# Disparities in Myeloma and Its Precursors in African Americans

Timothy R. Rebbeck, PhD

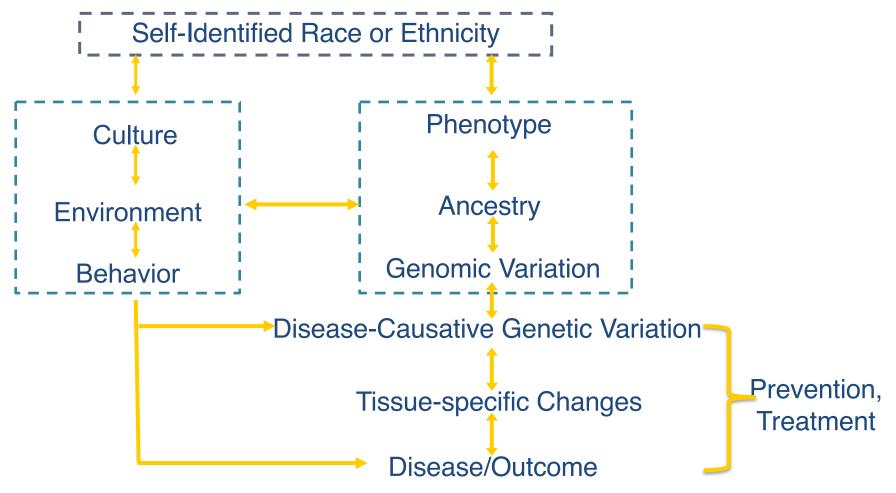




# **Disclosures**

None

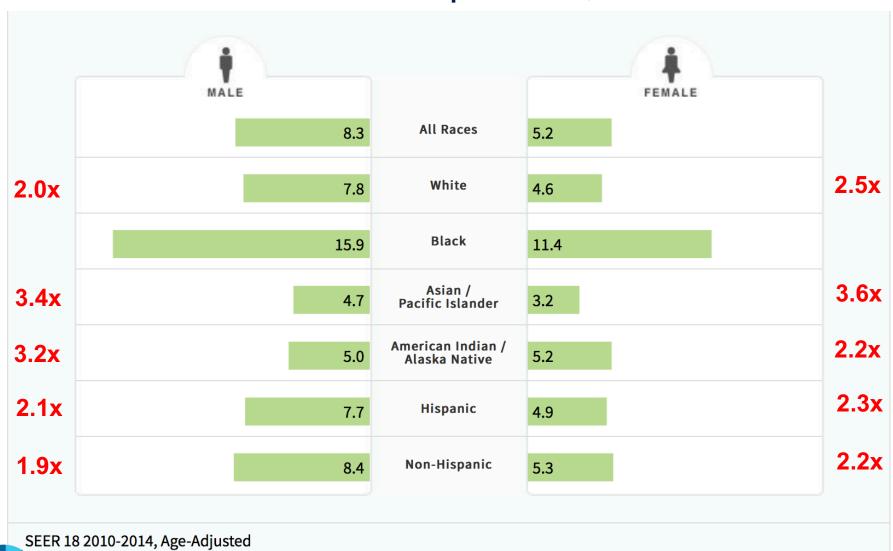
# Disparities Framework



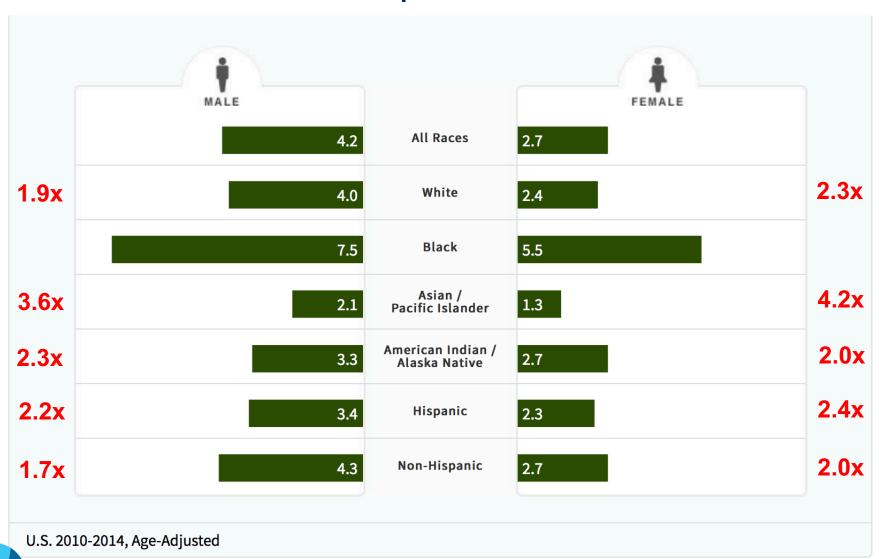


Adapted from: Rebbeck and Sankar CEBP 2005, Rebbeck et al. JCO 2006

#### Number of New Cases per 100,000 Persons



### Number of Deaths per 100,000 Persons

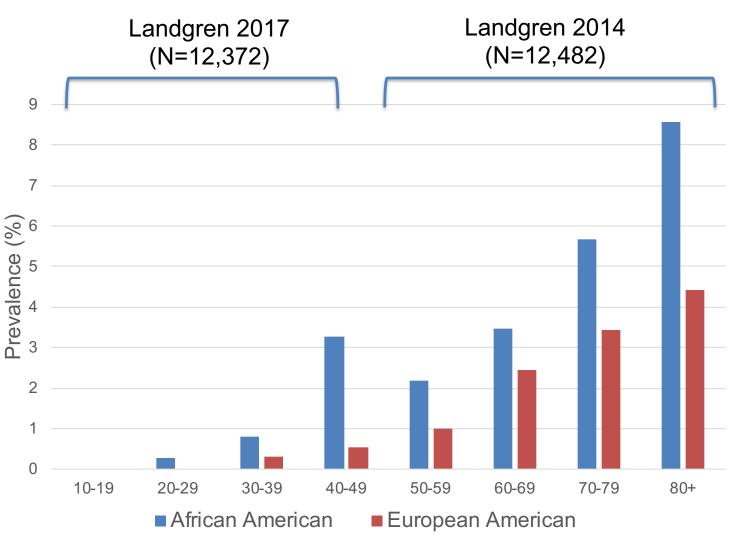




### Disparities in MGUS Prevalence

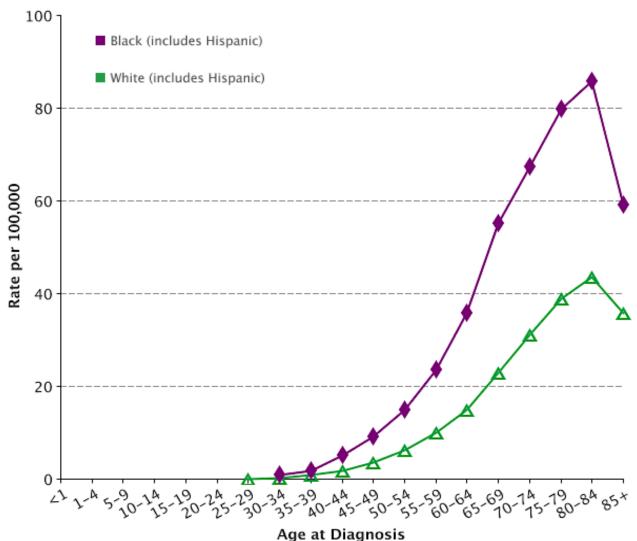
All Myeloma Patients have prior MGUS

(Landgren et al., Blood, 2009; Weiss et al; Blood 2009)



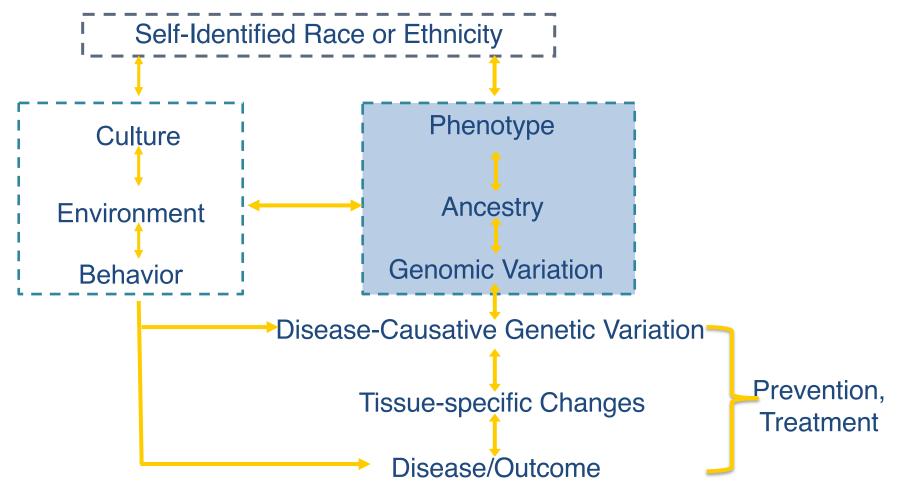


## Earlier Age at MM Diagnosis in Blacks





# Disparities Framework





Adapted from: Rebbeck and Sankar CEBP 2005, Rebbeck et al. JCO 2006

## Familial Myeloma

Trait		Citations
Familial Relative Risk of MM	2.5-fold excess risk	Altieri et al., 2006 Landgren et al. 2006 Hemminki et al. 2004 Frank et al. 2015
Proportion of MM that is familial	2.4%	Frank et al. 2016
Reported clustering of MM with other tumors	Tumor sites: colorectal*, breast and prostate cancers, non-thyroid endocrine tumors, leukemia (*a syndrome?)	Frank et al. 2016

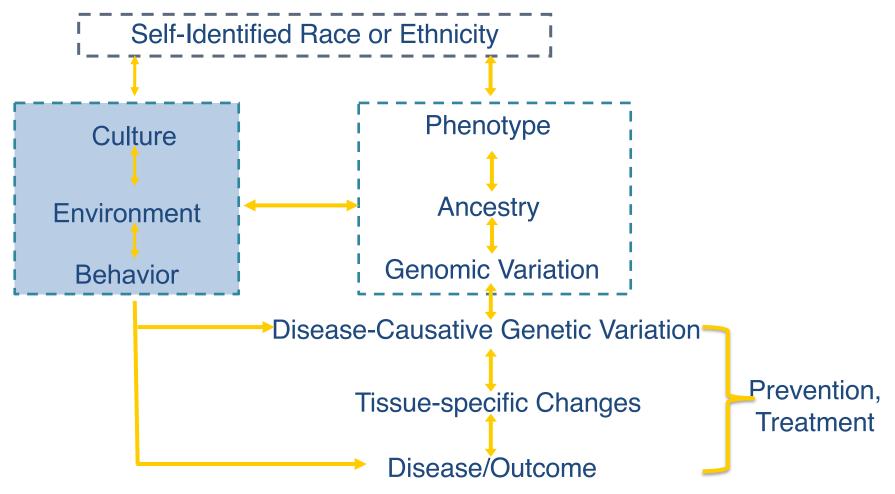


### Association of MM Family History with MM Risk

	European American	African American
Van Valkenburg et al. 2016	2.0 (0.83-5.04)	20.9 (2.59-168)
Brown et al. 1999	1.5 (0.3-6.4)	17.4 (2.4-348)



# Disparities Framework

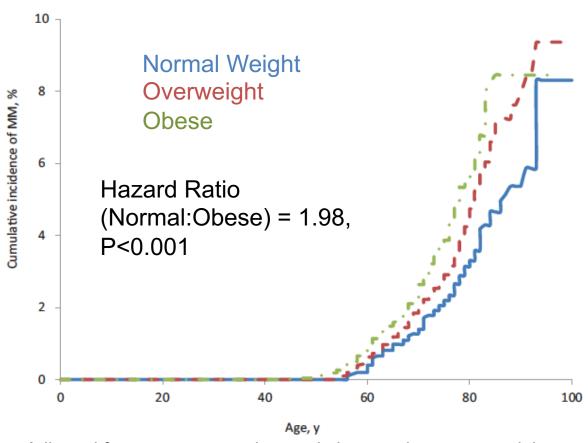




Adapted from: Rebbeck and Sankar CEBP 2005, Rebbeck et al. JCO 2006

## Obesity as a MM Risk Factor:

Cumulative Incidence of MM in 7,878 US Veterans with MGUS, 1999-2009





Adjusted for age, race, gender, marital status, income, creatinine, diabetes, and comorbidities

#### Selected MGUS Risk Factor Exposures

Exposure	Association	References
World Trade Center 9/11 Exposed vs. Olmstead County, MN	1.8-fold higher	Landgren et al. JAMA Oncology 2018
Pesticide exposed vs. Olmstead County, MN	1.9-fold higher	Landgren et al., <i>Blood</i> 2009
Agent Orange Exposed vs. Unexposed	7.1% vs. 3.1% (OR=2.4, 95%CI 1.3-4.4)	Landgren et al. JAMA Oncology 2015

Limitation: Associations largely unreported in African Americans



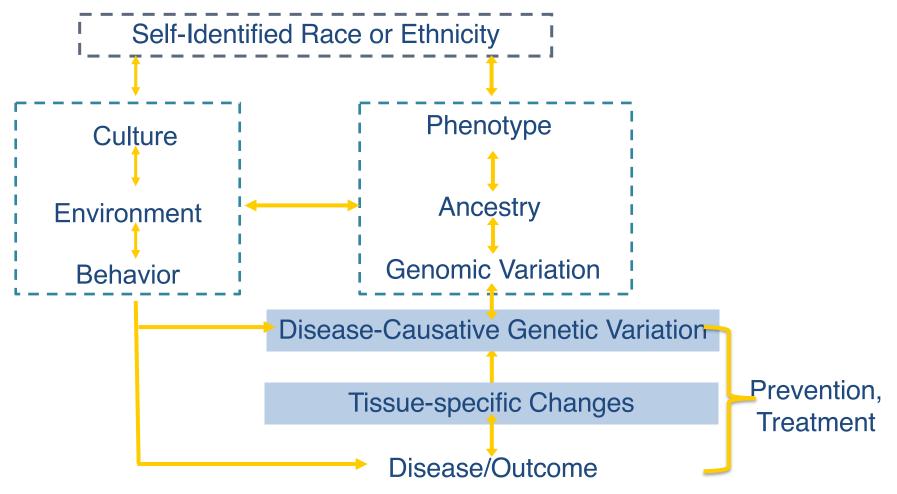
#### Selected Myeloma Risk Factor Exposures

Exposure	Association	References
World Trade Center 9/11 Exposed vs. General Population	7.63% in 9/11 Firefighters vs. 1.8% in Olmstead County	Landgren et al. <i>JAMA</i> Oncology 2018
Female Agricultural Workers	HR=2.25 (95%CI 1.16-4.37)	Kachuri et al. <i>BMC</i> Cancer 2017
Chernobyl Accident Clean-Up Workers	SIR=1.6 (96%CI: 1.01-2.2)	Bazyka et al. <i>Prob Rad Med Radiob</i> 2013
Hiroshima & Nagasaki Atomic Bomb Blast Survivors	No excess risk	Hsu et al., Radiation Research, 2013

Limitation: Associations largely unreported in African Americans



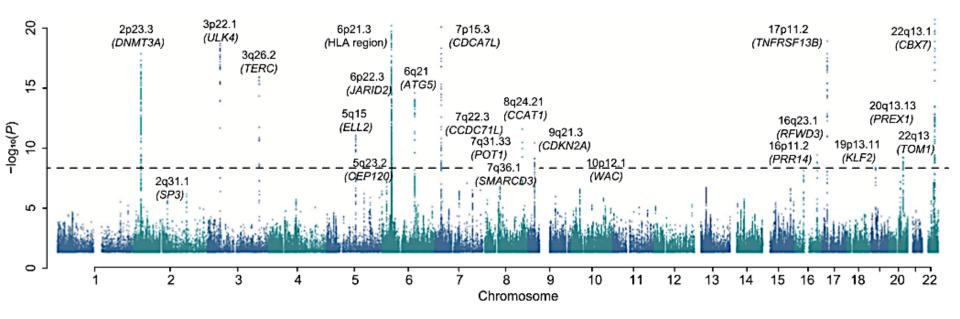
# Disparities Framework





Adapted from: Rebbeck and Sankar CEBP 2005, Rebbeck et al. JCO 2006

#### **Genetic Associations**



- 24 GWAS Loci Include: Telomere Regulation, Tumor Suppressor Genes, Oncogenes, Micro-RNAs, Linc RNAs, Carcinogen Metabolism Genes, MYC regulation, and others
- These explain about 16% of heritability.
- Common variants are enriched in familial myeloma
- Few rare loss of function variants have been observed (e.g., CDKN2A)

## Genome-Wide Association by Race

1,318 MM and 1,480 controls of European ancestry 1,305 MM and 7,078 controls of African ancestry

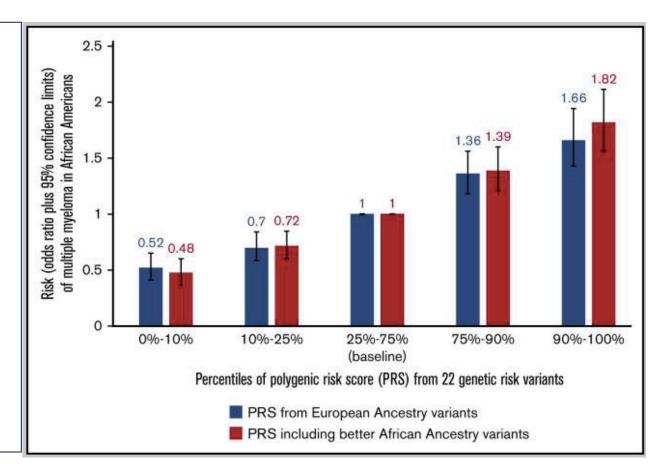
Index SNPs <sup>a</sup> /Most significantly associated SNPs <sup>b</sup>					Association in European ancestry			Association in African ancestry					
SNP	BP	Risk/Ref	Freq	OR	P	Freq	OR	P	Power	Freq	OR	P	Power
2p23.3													
rs6746082°	25659244	A/C	0.76	1.29	$1.22 \times 10^{-7}$	0.79	1.15	$5.17 \times 10^{-2}$	0.96	0.55	1.04	$3.77 \times 10^{-1}$	0.80
rs6761076 <sup>b</sup>	25607758	T/C				0.81	1.23	$7.23 \times 10^{-3}$		0.68	1.09	$8.33 \times 10^{-2}$	
2q12.3													
rs12614346a	107642482	A/G	0.33	1.39	$1.70 \times 10^{-5}$	0.31	1.00	$9.45 \times 10^{-1}$	0.99	0.16	1.00	$9.81 \times 10^{-1}$	0.99
rs13416655 <sup>b</sup>	107621925	C/T				0.50	1.01	$8.03 \times 10^{-1}$		0.39	1.10	$4.90 \times 10^{-2}$	
3p22.1													
rs1052501°	41925398	G/A	0.20	1.32	$7.47 \times 10^{-9}$	0.22	1.23	$4.42 \times 10^{-3}$	0.99	0.63	1.06	$2.21 \times 10^{-1}$	0.99
rs143531651 <sup>b</sup>	41816589	G/C				0.17	1.25	$4.91 \times 10^{-3}$		0.11	1.27	$1.37 \times 10^{-3}$	
3q26.2													
rs10936599a	169492101	G/A	0.75	1.26	$1.74 \times 10^{-13}$	0.79	1.12	$8.41 \times 10^{-2}$	0.92	0.93	1.08	$3.84 \times 10^{-1}$	0.73
rs9811216b	169487501	T/C				0.74	1.11	$1.10 \times 10^{-1}$		0.70	1.09	$8.46 \times 10^{-2}$	
6p21.33 <sup>d</sup>													
rs2285803°	31107258	A/G	0.28	1.19	$1.18 \times 10^{-10}$	0.29	1.11	$1.27 \times 10^{-1}$	0.84	0.26	1.06	$2.21 \times 10^{-1}$	0.95
7p15.3													
rs4487645a	21938240	C/A	0.65	1.38	$3.33 \times 10^{-15}$	0.70	1.23	$7.47 \times 10^{-4}$	0.99	0.89	1.37	8.30 × 10 <sup>-5</sup>	0.99
rs12540021 <sup>b</sup>	21945563	G/A				0.75	1.24	$6.30 \times 10^{-4}$		0.89	1.43	$2.27 \times 10^{-5}$	
17p11.2							=				_		
rs4273077ª	16849139	G/A	0.11	1.26	$1.41 \times 10^{-7}$	0.12	1.37	$2.46 \times 10^{-4}$	0.83	0.14	1.17	1.60 × 10 <sup>-2</sup>	0.97
rs34562254 <sup>b</sup>	16842991	A/G				0.11	1.45	$2.39 \times 10^{-5}$		0.13	1.25	$1.33 \times 10^{-3}$	
22q13.1													
rs877529a	39542292	A/G	0.44	1.23	$2.29 \times 10^{-16}$	0.45	1.21	$4.31 \times 10^{-4}$	0.97	0.48	1.11	1.47 × 10 <sup>-2</sup>	0.99
rs139425b	39559742	C/G				0.46	1.21	$4.43 \times 10^{-4}$		0.71	1.21	$5.54 \times 10^{-4}$	



#### Genome-Wide Association in African Americans

Meta-analysis of 2 GWAS of MM in 1,813 Cases and 8,871 Controls

- No genome-wide significant associations
- Novel locus at 2p24.1-23.1 in AA (from admixture mapping)
- Of 23 known EA risk variants:
  - 20 directionaly consistency
  - 9 replicated at *P* < .05





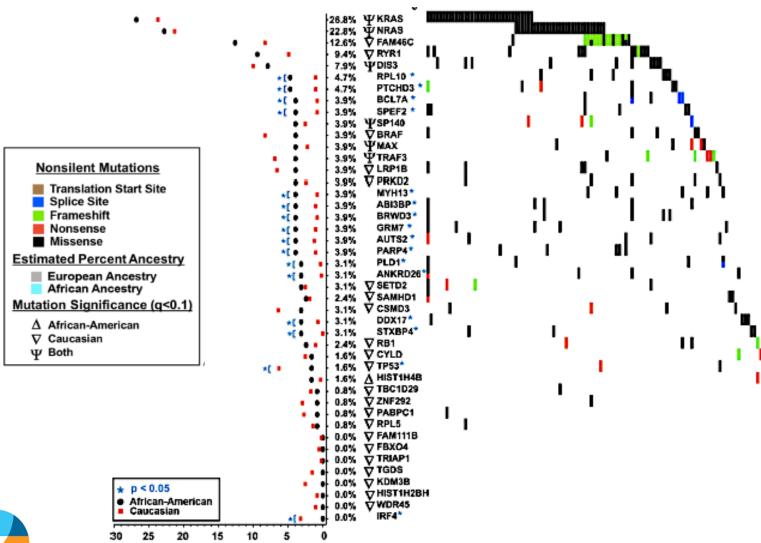
## Cytogenetic Abnormalities by Race

Cytogenetic abnormalities			Black			White		
		Total	With abnomality	%	Total	With abnomality	%	
t(11;14)								
< 60 years of age		151	8	5.3%	165	31	18.8%	< 0.001
60+ years of age		141	11	7.8%	307	52	16.9%	
t(4;14)								
< 60 years of age	*	151	7	4.6%	165	19	11.5%	0.04
60+ years of age		141	9	6.4%	307	28	9.1%	
Monosomy 13/del 13q								
< 60 years of age	**	151	46	30.5%	165	73	44.2%	< 0.001
60+ years of age		141	39	27.7%	307	150	48.9%	(0.00)
Monosomy 17/del17p								
< 60 years of age	***	151	15	9.9%	165	23	13.9%	0.027
60+ years of age		141	8	5.7%	307	38	12.4%	0.027
None of the studied abn	ormalities							
< 60 years of age		151	95	62.9%	165	57	34.5%	< 0.001
60+ years of age		141	90	63.8%	307	106	34.5%	< 0.001

Associated with \*adverse prognosis, \*\*earlier disease onset, \*\*\*disease progression



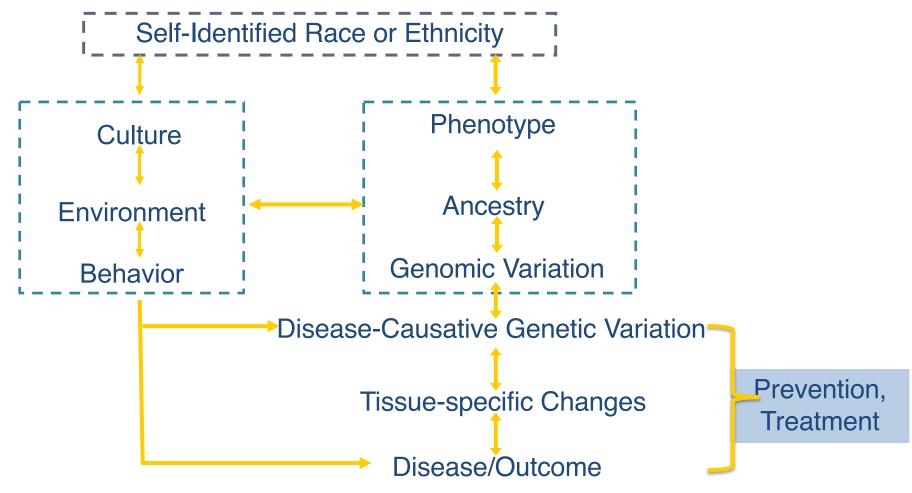
#### **Tumor Mutations by Race**



Percent Alterations



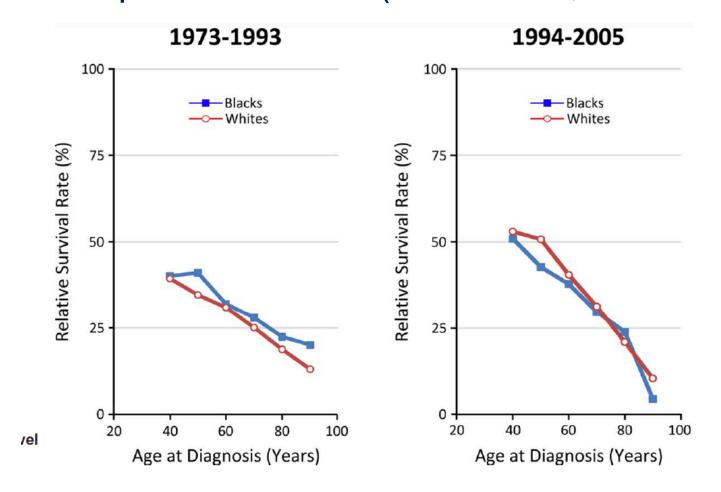
# Disparities Framework





Adapted from: Rebbeck and Sankar CEBP 2005, Rebbeck et al. JCO 2006

#### MM-Specific Survival (1973-2005, SEER 9)

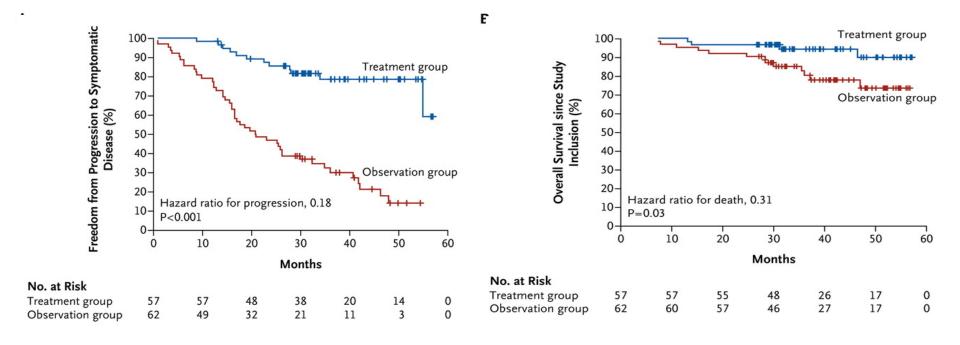


After introduction of ASCT and IMiDs (1990s), magnitude of survival improvement among Blacks was less than 50% of that in Whites



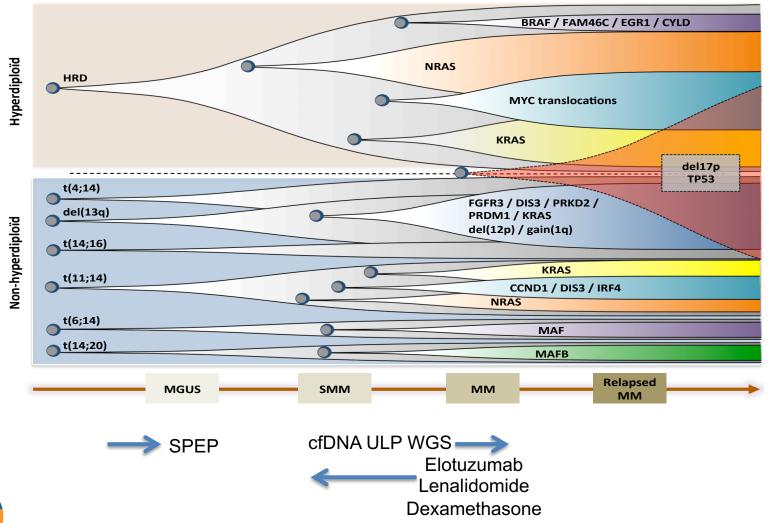
## Early Intervention May Benefit Pre-MM Patients

Example: RCT of Lenalidomide + Dexamethasone for the Treatment of High Risk SMM





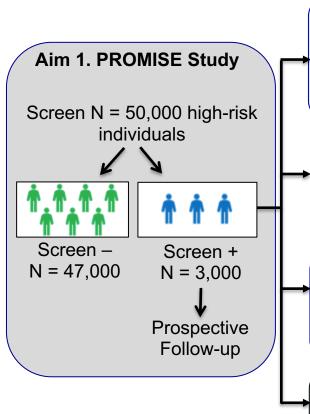
# Prevent or Delay Myeloma by Early Therapeutic Intervention of High-Risk Precursor Conditions







## Screening and Interception of PROMISE Precursor Myeloma



#### Aim 2. Genomic Characteristics

Viktor Adalsteinsson Benjamin Ebert Gaddy Getz

Irene Ghobrial David Liu Jihye Park

#### Aim 3. Race/Obesity

Tim Rebbeck Catherine Marinac David Liu

Lorelei Mucci

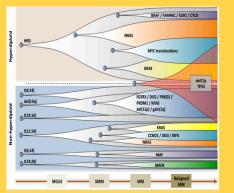
#### Aim 4. Microenvironment

Ivan Borrello Irene Ghobrial Jihye Park

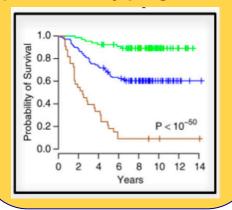
#### Aim 5. Imaging / Therapeutic

Irene Ghobrial Alexandre Detappe Jeremiah Johnson

#### **Develop novel biomarkers** & risk stratification tools



#### Develop new tools to prevent/delay progression















# Summary

- The disparity in MM mortality is complex but is in part driven by the increased incidence of MGUS and MM in Blacks as well as disparities in treatment.
- MM survival is equal in Whites and Blacks (or perhaps better in Blacks if treatment is equally applied).
- The genetic, molecular and epidemiological foundation of MGUS and MM risk is not understood, particularly in Blacks.
- Intercepting the progression of MGUS to MM and increasing engagement with Black communities in clinical research may reduce the Black-White disparity.



# Acknowledgements



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