

Supplementary Table 4 – Transcripts with expression levels correlated with *HOXA9*¹.

Affymetrix Array ID	GeneSymbol	GeneTitle	chr	kb	Pearson correlation MDA tumor set	Pearson correlation UCSF tumor set
226421_at	LOC286505	hypothetical protein LOC286505	23	109245	0,698444888	0,400127707
235209_at	RPESP	RPE-spondin	8	74144	0,662803926	0,387556682
204976_s_at	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1	23	109307	0,626641252	0,319824359
206289_at	HOXA4	homeo box A4	7	26942	0,59457904	0,504175544
214457_at	HOXA2	homeo box A2	7	26914	0,583776402	0,670022416
235753_at	---	---	7	26967	0,571266152	0,481704469
213844_at	HOXA5	homeo box A5	7	26955	0,570553259	0,600153467
227307_at	LOC90139	Tetraspanin similiar to uroplakin 1	11	44910	0,568012831	0,412540289
228642_at	---	---	7	26911	0,564053738	0,519325079
234269_at	---	CDNA FLJ20012 fis, clone ADKA03438	23	137717	0,563023913	0,317580479
213150_at	HOXA10	homeo box A10	7	26985	0,557265036	0,736818276
226743_at	FLJ34922	hypothetical protein FLJ34922	17	30703	0,556768125	0,422910701
235521_at	HOXA3	homeo box A3	7	26920	0,553093002	0,577449252
230935_at	LOC401022	Hypothetical LOC401022	2	176869	0,55065534	0,37843806
210074_at	CTSL2	cathepsin L2	9	96877	0,548943739	0,504752059
41037_at	TEAD4	TEA domain family member 4	12	2979	0,538223979	0,424683758
209220_at	GPC3	glypican 3	23	132620	0,530851416	0,447289109
239934_x_at	CDC27	Cell division cycle 27	7	27000	0,527929361	0,320123615
203417_at	MFAP2	microfibrillar-associated protein 2	1	17046	0,513248603	0,402105406
228783_at	BVES	Blood vessel epicardial substance	6	105652	0,512110154	0,359476395
228564_at	LOC375295	hypothetical gene supported by BC013438	2	177324	0,508413329	0,317196051
231906_at	HOXD8	homeo box D8	2	176821	0,507137859	0,336137678
206847_s_at	HOXA7	homeo box A7	7	26969	0,50517553	0,343191024
201096_s_at	ARF4	ADP-ribosylation factor 4	3	57545	0,50173134	0,32107530

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216212_s_a t	DKC1	dyskeratosis congenita 1, dyskerin	23	15356 2	0,49109564 8	0,41742132 1
203396_at	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4	15	76624	0,48784404 5	0,39060083 4
204195_s_a t	PKNOX1	PBX/knotted 1 homeobox 1	21	43296	0,48726595 9	0,31683425 8
206858_s_a t	HOXC6	homeo box C6	12	52710	0,48237499 6	0,44715413 9
227372_s_a t	BAIAP2L1	BAI1-associated protein 2- like 1	7	97620	0,48161569 5	0,58555324 9
218399_s_a t	CDCA4	cell division cycle associated 4	14	10454 8	0,47529232 4	0,31185558 5
225139_at	NFATC3	nuclear factor of activated T- cells, cytoplasmic, calcineurin-dependent 3	16	66819	0,47383921 4	0,31371622 2
31845_at	ELF4	E74-like factor 4 (ets domain transcription factor)	23	12894 7	0,47054249 7	0,52367036 4
204826_at	CCNF	cyclin F	16	2434	0,46292341 3	0,33603358 6
214639_s_a t	HOXA1	homeo box A1	7	26907	0,46104447 6	0,35324408 8
242979_at	---	Transcribed locus	2	22742 2	0,46026981 3	0,39760074 8
201589_at	SMC1L1	SMC1 structural maintenance of chromosomes 1-like 1 (yeast)	23	53310	0,45487917 4	0,45256457 8
213696_s_a t	MED8	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)	1	43520	0,45189743 6	0,43941410 1
212115_at	C16orf34	chromosome 16 open reading frame 34	16	1680	0,44991258 4	0,48633489 3
226936_at	C6orf173	CDNA clone IMAGE:4452583, partial cds	6	12670 7	0,44522902 2	0,47063534 5
235407_at	---	Hypothetical LOC402538	7	65595	0,44488999 3	0,35842337 7
226869_at	---	Full length insert cDNA clone ZD77F06	1	3428	0,44471461 8	0,34362809 8
207060_at	EN2	engrailed homolog 2	7	15475 3	0,44448097 4	0,56814649 9
205324_s_a t	FTSJ1	FtsJ homolog 1 (E. coli)	23	48096	0,44123931 1	0,41442192
220060_s_a t	FLJ20641	hypothetical protein FLJ20641	12	10105 5	0,43429171 2	0,35219278 5
209657_s_a t	HSF2	heat shock transcription factor 2	6	12277 9	0,43338441	0,37361620 8
216384_x_a t	---	---	2	23239 8	0,43241962 4	0,37613098 1
239537_at	ST8SIA2	ST8 alpha-N-acetyl- neuraminide alpha-2,8- sialyltransferase 2	15	90738	0,43149108 1	0,37970115 8
216899_s_a t	SCAP2	src family associated phosphoprotein 2	7	26518	0,42930717 1	0,56088789 5
218977_s_a t	SECP43	tRNA selenocysteine associated protein	1	28713	0,42930559 5	0,41520448 6

203714_s_at	TBCE	tubulin-specific chaperone e	1	231898	0,429187109	0,402747283
201994_at	MORF4L2	mortality factor 4 like 2	23	102742	0,428737704	0,321567714
218486_at	KLF11	Kruppel-like factor 11	2	10140	0,428550239	0,555702683
243367_at	---	Similar to D(1B) dopamine receptor (D(5) dopamine receptor) (D1beta dopamine receptor)	1	145732	0,428499767	0,464644935
223274_at	---	---	6	31237	0,424551623	0,342654107
213823_at	HOXA11	homeo box A11	7	26995	0,424373363	0,482038631
204268_at	S100A2	S100 calcium binding protein A2	1	150349	0,423423033	0,393187115
238323_at	TEAD2	TEA domain family member 2	19	54548	0,423107603	0,322342921
225662_at	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	2	173917	0,418192169	0,308754014
210416_s_at	CHEK2	CHK2 checkpoint homolog (S. pombe)	22	27432	0,41536613	0,320857476
203133_at	SEC61B	Sec61 beta subunit	9	99064	0,414289699	0,322464043
223749_at	C1QTNF2	C1q and tumor necrosis factor related protein 2	5	159719	0,414138416	0,313112547
216941_s_at	TAF1B	TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa	2	9979	0,413710211	0,452643613
223519_at	---	---	2	173839	0,408773818	0,324391263
208549_x_at	PTMA	prothymosin, alpha (gene sequence 28)	2	232398	0,408688007	0,412017224
202911_at	MSH6	mutS homolog 6 (E. coli)	2	47934	0,407218676	0,424293841
203358_s_at	EZH2	enhancer of zeste homolog 2 (Drosophila)	7	147962	0,405078359	0,409235925
203960_s_at	C1orf41	chromosome 1 open reading frame 41	1	54111	0,403961175	0,305744411
204033_at	TRIP13	thyroid hormone receptor interactor 13	5	959	0,401807675	0,431819825
219763_at	KIAA1608	KIAA1608	9	123508	0,401577829	0,385451226
203958_s_at	KIAA0478	KIAA0478 gene product	1	22594	0,401538586	0,324769785
228073_at	---	---	20	25543	0,400125885	0,363298475
212599_at	AUTS2	autism susceptibility candidate 2	7	69106	0,398358081	0,389296962
221190_s_at	C18orf8	chromosome 18 open reading frame 8	18	19352	0,398184545	0,310073707
204859_s_at	APAF1	apoptotic protease activating factor	12	97587	0,397233496	0,434388969
221520_s_at	CDCA8	cell division cycle associated 8	1	37836	0,39714743	0,395745753

239219_at	AURKB	aurora kinase B	17	8054	0,39552344 1	0,31148642 8
210046_s_at	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	15	88432	0,39545704 6	0,49584736 7
228004_at	---	Transcribed locus, strongly similar to XP_530276.1 LOC458136 [Pan troglodytes]	20	22493	0,39382002	0,50433414 2
229493_at	---	CDNA clone IMAGE:4131196, partial cds	2	17682 6	0,39167546 6	0,38941624 7
210220_at	FZD2	frizzled homolog 2 (Drosophila)	17	39991	0,39116543 4	0,38242147 4
238933_at	IRS1	Insulin receptor substrate 1	2	22748 3	0,38760939 3	0,35303360 5
227103_s_at	MGC2408	hypothetical protein MGC2408	3	18545 5	0,38639697 5	0,35032870 1
209709_s_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)	5	16283 6	0,38620471	0,32037493 5
228069_at	FAM54A	family with sequence similarity 54, member A	6	13660 3	0,38476965 4	0,30568706 9
202282_at	HADH2	hydroxyacyl-Coenzyme A dehydrogenase, type II	23	53343	0,38346247 3	0,34320951 7
204817_at	ESPL1	extra spindle poles like 1 (S. cerevisiae)	12	51961	0,37926265 5	0,32533439
219043_s_at	PDCL3 /// LOC285359	phosducin-like 3 /// hypothetical protein FLJ12205	2	10063 8	0,37901381 6	0,31172688 1
232278_s_at	DEPDC1	DEP domain containing 1	1	68654	0,37553973 4	0,44944078 9
201543_s_at	SARA1	SAR1a gene homolog 1 (S. cerevisiae)	10	71591	0,37467860 1	0,30592463 4
242056_at	TRIM45	tripartite motif-containing 45	1	11736 6	0,37305739 9	0,37098425 6
234904_x_at	ELAVL4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	1	50320	0,37247665 1	0,33791520 4
234863_x_at	FBXO5	F-box protein 5	6	15339 0	0,37175961 4	0,30119779 5
222039_at	LOC146909	hypothetical protein LOC146909	17	40358	0,37156136 2	0,37108551 7
209326_at	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	23	48521	0,37020227 5	0,30974583 4
206055_s_at	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	15	99639	0,36955741 9	0,31988216 1
208778_s_at	TCP1	t-complex 1	6	16017 0	0,36933392 1	0,39447691
221234_s_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2 /// BTB and CNC homology 1, basic leucine zipper transcription factor 2	6	90878	0,36872881 5	0,34137498 1
220668_s_at	DNMT3B	DNA (cytosine-5)-methyltransferase 3 beta	20	30837	0,36849990 4	0,36489577
222606_at	---	---	15	64605	0,36813621	0,40164237

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218708_at	NXT1	NTF2-like export factor 1	13	38642	0,367692238	0,304330801
218499_at	MST4	Mst3 and SOK1-related kinase	23	130909	0,365302967	0,477762835
231786_at	HOXA13	homeo box A13	7	27011	0,365108045	0,482800544
218349_s_at	FLJ10036	Zwilch	15	64610	0,364974979	0,556438305
218755_at	KIF20A	kinesin family member 20A	5	137547	0,36495469	0,404702338
214943_s_at	KIAA0117	KIAA0117 protein	1	231509	0,364253703	0,313038357
204315_s_at	GTSE1	G-2 and S-phase expressed 1	22	45031	0,362226364	0,328385621
211519_s_at	KIF2C	kinesin family member 2C	1	44892	0,360142872	0,344807171
229886_at	FLJ32363	FLJ32363 protein	5	43525	0,359936293	0,462986019
200944_s_at	HMG1	high-mobility group nucleosome binding domain 1	21	39636	0,359120217	0,412314036
226032_at	CASP2	caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2)	7	142521	0,359055024	0,301278178
206095_s_at	FUSIP1	FUS interacting protein (serine-arginine rich) 1	1	24038	0,357966086	0,322624075
228361_at	E2F2	E2F transcription factor 2	1	23579	0,35749393	0,389620632
220987_s_at	C11orf17 /// SNARK	chromosome 11 open reading frame 17 /// chromosome 11 open reading frame 17 /// likely ortholog of rat SNF1/AMP-activated protein kinase /// likely ortholog of rat SNF1/AMP-activated protein kinase	1	202013	0,357348615	0,402935602
222902_s_at	FLJ21144	hypothetical protein FLJ21144	1	40647	0,355701957	0,336605035
222640_at	DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	2	25422	0,354878648	0,379813806
227174_at	FLJ38736	hypothetical protein FLJ38736	15	51596	0,354144762	0,302984008
229549_at	OPN1SW	Opsin 1 (cone pigments), short-wave-sensitive (color blindness, tritan)	7	128007	0,352986344	0,310334197
239657_x_at	---	---	1	41518	0,35199216	0,442305991
244771_at	FLJ46299	FLJ46299 protein	3	129189	0,350920545	0,303019785
219248_at	THUMPD2	THUMP domain containing 2	2	39897	0,350751258	0,369023416
202412_s_at	USP1	ubiquitin specific protease 1	1	62623	0,35067725	0,48071165

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204005_s_at	PAWR	PRKC, apoptosis, WT1, regulator	12	78538	0,349604447	0,355877501
200698_at	KDEL2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	7	6285	0,349425336	0,339465988
223627_at	RKHD3	ring finger and KH domain containing 3	15	80123	0,349348413	0,459386644
213729_at	FNBP3	formin binding protein 3	2	153377	0,349297023	0,305131027
213523_at	CCNE1	cyclin E1	19	35001	0,348747137	0,305143243
218848_at	MGC2655	hypothetical protein MGC2655	16	3016	0,347981961	0,303818302
219459_at	POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	12	105379	0,347464119	0,380395005
220959_s_at	OBP2B /// OBP2A	odorant binding protein 2B /// odorant binding protein 2A	9	133110	0,346663876	0,352084933
213007_at	FLJ10719	hypothetical protein FLJ10719	15	87650	0,346236091	0,396674072
215227_x_at	ACP1	acid phosphatase 1, soluble	2	261	0,345581378	0,343726451
230472_at	IRX1	iroquois homeobox protein 1	5	3654	0,345539355	0,330864739
242133_s_at	---	Clone pp9372 unknown mRNA	2	91253	0,344661666	0,353108687
242626_at	---	---	6	147931	0,34418414	0,355821584
236681_at	HOXD13	Homeo box D13	2	176786	0,342850633	0,404518826
200934_at	DEK	DEK oncogene (DNA binding)	6	18353	0,34227273	0,300876097
219740_at	FLJ12505	hypothetical protein FLJ12505	1	209532	0,340248397	0,338482949
204998_s_at	ATF5	activating transcription factor 5	19	55127	0,339368928	0,36331672
218781_at	SMC6L1	SMC6 structural maintenance of chromosomes 6-like 1 (yeast)	2	17812	0,338242403	0,314601984
220161_s_at	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	9	109116	0,338130094	0,503294551
202179_at	BLMH	bleomycin hydrolase	17	25621	0,337928472	0,361677149
223811_s_at	C7orf20	chromosome 7 open reading frame 20	7	699	0,337563842	0,345002585
209339_at	SIAH2	seven in absentia homolog 2 (Drosophila) /// seven in absentia homolog 2 (Drosophila)	3	151942	0,336700991	0,305611564
226452_at	PDK1	pyruvate dehydrogenase kinase, isoenzyme 1	2	173288	0,336294315	0,303312871
218766_s_at	WARS2	tryptophanyl tRNA synthetase 2 (mitochondrial)	1	119341	0,335772011	0,337741321
201930_at	MCM6	MCM6 minichromosome maintenance deficient 6	2	136450	0,334908118	0,377523309

		(MIS5 homolog, <i>S. pombe</i>) (<i>S. cerevisiae</i>)				
227111_at	ZBTB34	zinc finger and BTB domain containing 34	9	126727	0,334813253	0,31358606
201277_s_at	HNRPAB	heterogeneous nuclear ribonucleoprotein A/B	5	177567	0,334230947	0,434186317
203764_at	DLG7	discs, large homolog 7 (<i>Drosophila</i>)	14	54705	0,333450544	0,330678276
221952_x_at	KIAA1393	KIAA1393	14	60512	0,333404821	0,415564621
222893_s_at	FLJ13150	hypothetical protein FLJ13150	1	92521	0,332120153	0,310121328
208079_s_at	STK6	serine/threonine kinase 6	10	115997	0,332105975	0,352617567
201088_at	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	17	6346	0,331391204	0,323773149
222684_s_at	FLJ14075	hypothetical LOC79954	2	10721	0,330625652	0,361527662
204224_s_at	GCH1	GTP cyclohydrolase 1 (dopa-responsive dystonia)	14	54409	0,330409894	0,371590474
226299_at	PKN3	protein kinase N3	9	128554	0,330259335	0,468578899
219814_at	MBNL3	muscleblind-like 3 (<i>Drosophila</i>)	23	131256	0,330062809	0,369217325
222430_s_at	YTHDF2	YTH domain family, member 2	1	28884	0,329258082	0,364494997
210732_s_at	LGALS8	lectin, galactoside-binding, soluble, 8 (galectin 8)	1	233026	0,328894426	0,347864594
201291_s_at	TOP2A	topoisomerase (DNA) II alpha 170kDa	17	35744	0,326358338	0,318933074
225154_at	SYAP1	synapse associated protein 1, SAP47 homolog (<i>Drosophila</i>)	23	16518	0,325944344	0,309555824
204835_at	POLA	polymerase (DNA directed), alpha	23	24623	0,325232988	0,428399322
209463_s_at	TAF12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa	1	28760	0,325111399	0,492364171
200790_at	ODC1	ornithine decarboxylase 1	2	10535	0,325075378	0,470260562
223429_x_at	KIAA1160	KIAA1160 protein	3	130345	0,3246821	0,353394908
227236_at	TSPAN2	tetraspan 2	1	115304	0,324511056	0,399228113
216973_s_at	HOXB7	homeo box B7	17	44041	0,323618864	0,46614351
205107_s_at	EFNA4	ephrin-A4	1	151852	0,322329244	0,314177747
207558_s_at	PITX2	paired-like homeodomain transcription factor 2	4	111906	0,321920987	0,380154849
205578_at	ROR2	receptor tyrosine kinase-like orphan receptor 2	9	91678	0,321808289	0,321851078
205807_s_at	TUFT1	tuftelin 1	1	148347	0,32148082	0,517013483
219588_s_at	MTB	more than blood homolog	7	157953	0,321330375	0,493523325

203574_at	NFIL3	nuclear factor, interleukin 3 regulated	9	91258	0,321000068	0,369487316
217640_x_at	C18orf24	chromosome 18 open reading frame 24	18	46174	0,320294019	0,353456961
215903_s_at	MAST2	microtubule associated serine/threonine kinase 2	1	46153	0,31979254	0,329717592
212300_at	DKFZp451J0118	taxilin	1	32326	0,319496848	0,314372543
209172_s_at	CENPF	centromere protein F, 350/400ka (mitosin) /// centromere protein F, 350/400ka (mitosin)	1	211165	0,319135743	0,339467439
218644_at	PLEK2	pleckstrin 2	14	66936	0,318934864	0,326256724
208668_x_at	HMG2	high-mobility group nucleosomal binding domain 2	1	26483	0,318134248	0,449791534
204775_at	CHAF1B	chromatin assembly factor 1, subunit B (p60)	21	36696	0,317584984	0,353815354
229490_s_at	---	---	1	153308	0,317512659	0,335776185
229498_at	---	"MRNA; cDNA DKFZp779M2422 (from clone DKFZp779M2422)"	23	131232	0,317486573	0,329235795
202107_s_at	MCM2	MCM2 minichromosome maintenance deficient 2, mitotin (<i>S. cerevisiae</i>)	3	128812	0,317355324	0,374428262
226823_at	PHACTR4	phosphatase and actin regulator 4	1	28643	0,316778233	0,367136653
221258_s_at	KIF18A	kinesin family member 18A /// kinesin family member 18A	11	28043	0,316770653	0,366950791
225844_at	POLE4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	2	75103	0,316536331	0,304414708
219296_at	ZDHHC13	zinc finger, DHHC domain containing 13	11	19125	0,316444986	0,331485583
1053_at	RFC2	replication factor C (activator 1) 2, 40kDa	7	73102	0,316164364	0,402082059
202095_s_at	BIRC5	baculoviral IAP repeat-containing 5 (survivin)	17	73727	0,316025945	0,310058657
224347_x_at	UBE2J2	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast) /// ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)	1	1230	0,315687823	0,307096621
202511_s_at	APG5L	APG5 autophagy 5-like (<i>S. cerevisiae</i>)	6	106810	0,315649942	0,306922844
233532_x_at	C20orf9	chromosome 20 open reading frame 9	20	41671	0,315434249	0,306859688
208690_s_at	PDLIM1	PDZ and LIM domain 1 (elfin)	10	97014	0,315426345	0,372654285
210821_x_at	CENPA	centromere protein A, 17kDa	2	26925	0,315030228	0,382959667
203974_at	HDHD1A	haloacid dehalogenase-like hydrolase domain containing 1A	23	6876	0,314981665	0,354135295

235425_at	SGOL2	shugoshin-like 2 (S. pombe)	2	201262	0,314843	0,32359315
224944_at	---	---	12	97446	0,314808933	0,35390311
221677_s_at	DONSON	downstream neighbor of SON	21	33877	0,313921996	0,331354324
211212_s_at	ORC5L	origin recognition complex, subunit 5-like (yeast)	7	103422	0,313638006	0,320577002
223234_at	MAD2L2	MAD2 mitotic arrest deficient-like 2 (yeast)	1	11672	0,313309027	0,311174644
201948_at	GNL2	guanine nucleotide binding protein-like 2 (nucleolar)	1	37716	0,313191293	0,390107115
215084_s_at	MGC8974	hypothetical protein MGC8974	1	54135	0,312842263	0,426165251
227604_at	LOC151146	hypothetical protein LOC151146	2	120693	0,31247291	0,359300567
219555_s_at	BM039	uncharacterized bone marrow protein BM039	16	79606	0,311890469	0,42301253
239002_at	ASPM	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	1	193846	0,311670017	0,382685145
223915_at	BCOR	BCL6 co-repressor	23	39700	0,311646297	0,389545163
219330_at	VANGL1	vang-like 1 (van gogh, Drosophila)	1	115948	0,311279889	0,315247936
210115_at	RPL39L	ribosomal protein L39-like	3	188331	0,311089308	0,363619341
213787_s_at	EBP	emopamil binding protein (sterol isomerase)	23	48141	0,310362639	0,362750039
203872_at	ACTA1	actin, alpha 1, skeletal muscle	1	225875	0,310270171	0,445830279
201710_at	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	20	41757	0,308912612	0,352105875
209773_s_at	RRM2	ribonucleotide reductase M2 polypeptide	2	10213	0,308809062	0,344624601
225544_at	TBX3	T-box 3 (ulnar mammary syndrome)	12	113578	0,308774755	0,330103432
205246_at	PEX13	peroxisome biogenesis factor 13	2	61172	0,307972196	0,335856808
228150_at	RGPR	regucalcin gene promotor region related protein	1	174630	0,307862056	0,347037577
202705_at	CCNB2	cyclin B2	15	57195	0,306436849	0,337162035
218009_s_at	PRC1	protein regulator of cytokinesis 1	15	89325	0,306412659	0,368305102
207856_s_at	FLJ20297 /// FLJ41352	hypothetical protein FLJ20297 /// FLJ41352 protein	2	130625	0,305854184	0,377722043
221854_at	PKP1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	1	198033	0,305307265	0,418611849
219978_s_at	NUSAP1	nucleolar and spindle associated protein 1	15	39425	0,305228734	0,321427043
218663_at	HCAP-G	chromosome condensation protein G	4	17505	0,304399405	0,332773859

223402_at	DUSP23	dual specificity phosphatase 23	1	156565	0,303872214	0,366234813
238035_at	SP3	Sp3 transcription factor	2	174597	0,303748593	0,308716263
229407_at	SDK1	sidekick homolog 1 (chicken)	7	4081	0,303627203	0,435551167
204914_s_at	SOX11	SRY (sex determining region Y)-box 11	2	5788	0,303581555	0,310954355
201303_at	DDX48	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48	17	75730	0,30334831	0,335678077
214720_x_at	SEPT10	septin 10	2	109659	0,30288458	0,413612112
228774_at	C9orf81	chromosome 9 open reading frame 81	9	78111	0,302610223	0,301222741
222975_s_at	UNR	upstream of NRAS	1	114992	0,302008626	0,332827023
236609_at	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	2	190475	0,301963344	0,405338776
218770_s_at	TMEM39B	transmembrane protein 39B	1	32223	0,301802068	0,319563575
228252_at	C15orf20	chromosome 15 open reading frame 20	15	62898	0,301724106	0,416103653
212825_at	PAXIP1L	PAX transcription activation domain interacting protein 1 like	7	154189	0,300778375	0,421045263
211804_s_at	CDK2	cyclin-dependent kinase 2	12	54649	0,30067678	0,319166963
202466_at	POLS	polymerase (DNA directed) sigma	5	6800	0,300289472	0,393745182
33322_i_at	SFN	stratifin	1	26874	0,300218193	0,329652294
228831_s_at	GNG7	guanine nucleotide binding protein (G protein), gamma 7	19	2463	-0,59076879	-0,380026769
217199_s_at	STAT2	signal transducer and activator of transcription 2, 113kDa	12	55027	-0,537398751	-0,313437778
213093_at	PRKCA	protein kinase C, alpha	17	62236	-0,49999193	-0,37465126
210976_s_at	PFKM	phosphofructokinase, muscle	12	46813	-0,497004587	-0,313674926
219738_s_at	PCDH9	protocadherin 9	13	66238	-0,496338089	-0,311996964
221508_at	TAOK3	TAO kinase 3	12	117162	-0,486440341	-0,372025416
212598_at	WDFY3	WD repeat and FYVE domain containing 3	4	85959	-0,483266055	-0,309255676
211494_s_at	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	4	72609	-0,47034237	-0,314878155
203845_at	PCAF	p300/CBP-associated factor	3	20114	-	-

					0,458041505	0,350609203
203889_at	SGNE1	secretory granule, neuroendocrine protein 1 (7B2 protein)	15	30749	-0,45561759	-0,39100611
208873_s_at	C5orf18	chromosome 5 open reading frame 18	5	112263	-0,450979824	-0,384918325
212090_at	GRINA	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	8	145138	-0,44679608	-0,309763069
32259_at	EZH1	enhancer of zeste homolog 1 (Drosophila)	17	38121	-0,441727612	-0,311125727
39817_s_at	C6orf108	chromosome 6 open reading frame 108	6	43303	-0,438822876	-0,321248719
200847_s_at	MGC8721	hypothetical protein MGC8721	8	30050	-0,436699638	-0,38654443
207761_s_at	DKFZP586A0522	DKFZP586A0522 protein	12	49609	-0,432744265	-0,401962973
205331_s_at	C5orf19	chromosome 5 open reading frame 19	5	137808	-0,429978918	-0,345800385
204610_s_at	DIPA	hepatitis delta antigen-interacting protein A	11	65415	-0,429338005	-0,39540242
208248_x_at	APLP2	amyloid beta (A4) precursor-like protein 2	11	129482	-0,427545057	-0,345759705
221588_x_at	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	14	73596	-0,42567226	-0,338332736
217732_s_at	ITM2B	integral membrane protein 2B	13	47719	-0,424265932	-0,346875828
225561_at	SELT	selenoprotein T	3	151829	-0,413664603	-0,403853601
228832_at	LOC90024	hypothetical LOC90024	4	102627	-0,410897546	-0,381320644
226463_at	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C, isoform 1	8	104154	-0,408264874	-0,303381652
206387_at	---	---	13	27438	-0,406437863	-0,364458078
213197_at	ASTN	astrotactin	1	173714	-0,405327617	-0,35895356
212660_at	PHF15	PHD finger protein 15	5	133923	-0,40452322	-0,36933123

					6	3
202523_s_at	SPOCK2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	10	73504	-0,399699787	-0,347694091
221511_x_at	CCPG1	cell cycle progression 1	15	53461	-0,399666085	-0,323426361
238569_at	GABBR1	Gamma-aminobutyric acid (GABA) B receptor, 1	6	29706	-0,396554947	-0,334851352
235885_at	P2RY12	purinergic receptor P2Y, G-protein coupled, 12	3	152538	-0,396201838	-0,349978071
214334_x_at	DAZAP2	DAZ associated protein 2	12	49924	-0,393469743	-0,471500116
213034_at	KIAA0999	KIAA0999 protein	11	116347	-0,390286419	-0,379807042
202608_s_at	NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	5	149891	-0,389649875	-0,327452761
221941_at	PAOX	polyamine oxidase (exo-N4-amino)	10	135088	-0,38931347	-0,349259938
222423_at	NDFIP1	Nedd4 family interacting protein 1	5	141491	-0,384741529	-0,444657626
220488_s_at	BCAS3	breast carcinoma amplified sequence 3	17	56624	-0,383730877	-0,316052569
225810_at	FLJ20313	hypothetical protein FLJ20313	15	29019	-0,382108609	-0,346226152
219021_at	RNF121	ring finger protein 121	11	71383	-0,381814894	-0,480815499
203292_s_at	VPS11	vacuolar protein sorting 11 (yeast)	11	118451	-0,379433909	-0,32863547
229926_at	---	Transcribed locus, moderately similar to XP_517655.1 similar to KIAA0825 protein [Pan troglodytes]	2	53988	-0,378936735	-0,329998356
230305_at	---	Transcribed locus, strongly similar to NP_001055.1 transketolase (Wernicke-Korsakoff syndrome) [Homo sapiens]	13	42586	-0,374819059	-0,307299537
218511_s_at	PNPO	pyridoxine 5'-phosphate oxidase	17	43377	-0,369625465	-0,395393892
205818_at	DBC1	deleted in bladder cancer 1	9	119110	-0,369536751	-0,300390305

238360_s_at	---	CDNA clone IMAGE:3877454, partial cds	17	34336	-0,369041527	-0,360583696
203261_at	DCTN6	dynactin 6	8	30147	-0,366446493	-0,313986907
202897_at	PTPNS1	protein tyrosine phosphatase, non-receptor type substrate 1	20	1846	-0,364329316	-0,350400791
201989_s_at	CREBL2	cAMP responsive element binding protein-like 2	12	12673	-0,363513755	-0,31394005
218974_at	FLJ10159	Hypothetical protein FLJ10159	6	108075	-0,362800576	-0,326626113
203657_s_at	CTSF	cathepsin F	11	66090	-0,362511307	-0,530210202
219074_at	TMEM34	transmembrane protein 34	4	148905	-0,358143235	-0,305903341
222391_at	TMEM30A	transmembrane protein 30A	6	76035	-0,357755385	-0,333485671
203188_at	B3GNT6	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6	11	65871	-0,356252681	-0,348646006
239300_at	---	Homo sapiens, clone IMAGE:4798675, mRNA	18	37918	-0,355710271	-0,348392872
218899_s_at	BAALC	brain and acute leukemia, cytoplasmic	8	104267	-0,354677341	-0,464172422
205003_at	DOCK4	dedicator of cytokinesis 4	7	110989	-0,353908458	-0,492045542
220116_at	KCNN2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	5	113793	-0,351102518	-0,302330389
219643_at	LRP1B	low density lipoprotein-related protein 1B (deleted in tumors)	2	141773	-0,350315743	-0,301135138
204735_at	PDE4A	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)	19	10433	-0,347036387	-0,385126303
209590_at	BMP7	Bone morphogenetic protein 7 (osteogenic protein 1)	20	55226	-0,346145762	-0,309300937
239753_at	LOC441383	"hypothetical gene supported by AF086559; BC065734"	8	146196	-0,345441506	-0,304398754
225512_at	FLJ35036	hypothetical protein	3	14264	-	-

		FLJ35036		9	0,344220229	0,318709425
204541_at	SEC14L2	SEC14-like 2 (<i>S. cerevisiae</i>)	22	29131	-0,337628365	-0,393039354
226001_at	KLHL5	kelch-like 5 (<i>Drosophila</i>)	4	38917	-0,337075247	-0,414146163
220884_at	---	---	10	98676	-0,336394816	-0,363051408
228863_at	PCDH17	Hypothetical protein LOC144997	13	57201	-0,335836676	-0,485920611
209598_at	PNMA2	paraneoplastic antigen MA2	8	26420	-0,335258798	-0,345275331
212561_at	RAB6IP1	RAB6 interacting protein 1	11	9180	-0,329332146	-0,335308475
227962_at	ACOX1	Acyl-Coenzyme A oxidase 1, palmitoyl	17	71450	-0,327672043	-0,368503165
200612_s_at	AP2B1	adaptor-related protein complex 2, beta 1 subunit	17	31008	-0,327669496	-0,307260674
203708_at	PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, <i>Drosophila</i>)	1	66531	-0,324552237	-0,438745759
203349_s_at	ETV5	ets variant gene 5 (ets-related molecule)	3	187278	-0,324458987	-0,334730834
216533_at	PCCA	Propionyl Coenzyme A carboxylase, alpha polypeptide	13	99967	-0,323840352	-0,306702672
213195_at	LOC201229	hypothetical protein LOC201229	17	23232	-0,322095197	-0,304836705
203562_at	FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	11	124846	-0,320117044	-0,365912645
225387_at	TM4SF9	transmembrane 4 superfamily member 9	4	99750	-0,319711008	-0,30093189
228692_at	---	CDNA FLJ13569 fis, clone PLACE1008369	8	69311	-0,317409048	-0,369041797
202800_at	SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	5	36683	-0,315610178	-0,336006753
209000_s_at	SEPT8	septin 8	5	132125	-0,315396482	-0,307467877
223155_at	HDHD2	haloacid dehalogenase-like hydrolase domain containing	18	42909	-0,31435678	-0,31645661

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225840_at	TEF	thyrotrophic embryonic factor	22	40118	-0,314083669	-0,321532794
208206_s_at	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	11	64260	-0,313357309	-0,339635242
201116_s_at	CPE	carboxypeptidase E	4	166718	-0,313300091	-0,381023982
200810_s_at	CIRBP	cold inducible RNA binding protein	19	1222	-0,312948512	-0,455354862
204592_at	DLG4	discs, large homolog 4 (Drosophila)	17	7049	-0,311113838	-0,388407383
202814_s_at	HIS1	HMBA-inducible	17	40583	-0,310915223	-0,33776201
203682_s_at	IVD	isovaleryl Coenzyme A dehydrogenase	15	38492	-0,306128475	-0,321690253
202920_at	ANK2	ankyrin 2, neuronal	4	114495	-0,303416996	-0,393696377

¹ Array probes with expression levels that are directly (Pearson correlation coefficient > +0.3) and inversely (Pearson correlation coefficient < -0.3) correlated with *HOXA9* expression are indicated for both UCSF and MDA sets.