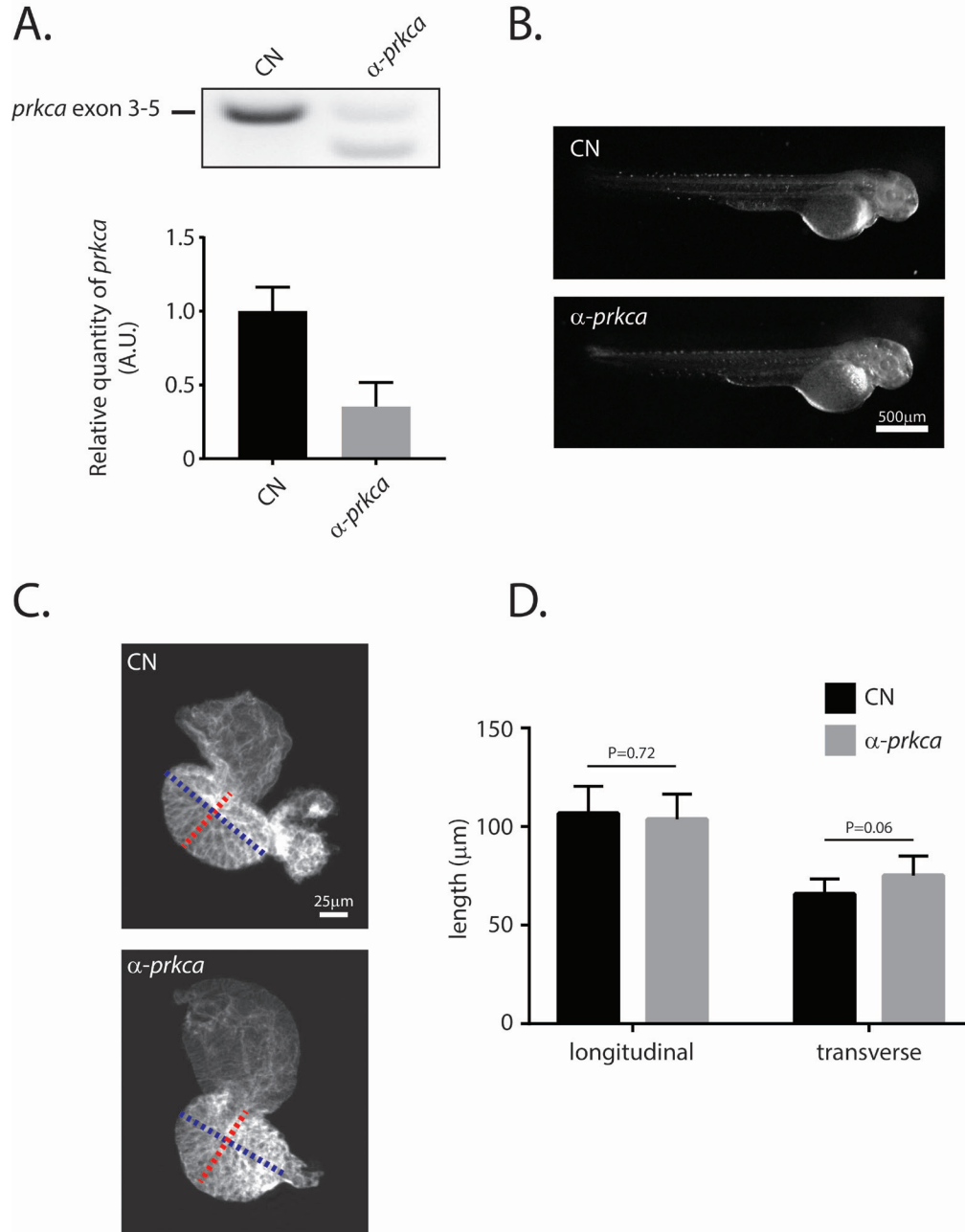


SUPPLEMENTAL MATERIAL



Supplemental Figure: *prkca* morpholino knockdown in zebrafish embryos does not affect ventricular structure. **A**, Efficacy of knockdown was assayed by semi-quantitative PCR in control (CN) and *prkca* morphant (α -*prkca*) cDNA with densitometric measurement of amplicons used to quantify percent knockdown (65% knockdown at 72 hours post fertilization). **B**, Light micrographs detailing gross morphology of control and *prkca* knockdown embryos show no overt changes. **C**, Analysis of ventricular dimensions of excised zebrafish hearts using 2D. Blue dashed line displays the longitudinal axis and the red dashed line indicates the transverse axis of the 72 hour post fertilization ventricle. **D**, quantification of ventricular chamber dimensions. Neither longitudinal nor transverse dimensions were significantly altered by *prkca* suppression. Error bars indicate the standard deviation.

Supplemental Table

Results from variant effect prediction on transcription binding sites using The R package motifbreakR. DNA sequences surrounding SNPs rs9303504 and rs9910355 were queried against the HOCOMOCO motif database with tests for both the reference and alternative alleles. Scores, nominal P-values, and P-values adjusted for multiple comparisons are reported for matches for both reference and alternative alleles. We did not observe any significant motifs matches with either the reference or alternative allele. Differences in scores between the reference and alternative alleles were not examined given the low confidence of the initial matches.

rsid	REF	ALT	snpPos	motifPos	motif	seqMatch	pctRef	pctAlt	scoreRef	scoreAlt	Refpvalue	Refpvalue.adj	Altpvalue	Altpvalue.adj
rs9910355	A	C	64315205	1	ANDR_HUMAN	gaaccgcgagattgtgcA	0.688927722	0.717312839	5.728839335	5.964488257	0.011409383	1	0.006762938	1
rs9910355	A	C	64315205	8	ATF6A_HUMAN	attgtgcAgctgc	0.514771558	0.647912798	6.337545879	9.766976566	0.065726459	1	0.009032071	1
rs9910355	A	C	64315205	7	BACH1_HUMAN	attgtgcAgctgca	0.654522336	0.699929111	8.224705817	8.795285824	0.0043406	1	0.001603637	1
rs9910355	A	C	64315205	8	CEBPB_HUMAN	attgtgcAgc	0.787600917	0.594537186	7.388298378	5.577213064	0.004335403	1	0.05222402	1
rs9910355	A	C	64315205	2	CEBPB_HUMAN	gagagattgtgcAg	0.821297275	0.674148554	6.813322737	5.592605521	0.001915753	1	0.02052442	1
rs9910355	A	C	64315205	1	CXXC1_HUMAN	Agctgca	0.734801565	0.859133224	3.209774909	3.752882951	0.040344238	1	0.008361816	1
rs9910355	A	C	64315205	8	DBP_HUMAN	attgtgcAgct	0.737942543	0.578755909	4.94051644	3.874763839	0.007895231	1	0.06472683	1
rs9910355	A	C	64315205	8	E2F1_HUMAN	ttgtgcAgctgcac	0.590778418	0.734520671	4.651649281	5.783441728	0.042850267	1	0.05073417	1
rs9910355	A	C	64315205	3	E2F3_HUMAN	gcAgctgcac	0.595519178	0.798091223	4.315641503	5.783651864	0.056879997	1	0.003631592	1
rs9910355	A	C	64315205	8	E2F4_HUMAN	ttgtgcAgctgcac	0.568329519	0.679223145	5.503972615	6.752239625	0.042521134	1	0.00635625	1
rs9910355	A	C	64315205	4	E2F5_HUMAN	ttgtgcAgct	0.625689563	0.774152046	6.186874568	7.65488493	0.020145416	1	0.001913071	1
rs9910355	A	C	64315205	6	E2F6_HUMAN	ttgtgcAgctgc	0.576882935	0.700614382	5.374174252	6.526842006	0.044429243	1	0.00798285	1
rs9910355	A	C	64315205	7	E2F7_HUMAN	ttgtgcAgctgca	0.540588287	0.651690037	5.102158451	6.150754488	0.053208113	1	0.009762901	1
rs9910355	A	C	64315205	3	ESR2_HUMAN	ccgagattgtgcAgc	0.533732029	0.679972207	5.495373733	6.980905988	0.070337934	1	0.009021515	1
rs9910355	A	C	64315205	9	FOXQ1_HUMAN	gattgtgcAgct	0.645979309	0.524298943	7.954989674	6.456542212	0.009675324	1	0.056813002	1
rs9910355	A	C	64315205	8	HIC1_HUMAN	attgtgcAg	0.58125932	0.765101925	5.673403492	7.46780616	0.048988342	1	0.00421524	1
rs9910355	A	C	64315205	1	ZEP1_HUMAN	cgagattgtgcA	0.689791947	0.674326011	6.445352329	6.300840051	0.006339967	1	0.008115947	1
rs9910355	A	C	64315205	9	HLF_HUMAN	gattgtgcAgctgc	0.740238506	0.557573141	7.174038315	5.403732776	0.00664252	1	0.06993778	1
rs9910355	A	C	64315205	12	IRF1_HUMAN	Agctgcacttta	0.678979014	0.668114636	8.716130994	8.576663728	0.009792026	1	0.009955645	1
rs9910355	A	C	64315205	12	IRF9_HUMAN	Agctgcacttta	0.696457696	0.650429233	6.309770832	5.892761937	0.004012108	1	0.00947845	1
rs9910355	A	C	64315205	17	KLF15_HUMAN	tgagccgagattgtgcA	0.757777928	0.778206856	5.807342541	5.963902636	0.01570517	1	0.000882102	0.747140396
rs9910355	A	C	64315205	15	KLF3_HUMAN	Agctgcactttacc	0.719741925	0.674273079	5.66944953	5.311288749	0.05066881	1	0.0118321	1
rs9910355	A	C	64315205	5	MAMA_HUMAN	tgagccgagattgtgcAgctgc	0.749232313	0.605540165	6.353031924	5.13461162	0.003093987	1	0.03920729	1
rs9910355	A	C	64315205	7	MAFK_HUMAN	tgacAgctgca	0.640078544	0.706568684	7.795070517	6.604807592	0.010317802	1	0.003321238	1
rs9910355	A	C	64315205	7	MIF6_HUMAN	tgacAgctgca	0.806597972	0.623131178	7.550174839	5.832830608	0.003271103	1	0.031405449	1
rs9910355	A	C	64315205	6	MYF6_HUMAN	cAgctgc	1	0.829403396	7.193737088	5.966509971	6.10352E-05	0.052001953	0.009097653	0.823242188
rs9910355	A	C	64315205	7	MYOD1_HUMAN	gcAgctgca	0.936470654	0.736609424	7.820304428	6.151297869	0.00050354	0.422973633	0.010959625	1
rs9910355	A	C	64315205	8	MYO6_HUMAN	ttgtgcAgctgcac	0.885811035	0.751718807	9.526265743	8.065987957	0.000151917	0.128825903	0.002767771	1
rs9910355	A	C	64315205	8	NDF1_HUMAN	gtgcAgctgcac	0.900527178	0.730360066	7.98681658	6.325012493	0.000450552	0.379814923	0.008978128	1
rs9910355	A	C	64315205	2	NFAT5_HUMAN	ccgagattgtgcAg	0.727601848	0.688155897	7.312028689	6.915616934	0.003228103	1	0.006108461	1
rs9910355	A	C	64315205	8	NFE2_HUMAN	attgtgcAgctgca	0.63877372	0.702076503	6.842821465	7.520948369	0.00940571	1	0.002801131	1
rs9910355	A	C	64315205	1	NF2L2_HUMAN	cgagattgtgcA	0.744761913	0.672338217	5.822442691	5.25624454	0.00285387	1	0.01051867	1
rs9910355	A	C	64315205	2	NFKB2_HUMAN	agattgtgcA	0.61472145	0.72349246	3.78839519	4.458727375	0.00386884	1	0.00759244	1
rs9910355	A	C	64315205	9	HEN1_HUMAN	gattgtgcAgctgcacttta	0.704718404	0.604741419	11.06004942	9.49098241	0.000925663	0.770151391	0.008928075	1
rs9910355	A	C	64315205	5	NROB1_HUMAN	ttgtgcAgctgc	0.573878254	0.82004382	3.14053378	4.487668421	0.095159531	1	0.002552986	1
rs9910355	A	C	64315205	10	COT2_HUMAN	ttgtgcAgctgcactt	0.688587118	0.783616965	4.619029453	5.266487881	0.013494324	1	0.00193009	1
rs9910355	A	C	64315205	12	PAX8_HUMAN	gcAgctgcacttta	0.737422049	0.809025057	2.837877051	3.113432322	0.01849779	1	0.004172854	1
rs9910355	A	C	64315205	4	PLAG1_HUMAN	ccgagattgtgcAgct	0.565865	0.739739506	5.525389373	7.2231801	0.058200531	1	0.004170279	1
rs9910355	A	C	64315205	5	PIT1_HUMAN	gattgtgcAgctgc	0.764144112	0.806216723	6.314653462	5.00958977	0.003935114	1	0.04234229	1
rs9910355	A	C	64315205	3	PO2F2_HUMAN	ttgtgcAgctgc	0.661147624	0.516017611	9.064375066	7.074633553	0.009170532	1	0.063140869	1
rs9910355	A	C	64315205	7	PO5F1_HUMAN	ttgtgcAgctgcactt	0.669427575	0.516773943	7.339320915	5.665691034	0.005407141	1	0.066713491	1
rs9910355	A	C	64315205	13	PPARG_HUMAN	ttgtgcAgctgcactttg	0.57996982	0.714707076	5.248988015	6.492857068	0.049895844	1	0.005434798	1
rs9910355	A	C	64315205	12	PRDM1_HUMAN	gcAgctgcacttta	0.662428719	0.637003783	10.27365645	9.879339225	0.004847728	1	0.007763565	1
rs9910355	A	C	64315205	17	PTF1A_HUMAN	gtgcAgctgcactttgca	0.831289503	0.747770461	7.094510383	6.65158399	0.000111651	0.094791879	0.001486338	1
rs9910355	A	C	64315205	6	RF2_HUMAN	ttgtgcAgctgcac	0.539220652	0.700483304	5.12421224	6.508868686	0.066211417	1	0.006340966	1
rs9910355	A	C	64315205	9	RXRα_HUMAN	gtgcAgctgcact	0.644390581	0.753180054	5.741148206	6.710399631	0.019759983	1	0.003030837	1
rs9910355	A	C	64315205	6	SNAI1_HUMAN	gcAgctgc	0.833212741	0.678593911	5.650693243	4.602097206	0.002441406	1	0.021118164	1
rs9910355	A	C	64315205	6	SNAI2_HUMAN	cAgctgc	0.837741453	0.679247151	6.066139321	4.918471966	0.003540039	1	0.02355791	1
rs9910355	A	C	64315205	13	STAT2_HUMAN	gcAgctgcactttg	0.711090666	0.678883299	6.734595463	6.429566016	0.005171079	1	0.009059899	1
rs9910355	A	C	64315205	4	TAL1_HUMAN	tgacAgctgcactttgca	0.686463235	0.562641327	9.843820554	8.068225609	0.004198446	1	0.03604778	1
rs9910355	A	C	64315205	8	TAL1_HUMAN	gtgcAgctgcac	0.668178572	0.54218551	9.654058566	7.833670345	0.006356239	1	0.041055918	1
rs9910355	A	C	64315205	16	TBX3_HUMAN	gattgtgcAgctgcactttgct	0.645690353	0.528763548	7.137610511	5.845074563	0.008701532	1	0.075896678	1
rs9910355	A	C	64315205	7	HTF4_HUMAN	gcAgctgca	0.96385849	0.797093525	11.51554788	9.523149655	6.8664E-05	0.058433533	0.00194931	1
rs9910355	A	C	64315205	7	TFE2_HUMAN	gtgcAgctgca	0.87890285	0.75120696	8.211252114	7.018238413	0.00079608	0.663930416	0.007889271	1
rs9910355	A	C	64315205	6	TF2_HUMAN	tgacAgctgc	0.843449419	0.688755236	10.70458648	8.741294759	0.000484467	0.009792037	0.005153656	1
rs9910355	A	C	64315205	4	TEAD3_HUMAN	ttgtgcAgctgcacttta	0.773464566	0.759777061	5.184927392	5.093173063	0.002910491	1	0.00385899	1
rs9910355	A	C	64315205	7	AP2B_HUMAN	tgacAgctgca	0.680632548	0.79627408	5.05750319	5.916788309	0.01263123	1	0.003851891	1
rs9910355	A	C	64315205	8	AP2D_HUMAN	ttgtgcAgctgcac	0.585664777	0.711440701	4.882897275	5.931293312	0.033894643	1	0.004139978	1
rs9910355	A	C	64315205	7	TFAP4_HUMAN	gtgcAgctgca	0.905458927	0.811829904	9.41275788	8.439431211	0.000104904	0.089168549	0.001180887	0.993126154
rs9910355	A	C	64315205	8	TFDP1_HUMAN	ttgtgcAgctgcac	0.611522451	0.764226643	4.914579764	6.141806881	0.031618025	1	0.00204102	1
rs9910355	A	C	64315205	8	TFE3_HUMAN	gcAgctgcac	0.793245742	0.646043675	6.656684007	5.421407733	0.003459576	1	0.028273582	1
rs9910355	A	C	64315205	13	TLX1_HUMAN	ccgagattgtgcAgctgc	0.620044684	0.720387679	3.134598143	3.642639873	0.04824774			

rs9303504	G	C	64315366	10	HXA5_HUMAN	Gagtaaatg	0.832482669	0.853989502	7.237346167	7.424319904	0.00241375	1	0.001530647	1
rs9303504	G	C	64315366	9	HXA7_HUMAN	aaatttctGagtaat	0.704340127	0.565948821	4.078743108	3.277336851	0.008429697	1	0.071082252	1
rs9303504	G	C	64315366	13	HXA9_HUMAN	tGaglaaatgaca	0.757343761	0.785605265	8.88834689	9.220029891	0.000762213	0.636447873	0.000371393	0.316055287
rs9303504	G	C	64315366	4	HXB6_HUMAN	ttctGagtaaatg	0.70941389	0.623282726	6.578653502	5.779927841	0.004332125	1	0.019075185	1
rs9303504	G	C	64315366	3	HXB7_HUMAN	ctGagtaata	0.802135685	0.693528621	9.67564777	8.365590495	0.001125336	0.93290329	0.007572174	1
rs9303504	G	C	64315366	3	HXB8_HUMAN	ctGagtaaat	0.786773788	0.683662209	9.784798098	8.502439694	0.00103569	0.859622955	0.00658226	1
rs9303504	G	C	64315366	8	HXD13_HUMAN	aatttctGagt	0.73289688	0.67739657	4.02318265	3.718517843	0.007205963	1	0.018604279	1
rs9303504	G	C	64315366	9	HXD9_HUMAN	aaatttctGa	0.802440327	0.756053391	4.661551392	4.392079532	0.005477905	1	0.010681152	1
rs9303504	G	C	64315366	3	IKZF1_HUMAN	tttctGag	0.578853255	0.781962491	4.237394787	5.724220697	0.077331543	1	0.008102417	1
rs9303504	G	C	64315366	5	IRF5_HUMAN	ttgtttaatttctGagta	0.55603264	0.600589076	7.082689248	7.650244757	0.022746693	1	0.008951389	1
rs9303504	G	C	64315366	3	JUN_HUMAN	ctGagtaat	0.843781083	0.737706067	8.419728701	7.361795954	0.000801086	0.667304993	0.004753113	1
rs9303504	G	C	64315366	4	JUNB_HUMAN	ttctGagtaat	0.862665697	0.757302076	8.184780319	7.185113712	0.000616074	0.516269684	0.00383091	1
rs9303504	G	C	64315366	4	JUND_HUMAN	ttctGagtaata	0.857343351	0.727924221	9.902873082	8.407997988	0.000360727	0.304814577	0.003535032	1
rs9303504	G	C	64315366	6	MAF_HUMAN	ctGagtaa	0.588013698	0.788658736	4.32190259	5.796644272	0.048934937	1	0.003616333	1
rs9303504	G	C	64315366	6	MAFA_HUMAN	tttctGaglaaatgacaatt	0.718784928	0.59374846	6.094858204	5.034625145	0.00600836	1	0.04651241	1
rs9303504	G	C	64315366	5	MAFK_HUMAN	ttctGagtaa	0.741996351	0.667594055	9.03625647	8.130162747	0.001520157	1	0.006297112	1
rs9303504	G	C	64315366	3	EV11_HUMAN	ttgttaatttctGag	0.66775648	0.754861687	9.289081575	10.50079183	0.004177646	1	0.000609669	0.518218963
rs9303504	G	C	64315366	13	MEIS1_HUMAN	Gagtaaatgaca	0.773747191	0.784939359	8.762511672	8.889260439	0.001323909	1	0.001039162	0.874974638
rs9303504	G	C	64315366	18	MLXPL_HUMAN	tGaglaaatgacaattga	0.624938198	0.700806099	6.444009938	7.226316904	0.015123802	1	0.003066653	1
rs9303504	G	C	64315366	7	NANOG_HUMAN	tGagtaat	0.604255339	0.763303303	3.983828143	5.03242418	0.04309082	1	0.00554199	1
rs9303504	G	C	64315366	10	NFE2_HUMAN	tttctGaglaaatg	0.76532252	0.694735285	8.198467159	7.442306053	0.000674225	0.564326651	0.003249746	1
rs9303504	G	C	64315366	5	NF2L2_HUMAN	ttctGaglaata	0.761049732	0.7268794	5.949778546	5.682639747	0.002046108	1	0.004050672	1
rs9303504	G	C	64315366	11	NR1D1_HUMAN	ttaatttctGagt	0.561085029	0.666905714	6.192571091	7.360490538	0.037104957	1	0.006995115	1
rs9303504	G	C	64315366	6	NR2E3_HUMAN	aaatttctGagtaa	0.667470282	0.561685164	6.658779686	5.603452111	0.004504956	1	0.031488061	1
rs9303504	G	C	64315366	2	NR2F6_HUMAN	tttttgaatttctGa	0.599009803	0.690509502	5.115647449	5.897070722	0.039458344	1	0.00999495	1
rs9303504	G	C	64315366	20	ONEC2_HUMAN	ctttttgttaatttctGa	0.701344342	0.727385602	6.927604643	7.184829999	0.004290333	1	0.002391946	1
rs9303504	G	C	64315366	5	PAX5_HUMAN	ttctGagta	0.689718959	0.910488481	6.237119415	8.233535277	0.019378662	1	0.000900269	0.761627197
rs9303504	G	C	64315366	6	PBX1_HUMAN	tttctGaglaaatg	0.720122921	0.561297666	5.985440457	4.665333744	0.003663374	1	0.048244506	1
rs9303504	G	C	64315366	9	PBX3_HUMAN	tttctGaglaaat	0.53065364	0.729054948	5.03522188	6.917795619	0.091790926	1	0.00893376	1
rs9303504	G	C	64315366	6	PKNX1_HUMAN	tttctGaglaata	0.773573925	0.584388378	5.508392411	4.16125777	0.006090686	1	0.068479404	1
rs9303504	G	C	64315366	10	PO3F2_HUMAN	Gagtaaatg	0.760259202	0.77800293	4.774813257	4.886252863	0.013281822	1	0.010290146	1
rs9303504	G	C	64315366	8	PO4F2_HUMAN	tttctGaglaata	0.744917374	0.813257596	8.174580304	8.924532791	0.003579408	1	0.000971526	0.819967866
rs9303504	G	C	64315366	15	PO5F1_HUMAN	tGaglaaatgacaat	0.677397807	0.699313971	7.426703164	7.666982728	0.004595324	1	0.002920338	1
rs9303504	G	C	64315366	5	PRDM1_HUMAN	taatttctGagta	0.56870554	0.682793513	8.20096664	10.58949556	0.02366719	1	0.003384173	1
rs9303504	G	C	64315366	4	SUH_HUMAN	tttctGagt	0.681097997	0.843411275	5.709467841	7.070097953	0.012828827	1	0.000675201	0.573246002
rs9303504	G	C	64315366	10	SMAD1_HUMAN	taatttctGag	0.712192456	0.569311981	5.235571688	4.185208175	0.006316662	1	0.056243718	1
rs9303504	G	C	64315366	7	SMAD2_HUMAN	tttctGagta	0.758699327	0.528329565	5.29649711	3.688280606	0.009328127	1	0.117516756	1
rs9303504	G	C	64315366	7	SMAD3_HUMAN	tttctGagt	0.817303306	0.683801157	5.667779317	4.741977699	0.004606247	1	0.02152729	1
rs9303504	G	C	64315366	6	SMAD4_HUMAN	tttctGagt	0.818345403	0.695291447	6.960077267	5.913495908	0.004341125	1	0.019447327	1
rs9303504	G	C	64315366	3	SMRC1_HUMAN	ctGagtaat	0.845978443	0.692027346	7.786658258	6.369642741	0.000759125	0.634628296	0.010631561	1
rs9303504	G	C	64315366	6	SPI1_HUMAN	tttaatttctGagtaa	0.607205586	0.659842183	7.907930555	8.59344229	0.016963508	1	0.006711473	1
rs9303504	G	C	64315366	9	SRBP1_HUMAN	aaatttctGag	0.764813027	0.514569583	5.028571011	3.38324479	0.006695271	1	0.1367383	1
rs9303504	G	C	64315366	8	STAT1_HUMAN	aatttctGagtaata	0.730497812	0.776530325	8.18070382	8.696213038	0.003882506	1	0.001657122	1
rs9303504	G	C	64315366	7	STAT3_HUMAN	tttctGagtaat	0.566818557	0.696997224	6.154447068	7.56791122	0.034141064	1	0.004616499	1
rs9303504	G	C	64315366	19	BRAC_HUMAN	tttctGaglaaatgacaattgaa	0.508851877	0.571776404	13.80553667	15.51272671	0.014304097	1	0.002873678	1
rs9303504	G	C	64315366	6	TEAD3_HUMAN	tttctGaglaaatg	0.77110102	0.89357317	5.169083338	5.99007661	0.003058624	1	0.000132659	0.113025852
rs9303504	G	C	64315366	2	UBIP1_HUMAN	tttctGa	0.966352966	0.819855159	4.18831464	3.553371784	0.000488281	0.410644531	0.007446289	1