Chromothripsis is linked to *TP53* alteration, cell cycle impairment, and dismal outcome in acute myeloid leukemia with complex karyotype

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Supplementary Table 1

Top 200 differentially expressed genes in chromothripsis-positive (n=13) vs –negative (n=14) CK-AML (p-value <.05)

Symbol	ID	LogFC	p value
PSMB10	5699	-1,652	4,81E-05
ADAMTS6	11174	-1,736	1,50E-04
SLC7A6	9057	-1,317	6,80E-04
VANGL1	81839	2,403	6,94E-04
ZNF197	10168	1,409	7,30E-04
TAS2R62P	338399	-1,404	9,22E-04
PLA2G15	23659	-1,455	0,001
CBFB	865	-1,453	0,001
CNOT8	9337	-1,449	0,001
ACD	65057	-1,329	0,001
CKLF	51192	-1,657	0,002
CMTM3	123920	-1,48	0,002
FAM192A	80011	-1,408	0,002
SSH3	54961	-1,279	0,002
ZNF415	55786	1,425	0,002
BEX2	84707	1,57	0,002
GCNT2	2651	1,732	0,002
PIM1	5292	1,935	0,002
POLR2C	5432	-1,326	0,003
HGS	9146	-1,208	0,003
OR5P2	120065	-1,171	0,003
LSM3	27258	1,303	0,003
SERAC1	84947	1,436	0,003
CDK5	1020	-1,434	0,004
KIAA0141	9812	-1,274	0,004
SNX19	399979	-1,223	0,004
RNF44	22838	-1,222	0,004
FAM221A	340277	1,29	0,004
AGPAT4-IT1	79992	1,414	0,004
AGPAT4	56895	1,749	0,004
ZNF655	79027	-1,355	0,005
VPS11	55823	-1,251	0,005
SPRR4	163778	-1,2	0,005
PARP14	54625	-1,622	0,006
TK2	7084	-1,48	0,006
MYO15B	80022	-1,459	0,006
EDC4	23644	-1,3	0,006
TEN1-CDK3	100529145	-1,292	0,006
RNF31	55072	-1,268	0,006
SNORA70	26778	1,297	0,006
VTI1B	10490	1,314	0,006
SH3PXD2A	9644	1,345	0,006
EMC6	83460	1,436	0,006
HOOK1	51361	1,553	0,006
UBE2L6	9246	-1,319	0,007
PHKG2	5261	-1,281	0,007
TMCO4	255104	-1,238	0,007
TEN1	100134934	-1,225	0,007
BCL9	607	1,318	0,007
ZFP3	124961	1,622	0,007
KLF12	11278	1,685	0,007
NAP1L3	4675	2,05	0,007
ARPC1B	10095	-1,585	0,008
DHODH	1723	-1,257	0,008
TRIM41	90933	-1,205	0,008
AASDH	132949	1,395	0,008
FAM46C	54855	2,069	0,008
CCNA1	8900	-2,923	0,009
BST2	684	-1,541	0,009
STAT2	6773	-1,525	0,009

OR7G3	390883	-1,379	0,009
FHOD1	29109	-1,374	0,009
ARMC7	79637	-1,196	0,009
RABGAP1L	9910	1,241	0,009
CYP20A1	57404	1,306	0,009
RHBDD1	84236	1,344	0,009
SELRC1	65260	1,354	0,009
FGFR1OP2	26127	1,469	0,009
VPS26B	112936	-1,396	0,01
MAML1	9794	-1,203	0,01
ATF7IP	55729	1,321	0,01
C6orf89	221477	1,346	0,01
PRTFDC1	56952	1,397	0,01
PCMTD2	55251	1,409	0,01
ELOVL6	79071	1,996	0,01
PRDM9	56979	-1,262	0,011
PHF8	23133	-1,156	0,011
PDE6D	5147	1,226	0,011
PRKAR2B	5577	1,661	0,011
RNF213	57674	-1,523	0,012
CEBPA	1050	-1,495	0,012
DHX38	9785	-1,295	0,012
PARP10	84875	-1,285	0,012
INPPL1	3636	-1,256	0,012
AP1S1	1174	-1,152	0,012
SLC30A9	10463	1,355	0,012
ZNF681	148213	1,384	0,012
ZNF542	147947	1,655	0,012
TIMP3	7078	1,813	0,012
TBC1D16	125058	-1,504	0,013
B3GAT3	26229	-1,327	0,013
OR8H3	390152	-1,198	0,013
ZBTB48	3104	-1,115	0,013
TRIM67	440730	1,259	0,013
PRR5	55615	1,264	0,013
ZDHHC3	51304	1,403	0,013
ARHGAP21	57584	2,31	0,013
CD300LB	124599	-1,53	0,014
FAM223A	100132967	-1,487	0,014
FES	2242	-1,307	0,014
QPCTL	54814	-1,19	0,014
FBXO16	157574	-1,162	0,014
ZNF286A	57335	1,618	0,014
SEC62	7095	1,7	0,014
IRF1	3659	-1,551	0,015
ANP32A-IT1	80035	-1,476	0,015
DBI	1622	-1,462	0,015
CPEB3	22849	-1,313	0,015
KATNB1	10300	-1,19	0,015
PHYHIPL	84457	-1,16	0,015
HPGD	3248	2,114	0,015
DPEP2	64174	-1,411	0,016
COG5	10466	-1,358	0,016
OR6N1	128372	-1,305	0,016
C11orf45	219833	-1,263	0,016
TMEM208	29100	-1,234	0,016
NT5C3L	115024	1,279	0,016
SH3BGRL2	83699	1,585	0,016
SUMO1P3	474338	1,824	0,016
KIAA1468	57614	-1,43	0,017
CUX1	1523	-1,226	0,017
INSL4	3641	-1,19	0,017
PKIA	5569	1,27	0,017
MPP6	51678	1,678	0,017
RASGRP2	10235	-1,278	0,018

C15orf27	123591	-1,144	0,018
ZNF135	7694	1,219	0,018
GSTM5	2949	1,912	0,018
PTH2R	5746	2,251	0,018
TM4SF1	4071	2,3	0,018
CNOT1	23019	-1,381	0,019
WWP2	11060	-1,317	0,019
TULP4	56995	1,253	0,019
NGFRAP1	27018	1,458	0,019
NFATC3	4775	-1,379	0,02
FDPS	2224	-1,327	0,02
FCHSD1	89848	-1,304	0,02
CES2	8824	-1,206	0,02
PANK2	80025	-1,148	0,02
DNM3	26052	1,208	0,02
MUT	4594	1,402	0,02
MTFR1	9650	1,512	0,02
EML4	27436	1,604	0,02
ATG4A	115201	1,673	0,02
PILRB	29990	-1,373	0,021
OR51A4	401666	-1,295	0,021
USP29	57663	-1,282	0,021
TMED6	146456	-1,24	0,021
FIBP	9158	-1,185	0,021
IKZF4	64375	-1,163	0,021
BMPR2	659	1,734	0,021
SSBP3	23648	1,737	0,021
TCP11L2	255394	1,834	0,021
KDELC1	79070	-1,705	0,022
HHEX	3087	-1,311	0,022
SLC25A14	9016	-1,226	0,022
LYPLAL1	127018	1,279	0,022
ORMDL3	94103	1,505	0,022
FBXO30	84085	1,517	0,022
MTSS1	9788	1,699	0,022
MTERFD3	80298	1,286	0,023
ZNF318	24149	1,322	0,023
SLC40A1	30061	2,037	0,023
TGIF1	7050	-1,238	0,024
ARMC10	83787	-1,219	0,024
VPS39	23339	-1,206	0,024
IRF3	3661	-1,182	0,024
JMJD7-	8681	-1,181	0,024
CARKD	55739	1,221	0,024
MRPL14	64928	1,237	0,024
BIN1	274	1,247	0,024
KATNA1	11104	1,281	0,024
FHL2	2274	1,525	0,024
TMEM170A	124491	-1,312	0,025
TBC1D9B	23061	-1,282	0,025
ZFAND4	93550	1,769	0,025
CPED1	79974	-1,731	0,026
MT1H	4496	-1,565	0,026
MDGA1	266727	-1,246	0,026
PYGB	5834	-1,172	0,026
TRIM69	140691	-1,133	0,026
ZNF324B	388569	-1,129	0,026
PRKCI	5584	1,159	0,026
ZNF471	57573	1,204	0,026
ZNF566	84924	1,345	0,026
EHHADH	1962	1,369	0,026
ASF1A	25842	1,697	0,026
LAPTM4B	55353	2,332	0,026
ZNF711	7552	2,426	0,026
LGALS1	3956	-1,934	0,027

FER1L6-AS1	439941	-1,21	0,027
NAA60	79903	-1,176	0,027
RBX1	9978	1,191	0,027
CCDC144C	348254	1,363	0,027
RAB3IP	117177	1,409	0,027
WNK1	65125	1,549	0,027
FZD5	7855	1,706	0,027
RSU1	6251	1,29	0,028
ALDH5A1	7915	1,438	0,028
NRIP1	8204	1,887	0,028

Supplementary Table 2

Pathways significantly impacted in chromothripsis-positive (n=13) vs –negative (n=14) CK-AML (p-value <.05)

Pathway name	p value	No of deregulated genes	downregulated genes	upregulated genes
RNA degradation	0.012	6	*CNOT8, EDC4, CNOT1, ZCCHC7*	*LSM3, PFKM*
Acute myeloid leukemia	0.023	4	*CCNA1, CEBPA*	*PIM1, MYC*
Transcriptional misregulation in cancer	0.023	7	*CCNA1, CEBPA, HHEX*	*HPGD, BCL2L1, KLF3, MYC*
Hepatitis C	0.029	6	*STAT2, IRF1, IRF3, IRF9, OAS2, OAS3*	
Pentose phosphate pathway	0.032	3	*DERA*	*RPIA, PFKM*
Endocytosis	0.033	11	*HGS, ARPC1B, VPS26B, PSD3, ADRBK1, WIPF3, IST1*	*DNM3, BIN1, PRKCI, RABEP1*
Notch signaling pathway	0.038	4	*MAML1, APH1B*	*KAT2B, DTX3*
Mineral absorption	0.040	3	*MT1H, ATOX1*	*SLC40A1*
Drug metabolism	0.046	4	*FMO1, ADH1C, GSTK1*	*GSTM5*
Olfactory transduction	0.048	12	*OR5P2, OR7G3, OR8H3, OR6N1, OR51A4, OR2M7, ADRBK1, OR13C3, OR6N2*	*OR10J3, CALM2, OR52N2*

Supplementary Table 3

Gene set enrichment analysis (GSEA) using the Molecular Signatures Database (MSigDB) in chromothripsis-positive (n=13) vs –negative (n=14) CK-AML (p-value <.05)

# overlaps shown:	88
# genesets in collections:	1454
# genes in comparison (n):	397
# genes in universe (N):	45956

Gene Set Name	# Genes in Ge	Description	# Genes in Overlap (k)	k/K	p-value	FDR q-value
CYTOPLASM	2131	Genes annotated by the GO term GO:0005737. All	56	0.0263	1.54E-13	2.23E-10
BIOPOLYMER_METABOLIC_PROCESS	1684	Genes annotated by the GO term GO:0043283. Th	44	0.0261	9.48E-11	6.89E-8
NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	1244	Genes annotated by the GO term GO:0006139. Th	35	0.0281	1.35E-9	6.56E-7
NEGATIVE_REGULATION_OF_CELLULAR_PROCESS	646	Genes annotated by the GO term GO:0048523. An	24	0.0372	3.28E-9	1.19E-6
NEGATIVE_REGULATION_OF_BIOLOGICAL_PROCESS	677	Genes annotated by the GO term GO:0048519. An	24	0.0355	8.08E-9	2.35E-6
CYTOPLASMIC_PART	1383	Genes annotated by the GO term GO:0044444. An	35	0.0253	1.95E-8	4.73E-6
CELL_PROLIFERATION_GO_0008283	513	Genes annotated by the GO term GO:0008283. Th	20	0.0390	3.11E-8	6.46E-6
TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	457	Genes annotated by the GO term GO:0006366. Th	18	0.0394	1.31E-7	2.21E-5
NUCLEUS	1430	Genes annotated by the GO term GO:0005634. A	34	0.0238	1.37E-7	2.21E-5
TRANSCRIPTION_DNA_DEPENDENT	636	Genes annotated by the GO term GO:0006351. Th	21	0.0330	2.27E-7	2.9E-5
TRANSCRIPTION	753	Genes annotated by the GO term GO:0006350. Th	23	0.0305	2.38E-7	2.9E-5
RNA_BIOSYNTHETIC_PROCESS	638	Genes annotated by the GO term GO:0032774. Th	21	0.0329	2.39E-7	2.9E-5
CYTOSOL	205	Genes annotated by the GO term GO:0005829. Th	12	0.0585	2.72E-7	3.04E-5
RNA_METABOLIC_PROCESS	841	Genes annotated by the GO term GO:0016070. Th	24	0.0285	4.41E-7	4.58E-5
REGULATION_OF_METABOLIC_PROCESS	799	Genes annotated by the GO term GO:0019222. An	23	0.0288	6.62E-7	6.42E-5
REGULATION_OF_CELLULAR_METABOLIC_PROCESS	787	Genes annotated by the GO term GO:0031323. An	22	0.0280	1.87E-6	1.7E-4
REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	618	Genes annotated by the GO term GO:0019219. An	19	0.0307	2.43E-6	2.08E-4
PROTEIN_COMPLEX	816	Genes annotated by the GO term GO:0043234. An	22	0.0270	3.33E-6	2.69E-4
SIGNAL_TRANSDUCTION	1634	Genes annotated by the GO term GO:0007165. Th	32	0.0196	1.79E-5	1.37E-3
REGULATION_OF_GENE_EXPRESSION	673	Genes annotated by the GO term GO:0010468. An	18	0.0267	2.87E-5	2.03E-3
CATABOLIC_PROCESS	225	Genes annotated by the GO term GO:0009056. Th	10	0.0444	2.99E-5	2.03E-3
MACROMOLECULAR_COMPLEX	945	Genes annotated by the GO term GO:0032991. A	22	0.0233	3.18E-5	2.03E-3
PROTEIN_METABOLIC_PROCESS	1231	Genes annotated by the GO term GO:0019538. Th	26	0.0211	3.23E-5	2.03E-3
TRANSCRIPTION_COFACTOR_ACTIVITY	228	Genes annotated by the GO term GO:0003712. Th	10	0.0439	3.34E-5	2.03E-3
REGULATION_OF_TRANSCRIPTION	566	Genes annotated by the GO term GO:0045449. An	16	0.0283	4.14E-5	2.41E-3
CELLULAR_HOMEOSTASIS	147	Genes annotated by the GO term GO:0019725. Th	8	0.0544	4.53E-5	2.54E-3
REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	289	Genes annotated by the GO term GO:0006357. An	11	0.0381	4.98E-5	2.68E-3
MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1049	Genes annotated by the GO term GO:0007275. Th	23	0.0219	5.27E-5	2.74E-3
REGULATION_OF_TRANSCRIPTIONDNA_DEPENDENT	461	Genes annotated by the GO term GO:0006355. An	14	0.0304	5.83E-5	2.92E-3
REGULATION_OF_RNA_METABOLIC_PROCESS	471	Genes annotated by the GO term GO:0051252. An	14	0.0297	7.32E-5	3.55E-3
TRANSPORT	795	Genes annotated by the GO term GO:0006810. Th	19	0.0239	7.78E-5	3.65E-3
TRANSCRIPTION_FACTOR_BINDING	307	Genes annotated by the GO term GO:0008134. Int	11	0.0358	8.54E-5	3.88E-3
MULTI_ORGANISM_PROCESS	165	Genes annotated by the GO term GO:0051704. Th	8	0.0485	1.02E-4	4.5E-3
ACID_AMINO_ACID_LIGASE_ACTIVITY	57	Genes annotated by the GO term GO:0016881. Ca	5	0.0877	1.36E-4	5.73E-3
ION_HOMEOSTASIS	129	Genes annotated by the GO term GO:0050801. An	7	0.0543	1.38E-4	5.73E-3
CELLULAR_MACROMOLECULE_METABOLIC_PROCESS	1131	Genes annotated by the GO term GO:0044260. Th	23	0.0203	1.59E-4	6.43E-3
NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY	14	Genes annotated by the GO term GO:0051346. An	3	0.2143	2.17E-4	8.53E-3
ESTABLISHMENT_OF_LOCALIZATION	870	Genes annotated by the GO term GO:0051234. Th	19	0.0218	2.45E-4	9.37E-3
TRANSCRIPTION_FACTOR_ACTIVITY	354	Genes annotated by the GO term GO:0003700. Th	11	0.0311	2.93E-4	1.09E-2
LIGASE_ACTIVITY_FORMING_CARBON_NITROGEN_BONDS	68	Genes annotated by the GO term GO:0016879. Ca	5	0.0735	3.13E-4	1.14E-2
CELLULAR_PROTEIN_METABOLIC_PROCESS	1117	Genes annotated by the GO term GO:0044267. Th	22	0.0197	3.41E-4	1.21E-2
CHROMATIN_REMODELING_COMPLEX	17	Genes annotated by the GO term GO:0016585. An	3	0.1765	3.98E-4	1.38E-2
CHEMICAL_HOMEOSTASIS	155	Genes annotated by the GO term GO:0048878. Th	7	0.0452	4.24E-4	1.43E-2
CELL_CYCLE_GO_0007049	315	Genes annotated by the GO term GO:0007049. Th	10	0.0317	4.63E-4	1.5E-2
NEGATIVE_REGULATION_OF_CELLULAR_METABOLIC_PROCESS	259	Genes annotated by the GO term GO:0031324. An	9	0.0347	4.64E-4	1.5E-2
HOMEOSTATIC_PROCESS	207	Genes annotated by the GO term GO:0042592. Th	8	0.0386	4.75E-4	1.5E-2
NEGATIVE_REGULATION_OF_METABOLIC_PROCESS	262	Genes annotated by the GO term GO:0009892. An	9	0.0344	5.04E-4	1.56E-2
NEGATIVE_REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	211	Genes annotated by the GO term GO:0045934. An	8	0.0379	5.38E-4	1.63E-2
CELLULAR_CATABOLIC_PROCESS	212	Genes annotated by the GO term GO:0044248. Th	8	0.0377	5.55E-4	1.65E-2
ADENYL_RIBONUCLEOTIDE_BINDING	163	Genes annotated by the GO term GO:0032559. Int	7	0.0429	5.72E-4	1.66E-2
HYDROLASE_ACTIVITY_ACTING_ON_ESTER_BONDS	269	Genes annotated by the GO term GO:0016788. Ca	9	0.0335	6.08E-4	1.73E-2
NEGATIVE_REGULATION_OF_CELL_CYCLE	79	Genes annotated by the GO term GO:0045786. An	5	0.0633	6.26E-4	1.75E-2
MEMBRANE	1994	Genes annotated by the GO term GO:0016020. D	32	0.0160	6.51E-4	1.79E-2
ADENYL_NUCLEOTIDE_BINDING	169	Genes annotated by the GO term GO:0030554. Int	7	0.0414	7.09E-4	1.91E-2
GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	123	Genes annotated by the GO term GO:0006091. Th	6	0.0488	7.27E-4	1.92E-2
INTRACELLULAR_SIGNALING_CASCADE	667	Genes annotated by the GO term GO:0007242. A	15	0.0225	8.03E-4	2.07E-2
TRANSCRIPTION_ACTIVATOR_ACTIVITY	173	Genes annotated by the GO term GO:0016563. An	7	0.0405	8.13E-4	2.07E-2
REGULATION_OF_APOPTOSIS	341	Genes annotated by the GO term GO:0042981. An	10	0.0293	8.51E-4	2.11E-2
UBIQUITIN_PROTEIN_LIGASE_ACTIVITY	49	Genes annotated by the GO term GO:0004842. Ca	4	0.0816	8.55E-4	2.11E-2
REGULATION_OF_PROGRAMMED_CELL_DEATH	342	Genes annotated by the GO term GO:0043067. An	10	0.0292	8.7E-4	2.11E-2
SMALL_CONJUGATING_PROTEIN_LIGASE_ACTIVITY	51	Genes annotated by the GO term GO:0019787. Ca	4	0.0784	9.95E-4	2.37E-2
SMALL_PROTEIN_CONJUGATING_ENZYME_ACTIVITY	52	Genes annotated by the GO term GO:0008639. Ca	4	0.0769	1.07E-3	2.51E-2
MACROMOLECULE_CATABOLIC_PROCESS	137	Genes annotated by the GO term GO:0009057. Th	6	0.0438	1.27E-3	2.92E-2
TRANSFERASE_ACTIVITY_TRANSFERRING_PHOSPHORUS_CONTAINING_GROUPS	424	Genes annotated by the GO term GO:0016772. Ca	11	0.0259	1.29E-3	2.92E-2
NEGATIVE_REGULATION_OF_TRANSCRIPTION	188	Genes annotated by the GO term GO:0016481. An	7	0.0372	1.32E-3	2.95E-2
TRANSCRIPTION_COREPRESSOR_ACTIVITY	94	Genes annotated by the GO term GO:0003714. Th	5	0.0532	1.37E-3	3.02E-2
CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	26	Genes annotated by the GO term GO:0006333. Th	3	0.1154	1.44E-3	3.11E-2
CYTOSKELETON	367	Genes annotated by the GO term GO:0005856. An	10	0.0272	1.47E-3	3.14E-2
CELL_CYCLE_ARREST_GO_0007050	57	Genes annotated by the GO term GO:0007050. An	4	0.0702	1.51E-3	3.14E-2
MEMBRANE_PART	1670	Genes annotated by the GO term GO:0044425. An	27	0.0162	1.53E-3	3.14E-2
KINASE_ACTIVITY	369	Genes annotated by the GO term GO:0016301. Ca	10	0.0271	1.53E-3	3.14E-2
REGULATION_OF_CELL_PROLIFERATION	308	Genes annotated by the GO term GO:0042127. An	9	0.0292	1.56E-3	3.14E-2
LIGASE_ACTIVITY	97	Genes annotated by the GO term GO:0016874. Ca	5	0.0515	1.58E-3	3.14E-2
REGULATION_OF_DEVELOPMENTAL_PROCESS	440	Genes annotated by the GO term GO:0050793. An	11	0.0250	1.72E-3	3.38E-2
BIOPOLYMER_MODIFICATION	650	Genes annotated by the GO term GO:0043412. Th	14	0.0215	1.77E-3	3.43E-2
NEGATIVE_REGULATION_OF_APOPTOSIS	150	Genes annotated by the GO term GO:0043066. An	6	0.0400	2.02E-3	3.86E-2
NEGATIVE_REGULATION_OF_PROGRAMMED_CELL_DEATH	151	Genes annotated by the GO term GO:0043069. An	6	0.0397	2.08E-3	3.94E-2
PURINE_RIBONUCLEOTIDE_BINDING	205	Genes annotated by the GO term GO:0032555. Int	7	0.0341	2.15E-3	3.97E-2
TRANSCRIPTION_REPRESSOR_ACTIVITY	152	Genes annotated by the GO term GO:0016564. An	6	0.0395	2.15E-3	3.97E-2
REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	30	Genes annotated by the GO term GO:0040029. An	3	0.1000	2.18E-3	3.97E-2
CELLULAR_CATION_HOMEOSTASIS	106	Genes annotated by the GO term GO:0030003. Th	5	0.0472	2.33E-3	4.18E-2
ATP_BINDING	156	Genes annotated by the GO term GO:0005524. Int	6	0.0385	2.45E-3	4.3E-2
NEGATIVE_REGULATION_OF_CELL_PROLIFERATION	156	Genes annotated by the GO term GO:0008285. An	6	0.0385	2.45E-3	4.3E-2
DNA_BINDING	602	Genes annotated by the GO term GO:0003677. Int	13	0.0216	2.49E-3	4.31E-2
PURINE_NUCLEOTIDE_BINDING	211	Genes annotated by the GO term GO:0017076. Int	7	0.0332	2.53E-3	4.33E-2
CATION_HOMEOSTASIS	109	Genes annotated by the GO term GO:0055080. Th	5	0.0459	2.63E-3	4.4E-2
VIRAL_INFECTIOUS_CYCLE	32	Genes annotated by the GO term GO:0019058. A	3	0.0938	2.64E-3	4.4E-2
ORGANELLE_ORGANIZATION_AND_BIOGENESIS	473	Genes annotated by the GO term GO:0006996. A	11	0.0233	3,00E-03	4.96E-2

Supplementary Table 4

Top 200 differentially expressed genes in chromothripsis-positive (n=10) vs –negative (n=7) TP53altered CK-AML cases (p-value <.05)

Symbol	ID	LogFC	p value
PSMB10	5699	-1,782	1,96E-04
ZNF516	9658	-1,961	2,41E-04
TMEM208	29100	-1,406	2,84E-04
BCL9	607	1,403	7,11E-04
ADAMTS6	11174	-1,679	9,77E-04
CPEB3	22849	-1,466	0,001
BAI3	577	-1,462	0,002
PLA2G15	23659	-1,43	0,002
MAML1	9794	-1,264	0,002
TPST2	8459	1,275	0,002
CABP5	56344	1,506	0,002
ACD	65057	-1,436	0,003
PHKG2	5261	-1,391	0,003
PPIP5K1	9677	-1,346	0,003
TRIM41	90933	-1,329	0,003
KIAA0141	9812	-1,326	0,003
PSKH1	5681	-1,293	0,003
HCFC1	3054	-1,241	0,003
POLR2F	5435	1,405	0,003
ZNF197	10168	1,52	0,003
CES2	8824	-1,323	0,004
TMEM217	221468	-1,281	0,004
RNF44	22838	-1,251	0,004
RNF31	55072	-1,215	0,004
ERCC1	2067	-1,202	0,004
CBFB	865	-1,617	0,005
CDK5	1020	-1,443	0,005
TAZ	6901	-1,221	0,005
ZNF681	148213	1,442	0,005
VTI1B	10490	1,463	0,005
SERAC1	84947	1,547	0,005
TNIK	23043	1,807	0,005
ZNF37A	7587	1,118	0,006
ERVK3-1	100507739	1,248	0,006
PIM1	5292	2,126	0,006
MYO15B	80022	-1,71	0,007
FAM192A	80011	-1,538	0,007
IMPA2	3613	-1,516	0,007
SLC7A6	9057	-1,394	0,007
IKZF4	64375	-1,226	0,007
GPD1L	23171	1,303	0,007
SELRC1	65260	1,36	0,007
CCS	9973	1,428	0,007
GPA33	10223	1,469	0,007
TK2	7084	-1,603	0,008
FCER1A	2205	-1,589	0,008
DPP7	29952	-1,259	0,008
WBP5	51186	1,45	0,008
TMEM242	729515	1,538	0,008
CNOT1	23019	-1,707	0,009
WWP2	11060	-1,42	0,009
GEM	2669	1,184	0,009
CYTL1	54360	3,58	0,009
RNF213	57674	-1,494	0,01
BIK	638	1,236	0,01
RBFOX2	23543	1,399	0,01
ZDHHC3	51304	1,453	0,01
VANGL1	81839	2,237	0,01
GRAMD1B	57476	-1,905	0,011
SPATA20	64847	-1,309	0,011
TBC1D9B	23061	-1,303	0,011
TMCO4	255104	-1,249	0,011
PTTG2	10744	-1,179	0,011
USP49	25862	1,268	0,011
DSTN	11034	1,624	0,011
P2RX5-	100533970	1,634	0,011
CCRL2	9034	1,728	0,011
PANX1	24145	-1,745	0,012
TMEM170A	124491	-1,437	0,012
CS	1431	-1,319	0,012

TMEM237	65062	1,267	0,012
BEX2	84707	1,671	0,012
OR4M2	390538	-2,081	0,013
FRY	10129	-2,042	0,013
EDC4	23644	-1,391	0,013
FFAR3	2865	-1,379	0,013
MON1B	22879	-1,336	0,013
FIBP	9158	-1,23	0,013
LAPTM4B	55353	2,447	0,013
CKLF	51192	-1,687	0,014
CYBA	1535	-1,428	0,014
SNRPB2	6629	1,29	0,014
RABGAP1L	9910	1,292	0,014
GCHFR	2644	1,293	0,014
ZNF286A	57335	1,591	0,014
VPS26B	112936	-1,583	0,015
VPS11	55823	-1,314	0,015
FGFR1OP2	26127	1,691	0,015
NOB1	28987	-1,413	0,016
AGPAT2	10555	-1,307	0,016
CREBBP	1387	-1,222	0,016
EP400	57634	-1,19	0,016
SIPA1	6494	-1,18	0,016
ASIC3	9311	-1,072	0,016
CHCHD6	84303	1,147	0,016
SH3PXD2A	9644	1,329	0,016
FAM46C	54855	2,506	0,016
ANKRD16	54522	-1,322	0,017
MPZL1	9019	1,389	0,017
LGALS1	3956	-1,949	0,018
TBC1D16	125058	-1,724	0,018
ARRDC1	92714	-1,345	0,018
FES	2242	-1,309	0,018
HMHA1	23526	-1,215	0,018
GLYR1	84656	-1,209	0,018
QR4	124222	-1,199	0,018
COQ2	27235	-1,231	0,019
SPTLC3	55304	1,611	0,019
ASCC2	84164	1,732	0,019
FANCA	2175	-1,461	0,02
CLTA	1211	-1,457	0,02
FAM78A	286336	-1,449	0,02
GINS3	64785	-1,424	0,02
CLDN20	49861	1,211	0,02
ZFP3	124961	1,258	0,02
EXOSC7	23016	1,291	0,02
ELAC2	60528	1,342	0,02
FBXO34	55030	1,549	0,02
OAS3	4940	-1,686	0,021
B4GALT6	9331	-1,646	0,021
ORAI3	93129	-1,373	0,021
TRIM52	84851	-1,351	0,021
MFSD11	79157	-1,263	0,021
OR5P2	120065	-1,219	0,021
PFKL	5211	-1,21	0,021
C19orf54	284325	-1,171	0,021
HGS	9146	-1,177	0,022
SBF1	6305	1,287	0,022
IFI6	2537	-2,102	0,023
SLITRK4	139065	-1,906	0,023
BST2	684	-1,448	0,023
CEBPA	1050	-1,366	0,023
B3GAT3	26229	-1,355	0,023
UTRN	7402	-1,352	0,023
LOC283588	283588	-1,256	0,023
C15orf63	25764	-1,227	0,023
TIMP3	7078	2,129	0,023
L3MBTL4	91133	-2,049	0,024
TAS2R62P	338399	-1,407	0,024
FDPS	2224	-1,334	0,024
CMTM1	113540	-1,296	0,024
NAA60	79903	-1,225	0,024
CRYGS	1427	-1,183	0,024
NGFRAP1	27018	1,469	0,024
MTSS1	9788	2,07	0,024

LRRK1	79705	-1,515	0,025
PARP14	54625	-1,436	0,025
PHKA2	5256	-1,214	0,025
ATF7	11016	-1,178	0,025
SYN2	6854	1,274	0,025
ETNK2	55224	1,294	0,025
TREML4	285852	1,402	0,025
ELN	2006	1,556	0,025
SPSB1	80176	1,589	0,025
KDELC1	79070	-1,805	0,026
LONRF3	79836	-1,499	0,026
CMTM3	123920	-1,477	0,026
ZRSR2	8233	-1,365	0,026
LRRC23	10233	-1,346	0,026
EME1	146956	-1,292	0,026
SLC4A4	8671	1,332	0,026
ZNF415	55786	1,364	0,026
ZNF502	91392	1,413	0,026
ZAP70	7535	1,533	0,026
GIPC2	54810	1,665	0,026
ARPC1B	10095	-1,792	0,027
KIAA1468	57614	-1,661	0,027
NIP7	51388	-1,564	0,027
OSBPL1A	114876	-1,457	0,027
POLR2C	5432	-1,325	0,027
UBIAD1	29914	1,154	0,027
LSM3	27258	1,287	0,027
RSPO2	340419	-1,575	0,028
OR7G3	390883	-1,467	0,028
ALDOA	226	-1,242	0,028
TOMM40	10452	-1,192	0,028
C4B	721	1,188	0,028
BMPR2	659	1,831	0,028
CMTM4	146223	-1,49	0,029
TDRD7	23424	-1,464	0,029
VAMP5	10791	-1,392	0,029
DIAPH1	1729	-1,336	0,029
SOGA1	140710	-1,29	0,029
TTLL3	26140	-1,269	0,029
SNX19	399979	-1,255	0,029
SMG9	56006	-1,219	0,029
JMJD7-	8681	-1,194	0,029
OXER1	165140	-1,184	0,029
CTH	1491	1,463	0,029
ELOVL6	79071	2,036	0,029
C16orf80	29105	-1,96	0,03
STAT2	6773	-1,559	0,03
ATP6V0D1	9114	-1,555	0,03
GHRLOS2	84657	-1,475	0,03
FBXO22	26263	-1,401	0,03
DHX38	9785	-1,4	0,03
VAC14	55697	-1,325	0,03
PYGB	5834	-1,19	0,03
ZNF839	55778	1,138	0,03
SELK	58515	1,326	0,03

Supplementary Table 5

Pathways significantly impacted in chromothripsis-positive (n=10) vs –negative (n=7) TP53altered CK-AML cases (p-value <.05)

Pathway name	p value	No of deregulated genes	downregulated genes	upregulated genes
Glycerophospholipid metabolism	9,12E-03	10	*PLA2G15, TAZ, AGPAT2, JMJD7-PLA2G4B, DGKH*	*GPD1L, ETNK2, AGPAT4, CDS1, C17orf48*
Biosynthesis of amino acids	0.002	6	*CS, PFKL, ALDOA*	*CTH, PSPH, PSAT1*
RNA degradation	0.005	6	*CNOT1, EDC4, PFKL, CNOT8*	*EXOSC7, LSM3*
Fanconi anemia pathway	0.017	4	*ERCC1, FANCA,EME1*	*MLH1*
RNA polymerase	0.020	3	*POLR2C, POLR3K*	*POLR2F*
Glycine, serine and threonine metabolism	0.035	3		*CTH, PSPH, PSAT1*
Transcriptional misregulation in cancer	0.041	1	*CEBPA*	
Phosphatidylinositol signaling system	0.042	5	*PPIP5K1, IMPA2, DGKH*	*PIP4K2C, CDS1*
Pyrimidine metabolism	0.043	5	*TK2, POLR2C, DHODH, POLR3K*	*POLR2F*
Phagosome	0.045	6	*CYBA, HGS, ATP6V0D1*	*RAB5A, HLA-DRB1, DYNC1LI1*
Asthma	0.046	2	*FCER1A*	*HLA-DRB1*