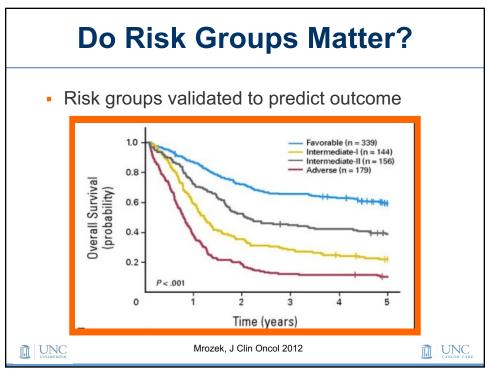
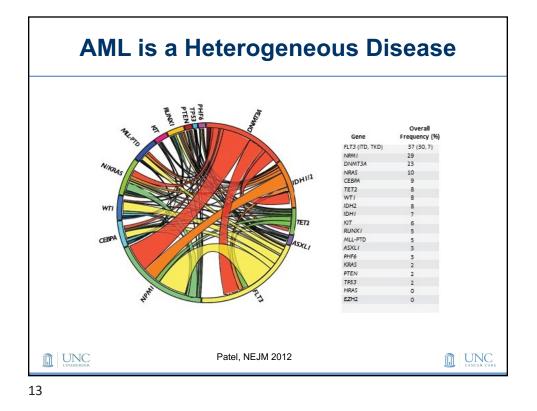


Classif	Classification/Prognostication							
 Genetic infe 	fication outdated (M0-M7 ormation critical for progr _eukemiaNet Classificatio	nosticatio	'n					
ELN Risk	Cytogenetic/Molecular	Incidence- Younger pts	Incidence- Older pts					
Favorable	 t(8;21); inv(16); t(16;16) NPM1 mutation w/o FLT3-ITD mut. OR with FLT3-ITD^{low} Biallelic mutated CEPBA 	41%	20%					
Intermediate	 Mutated NPM1 and FLT3-ITD^{high} Wild-type NPM1 w/o FLT3-ITD or with FLT3-ITD^{low} t(9;11) Other 	37%	49%					
Adverse	 Inv(3); t(3;3); t(6;9); t(v;11); -5; del(5q); -7; -17/abnl(17p); complex Wild type NPM1 & FLT3-ITD^{high} Mutated RUNX1, ASXL1, TP53 	22%	31%					
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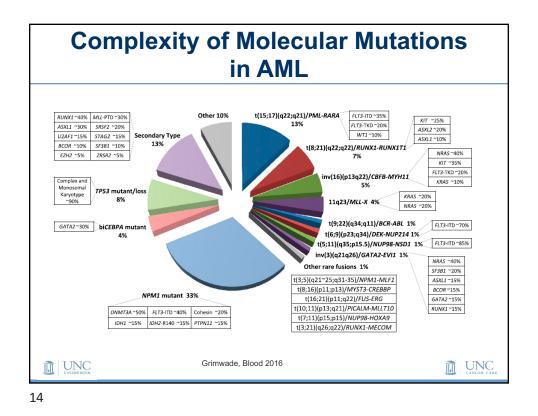
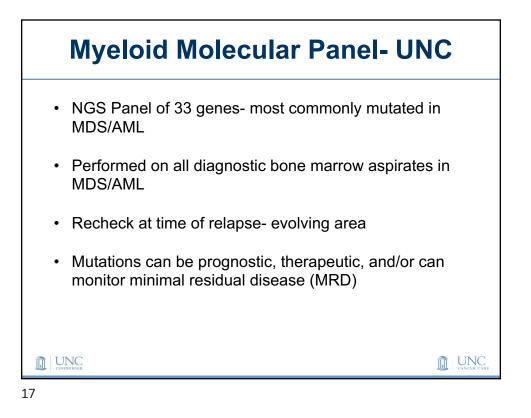
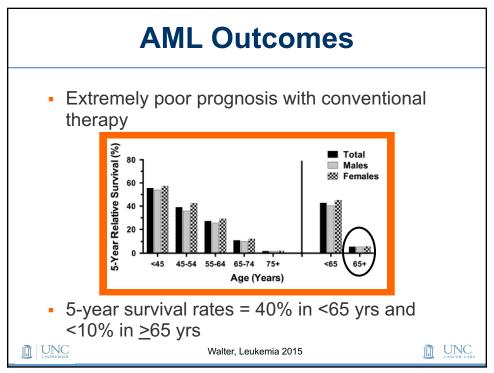


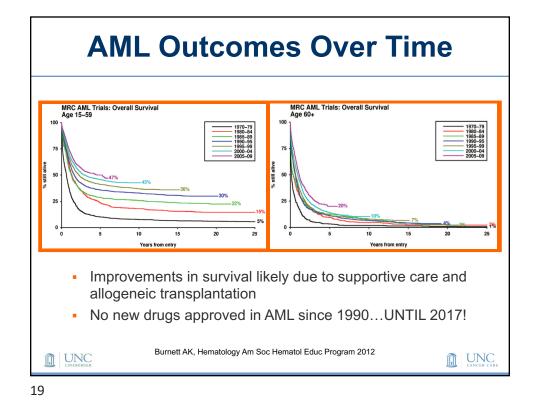
Table 1. Proposed Genomic Classification of Acute Myeloid Leukemia (AML).					
Genomic Subgroup	Frequency in the Study Cohort (N=1540)	Most Frequently Mutated Genes*			
	no. of patients (%)	gene (%)			
AML with NPM1 mutation	418 (27)	NPM1 (100), DNMT3A (54), FLT3 ^{ITD} (39), NRAS (19) TET2 (16), PTPN11 (15)			
AML with mutated chromatin, RNA-splicing genes, or both†	275 (18)	RUNX1 (39), MLL ^{PTD} (25), SRSF2 (22), DNMT3A (20 ASXL1 (17), STAG2 (16), NRAS (16), TET2 (15), FLT3 ^{ITD} (15)			
AML with TP53 mutations, chromosomal aneuploidy, or both‡	199 (13)	Complex karyotype (68), -5/5q (47), -7/7q (44), TP53 (44), -17/17p (31), -12/12p (17), +8/8q (16			
AML with inv (16) (p13.1q22) or t(16;16) (p13.1;q22); CBFB-MYH11	81 (5)	inv(16) (100), NRAS (53), +8/8q (16), +22 (16), KIT (15), FLT3 ^{TKD} (15)			
AML with biallelic CEBPA mutations	66 (4)	CEBPA biallelic (100), NRAS (30), WT1 (21), GATA2 (20			
AML with t(15;17)(q22;q12); PML-RARA	60 (4)	t(15;17) (100), FLT3 ^{ITD} (35), WT1 (17)			
AML with t(8;21)(q22;q22); RUNX1-RUNX1T1	60 (4)	t(8;21) (100), KIT (38), -Y (33), -9q (18)			
AML with MLL fusion genes; t(x;11)(x;q23)§	44 (3)	t(x;11q23) (100), NRAS (23)			
AML with inv(3) (q21q26.2) or t(3;3) (q21;q26.2); GATA2, MECOM(EVI1)	20 (1)	inv(3) (100), -7 (85), KRAS (30), NRAS (30), PTPN11 (30), ETV6 (15), PHF6 (15), SF3B1 (15)			
AML with IDH2R172 mutations and no other class-defining lesions	18 (1)	IDH2 ^{R172} (100), DNMT3A (67), +8/8q (17)			
AML with t(6;9) (p23;q34); DEK-NUP214	15 (1)	t(6;9) (100), FLT3 ^{ITD} (80), KRAS (20)			
AML with driver mutations but no detected class-defining lesions	166 (11)	FLT3 ^{ITD} (39), DNMT3A (16)			
AML with no detected driver mutations	62 (4)				
AML meeting criteria for ≥2 genomic subgroups	56 (4)				

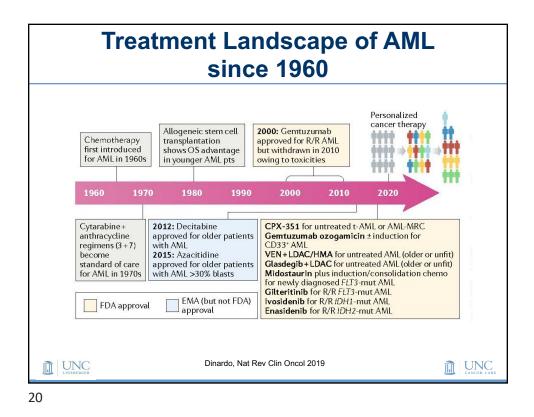
Driver Mutations With Effect on OS							
Table 2. Driver Mutations with th	e Strongest Effect on	Overall Survival a	nd Other Clas	Gene-gene interactions			
Variable	Frequency in Study Cohort (N=1540)	Hazard Ratio for Death (95% CI)	P Value	NPM1–FLT3 ^{ITD} –DNMT3A	93 (6)	1.5 (1.2–1.9)	0.0002
_	no. of patients (%)			MI I PTD_FI T3TKD	10 (1)	1.4 (1.2-1.8)	0.0005
Main effects	22 (2)		0.10.6			· · · ·	
inv(3), GATA2, MECOM(EVI1) TP53	23 (1)	2.9 (1.8-4.7)	9×10 ⁻⁶	DNMT3A-IDH2 ^{R140}	47 (3)	1.4 (1.1–1.8)	0.007
Complex karyotype	98 (6) 159 (10)	1.7 (1.4–2.2) 1.4 (1.2–1.7)	2×10 ⁻⁶	STAG2-IDH2R140	11 (1)	0.8 (0.6-0.9)	0.01
BRAF	9 (1)	1.4 (1.2-1.7)	0.009	NPM1-FLT3 ^{TKD}	53 (3)	0.7 (0.6-0.9)	0.009
SRSF2	89 (6)	1.4 (1.1–1.7)	0.003				
FLT3ITD	341 (22)	1.4 (1.2–1.7)	0.0008	DNMT3A-RAD21	19 (1)	0.7 (0.5–0.9)	0.0008
+21	39 (3)	1.3 (1.1-1.6)	0.001	Other class-defining lesions			
-5/5q	107 (7)	1.3 (1.1-1.5)	0.0007	t(x;11), not MLLT3-MLL	37 (2)	1.4 (1.0-2.1)	0.06
-17/17p	74 (5)	1.3 (1.1-1.5)	0.003	ASXL1	70 (5)	1.3 (1.0-1.6)	0.04
+13	21 (1)	1.3 (1.1–1.5)	0.004				
-7	88 (6)	1.3 (1.1–1.5)	0.003	ZRSR2	13 (1)	1.3 (1.0–1.7)	0.04
-9q†	53 (3)	1.2 (1.1–1.5)	0.01	RUNX1	133 (9)	1.1 (0.9-1.3)	0.5
+22†	26 (2)	1.2 (1.1–1.4)	0.008	t(9;11), MLLT3-MLL	18 (1)	0.8 (0.4-1.4)	0.5
NPM1	436 (28)	0.7 (0.6–0.9)	0.0004	A CONTRACT OF A CONTRACT.	()	· · · ·	
CEBPA ^{biallelic}	73 (5)	0.6 (0.4–0.7)	4×10 ⁻⁵	IDH 2 ^{R172}	39 (3)	0.8 (0.6–1.0)	0.07
t(15;17), PML-RARA	65 (4)	0.3 (0.2–0.4)	5×10 ⁻⁸	t(8;21), RUNX1-RUNX1T1	63 (4)	0.7 (0.4-1.0)	0.03
inv(16), CBFB–MYH11	82 (5)	0.3 (0.2–0.4)	4×10 ⁻⁹				
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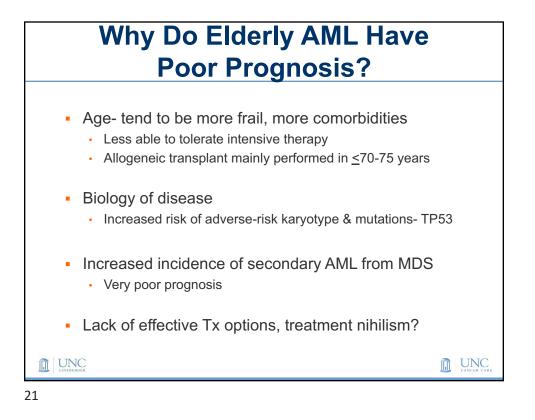


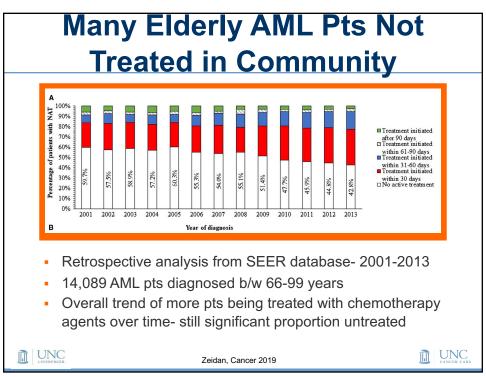














 Older ad toxicity 	dults have and lower	signifi	or <60 years cantly highe I efficacy wit	rates o		on	
Table 5. Mortality within 30 days Yo	ounger	Older	Table 6. Treatment outcomes	Youngerthan 56 y	56-65 y	66-75 y	Olderthan 75
No. patients :: Early death s' by performance status, no /no. total patients (%) : 0 : : 1 : : 2 : :	an 56 y 56-65 y 66-75 y 364 242 270 1129 (2) 8/72 (11) 9/73 (12) 180 (3) 6/12 (5) 20/126 (16) 146 (2) 8/34 (18) 16/52 (31) 0.9(0) 7/24 (29) 9/16 (14)) 7/40 (18)) 7/14 (50)	No. patients Response, no. (%) CR Resistant disease Median overal survival, no. (85% CI) No. patients with CR Median disease necessarikal, no. (85% CD)	388 235 (64) 99 (27) 18.8 (14.9-22.6) 235 21.6 (15.8-25.5)	246 113 (46) 91 (37) 9.0 (81-10.2) 113 7.4 (65-8.8)	274 108(39) 101(37) 6.9(5.47.7) 108 8.3(6.3-10.2)	80 26 (33) 29 (36) 3.5 (1.4-6.1) 26 8.9 (5.8-10.8

