

Probeset_ID	Gene Symbol (increased genes)	RefSeq sequence Release 46	Comment
552519_at	ACVR1C	NM_145259.2	ok
1554044_a_at	MRAP	NM_178817.3	ok
1555037_a_at	IDH1	NM_005896	ok
1556035_s_at	ZNF207	GNOMON 16744323.m, AL834501.1	ok, ZNF207c
1558964_at	FAT3	NM_001008781.2	ok
200650_s_at	LDHA	NM_005566.3	ok
200804_at	TMBIM6	NM_003217.2	ok
200871_s_at	PSAP	NM_002778.2	target sequence is downstream of first polyA- site and upstream of other polyA-site(s)
200880_at	DNAJA1	GNOMON 10894623.m	ok
201060_x_at	STOM	NM_004099.4	ok
201395_at	RBM5	NM_005778.2	ok
201432_at	CAT	NM_001752.3	ok
201625_s_at	INSIG1	NM_005542.4	ok
202127_at	PRPF4B	NM_003913.4	target sequence is downstream of first polyA- site and upstream of other polyA-site(s)
202350_s_at	MATN2	NM_002380.3	ok
202449_s_at	RXRA	NM_002957.4	ok
202605_at	GUSB	NM_000181.3	ok
202934_at	HK2	NM_000189.4	ok
202992_at	C7	NM_000587.2	ok
203296_s_at	ATP1A2	NM_000702.3	ok
203382_s_at	APOE	NM_000041.2	ok
203407_at	PPL	NM_002705.4	ok
203424_s_at	IGFBP5	NM_000599.3	ok, target sequence is upstream of CDS within exon 1
203548_s_at	LPL	NM_000237.2	ok
203627_at	IGF1R	NM_000875.3	ok
203980_at	FABP4	NM_001442.2	ok
204039_at	CEBPA	NM_004364.3	ok
204894_s_at	AOC3	NM_003734.2	ok
204997_at	GPD1	NM_005276.2	ok
205204_at	NMB	NM_021077.3	ok
205498_at	GHR	NM_000163.2	oligo#11 of target sequence is downstream of polyA - site

205913_at	PLIN1	NM_002666.4	ok
207175_at	ADIPOQ	NM_001177800.1	ok
207703_at	NLGN4Y	NM_014893.4	target sequence is downstream of first polyA-site and upstream of other polyA-site(s)
208016_s_at	AGTR1	NM_000685.4	ok
208510_s_at	PPARG	NM_138712.3	ok
208949_s_at	LGALS3	NM_002306.3	ok
209540_at	IGF1	NM_001111283.1	ok
209616_s_at	CES1	NM_001025195.1	ok
211162_x_at	SCD	NM_005063.4	ok
211454_x_at	FKSG49	GNOMON 19020193, XM_003118496.1	BLAST without hit
211569_s_at	HADH	NM_004998.2	target sequence is downstream of first polyA-site and upstream of other polyA-site(s)
212135_s_at	ATP2B4	NM_003247.2	ok
212218_s_at	FASN	NM_000303.2	ok
212510_at	GPD1L	NM_004454.2	ok
212793_at	DAAM2	NM_014782.5	ok
213236_at	SASH1	NM_001127500.1	ok
213436_at	CNR1	NM_014824.2	ok
213517_at	PCBP2	NM_005013.2	target sequence does not match with any of the 7 variants of mRNA sequences; maps to intron sequence of PCBP2
214721_x_at	CDC42EP4	GNOMON 19430213.m, AB209922.1	ok
217122_s_at	SLC35E2	NM_002526.3	ok
217882_at	TMEM111	GNOMON 17696263.m	ok
218245_at	TSKU	NM_006855.2	ok
218346_s_at	SESN1	NM_014942.3	ok
218975_at	COL5A3	NM_021226.2	ok
219398_at	CIDEC	NM_016938.4	ok
219547_at	COX15	NM_012090.4	ok

219697_at	HS3ST2	NM_012137.3	first polyA-site within target sequence, excludes oligo #9-11, next polyA-sites downstream of target sequence
219716_at	APOL6	NM_016073.2	ok
219761_at	CLEC1A	NM_015227.4	ok
220975_s_at	C1QTNF1	NM_006818.3	ok
221139_s_at	CSAD	NM_006618.3	ok
222750_s_at	SRD5A3	NR_033796.1	ok
222853_at	FLRT3	NM_197966.1	ok
223130_s_at	MYLIP	NM_198321.3	ok
223412_at	KBTBD7	NM_001128205.1	ok
226038_at	LONRF1	NM_015000.3	ok
226064_s_at	DGAT2	NM_020733.1	ok
226509_at	ZNF641	NM_001193329.1	ok
226547_at	MYST3	NM_052854.2	ok
226568_at	FAM102B	NM_015444.2	ok
226576_at	ARHGAP26	NM_001101.3	target sequence is downstream of first polyA-site and upstream of other polyA-site(s)
227899_at	VIT	NT_011295.11	ok
228410_at	GAB3	NM_018946.3	target sequence is downstream of first polyA-site and upstream of other polyA-site(s)
229487_at	EBF1	NM_024949.5	ok
229839_at	SCARA5	NM_017918.4	ok
230180_at	---	NM_013352.2	target sequence maps to intron sequence of DDX17 (NM_006386.4)
235306_at	GIMAP8	NM_024657.4	ok
235956_at	KIAA1377	NM_030917.3	target sequence is downstream of first polyA-site and upstream of other polyA-site(s)
236361_at	GALNTL2	NM_001130415.1	ok
237475_x_at	CCDC152	NM_024665.4	ok
239629_at	CFLAR	NM_033161.2	target sequence maps with first oligo to the 3' end of the last exon of NM_001127184.2

242738_s_at	ZFHX3	NM_003781.3	ok
244766_at	LOC100271836 /// LOC100288704 /// LOC440354 /// LOC595101 /// LOC641298 /// SMG1	NM_003255.4	ok
43427_at	ACACB	NM_170746.2	target sequence maps to different genomic areas (LOC...) but not to RNA sequences

Table S1. Controlling of Affymetrix probe set annotation (only for increased genes).

Probeset_ID	Gene Symbol (decreased genes)	RefSeq sequence Release 46	Comment
1558105_a_at	---	NT_079573.4	24477 bp at 5' side: carbohydrate sulfotransferase 76568 bp at 3' side: sodium hydrogen exchanger 7
200014_s_at	HNRNPC	NM_031314.2	ok
200606_at	DSP	NM_004415.2	ok
200654_at	P4HB	NM_000918.3	ok
200663_at	CD63	NM_001780.4	ok
200700_s_at	KDEL2	NM_006854.3	ok
200704_at	LITAF	NM_004862.3	ok
200734_s_at	ARF3	NM_001659.2	ok
200745_s_at	GNB1	NM_002074.3	ok
200757_s_at	CALU	NM_001219.4	ok
200816_s_at	PAFAH1B1	NM_000430.3	ok
200891_s_at	SSR1	NM_003144.3	ok
200902_at	SEP15	NM_004261.3	ok
200989_at	HIF1A	NM_001530.3	ok
200998_s_at	CKAP4	NM_006825.3	ok
201097_s_at	ARF4	NM_001660.3	ok
201099_at	USP9X	NM_001039590.2	target sequence is downstream of first polyA-site and upstream of other polyA-site(s)
201148_s_at	TIMP3	NM_000362.4	ok
201162_at	IGFBP7	NM_001553.1	ok
201261_x_at	BGN	NM_001711.4	ok
201278_at	DAB2	NM_001343.2	ok

201286_at	SDC1	NM_001006946.1	ok
201330_at	RARS	NM_002887.3	ok
201462_at	SCRN1	NM_001145513.1	ok
201470_at	GSTO1	NM_004832.2	ok
201560_at	CLIC4	NM_013943.2	ok
201594_s_at	PPP4R1	NM_001042388.1	ok
201719_s_at	EPB41L2	NM_001199388.1	ok
201994_at	MORF4L2	NM_001142418.1	ok
202052_s_at	RAI14	NM_015577.2	ok
202074_s_at	OPTN	NM_001008211.1	ok
202369_s_at	TRAM2	NM_012288.3	ok
202418_at	YIF1A	NM_020470.2	ok
202591_s_at	SSBP1	NM_003143.1	ok
202619_s_at	PLOD2	NM_182943.2	ok
202669_s_at	EFNB2	NM_004093.3	ok
202693_s_at	STK17A	NM_004760.2	ok
202696_at	OXSR1	NM_005109.2	ok
202722_s_at	GFPT1	NM_002056.2	ok
202986_at	ARNT2	NM_014862.3	ok
203020_at	RABGAP1L	GNOMON 19020193, XM_003118496.1	ok, target sequence is downstream of NM_014857.3
203072_at	MYO1E	NM_004998.2	ok
203083_at	THBS2	NM_003247.2	ok
203201_at	PMM2	NM_000303.2	ok
203349_s_at	ETV5	NM_004454.2	ok
203404_at	ARMCX2	NM_014782.5	ok
203510_at	MET	NM_001127500.1	ok
203620_s_at	FCHSD2	NM_014824.2	ok
203675_at	NUCB2	NM_005013.2	ok
203810_at	DNAJB4	GNOMON 19430213.m, AB209922.1	ok, target sequence overlaps with 3' end of NM_007034.3
203939_at	NT5E	NM_002526.3	ok
204004_at	PAWR	GNOMON 17696263.m	ok, target sequence is 1809 bp downstream of NM_002583.2
204017_at	KDEL3	NM_006855.2	ok
204671_s_at	ANKRD6	NM_014942.3	ok
206298_at	ARHGAP22	NM_021226.2	ok
206580_s_at	EFEMP2	NM_016938.4	ok
207358_x_at	MACF1	NM_012090.4	ok
209094_at	DDAH1	NM_012137.3	ok
209526_s_at	HDGFRP3	NM_016073.2	ok
209578_s_at	POFUT2	NM_015227.4	ok

211071_s_at	MLLT11	NM_006818.3	ok
211202_s_at	KDM5B	NM_006618.3	ok
211325_x_at	LOC171220 (DSTNP2)	NR_033796.1	ok
211725_s_at	BID	NM_197966.1	ok
212256_at	GALNT10	NM_198321.3	ok
212344_at	SULF1	NM_001128205.1	ok
212565_at	STK38L	NM_015000.3	ok
212822_at	HEG1	NM_020733.1	ok
212848_s_at	C9orf3	NM_001193329.1	ok
213059_at	CREB3L1	NM_052854.2	ok
213338_at	TMEM158	NM_015444.2	ok
213867_x_at	ACTB	NM_001101.3	ok
214316_x_at	---	NT_011295.11	207 bp at 5' side: calreticulin precursor; 1743 bp at 3' side: UV excision repair Protein RAD23 homolog A, invers to GNOMON 3910343
218189_s_at	NANS	NM_018946.3	ok
218775_s_at	WWC2	NM_024949.5	target sequence is downstream of first polyA-site and upstream of other polyA-site(s)
218802_at	CCDC109B	NM_017918.4	ok
218854_at	DSE	NM_013352.2	ok
219038_at	MORC4	NM_024657.4	ok
221007_s_at	FIP1L1	NM_030917.3	ok
221031_s_at	APOLD1	NM_001130415.1	ok
222634_s_at	TBL1XR1	NM_024665.4	ok
222978_at	SURF4	NM_033161.2	target sequence is downstream of first polyA-site and upstream of other polyA-site(s)
223374_s_at	B3GALNT1	NM_003781.3	target sequence includes first polyA site
224560_at	TIMP2	NM_003255.4	ok
224677_x_at	C11orf31	NM_170746.2	ok
224771_at	NAV1	NM_020443.4	ok
224955_at	TEAD1	NM_021961.5	ok
225152_at	ZNF622	NM_033414.2	ok
225188_at	RAPH1	NM_213589.1	ok
227280_s_at	CCNYL1	NM_001142300.1	ok
227320_at	FAM101A	NM_181709.4	ok
227566_at	NTM	NM_016522.2	ok
227638_at	KIAA1632 (EPG5)	NM_020964.2	ok
228293_at	DEPDC7	NM_001077242.1	ok
229555_at	GALNT5	NM_014568.1	ok
229582_at	INO80C	NM_001098817.1	ok

231841_s_at	KIAA1462	NM_020848.2	ok
231999_at	ANKRD11	NM_013275.4	ok
243864_at	CCDC80	GNOMON 6299293	ok, oligo #11 not matching to variant 1(NM_199511.1) and 2 (NM_199511.1), first polyA site upstream, second downstream

**Table S2. Controlling of Affymetrix probe set annotation
(only for decreased genes).**